

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 22, 2004, 15:11:01 ; Search time 56 Seconds
(without alignments)
427.709 Million cell updates/sec

Title: US-09-598-982-21

Perfect score: 1393

Sequence: 1 LEKRVGGQAPRSKWPQV.....IVTRYVYLDWIHHVVKKP 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1368	98.2	275	2 B35863	trypsin (EC 3.4.21)
2	1363	97.8	275	2 A35863	trypsin (EC 3.4.21)
3	1339	96.1	275	2 A35863	trypsin (EC 3.4.21)
4	1232.5	88.5	276	2 A45754	trypsin (EC 3.4.21)
5	1091	78.3	276	2 A38654	mast cell protease
6	1077	77.3	275	2 A32410	trypsin (EC 3.4.21)
7	1075	77.2	270	2 S56160	mast cell trypsin
8	1054	75.7	273	2 A47246	trypsin (EC 3.4.21)
9	1051	75.4	274	2 JC4171	trypsin (EC 3.4.21)
10	1005	72.1	237	2 S68702	trypsin (EC 3.4.21)
11	807	57.9	230	2 I48685	mast cell protease
12	684.5	49.1	269	2 B32410	mast cell protease
13	512	36.8	343	1 A57014	protease (EC 3.4.21)
14	467	33.5	625	1 KFHUI	coagulation factor
15	451	32.4	638	1 KQHUP	plasma kallikrein
16	448	32.2	455	2 A61545	plasma kallikrein
17	447	32.1	638	1 KQMSPL	plasma kallikrein
18	446.5	32.1	812	1 PLBO	plasma kallikrein
19	445	31.9	638	1 KQRPPL	plasma kallikrein
20	444.5	31.9	271	1 ELR22	pancreatic elastase
21	443	31.8	245	1 KYBOB	chymotrypsin (EC 3.4.21)
22	441	31.7	460	2 B61545	plasma kallikrein
23	437	31.4	1524	2 T30337	polyprotein - Afri
24	436.5	31.3	269	2 B26923	pancreatic elastase
25	430.5	30.9	271	2 A25528	pancreatic elastase
26	429	30.8	810	1 PLHU	plasma kallikrein
27	428	30.7	810	2 B30848	chymotrypsin (EC 3.4.21)
28	427	30.7	263	2 A21195	chymotrypsin (EC 3.4.21)
29	427	30.7	266	1 ELPG	pancreatic elastase

ALIGNMENTS

RESULT 1

B35863

trypsin (EC 3.4.21.59) II precursor - human

N:Alternate names: trypsin beta

C:Species: Homo sapiens (man)

C>Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #text_change 21-Jul-2000

C:Accession: B35863; A37193; I59473; I59473

R:Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, G.F. Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990

A:Title: Human mast cell trypsin: multiple cDNAs and genes reveal a multigene serine protease

A:Reference number: A35863; MUID:90251647; PMID:2187193

A:Accession: B35863

A:Molecule type: mRNA; DNA

A:Residues: 1-275 <VAN>

A:Cross-references: GB:M33492; NID:G339982; PIDN:AAA36779.1; PID:G339983

A>Note: residues 2-275 are derived from mRNA; residue one was inferred from the genomic DNA

R:Miller, J.S.; Moxley, G.; Schwartz, L.B.

J. Clin. Invest. 86, 864-870, 1990

A:Title: Cloning and characterization of a second complementary DNA for human trypsin.

A:Reference number: A37193; MUID:90369005; PMID:2203827

A:Accession: A37193

A:Molecule type: mRNA

A:Residues: 1-275 <MIL>

A:Cross-references: GB:M37488; NID:G179583; PIDN:AAA51843.1; PID:G179584

R:Blom, T.; Hellman, L.

Scand. J. Immunol. 37, 203-208, 1993

A:Title: Characterization of a trypsin mRNA expressed in the human basophil cell line K1

A:Reference number: I59473; MUID:93166209; PMID:8434231

A:Accession: I59473

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-275 <RES>

A:Cross-references: GB:S5551; NID:G265666; PIDN:AAI3876.1; PID:G4261576

A:Experimental source: basophil cell line KUB12

C:Genetics:

A:Gene: GDB:TFS1

A:Cross-references: GDB:125890; OMIM:191080

A:Map position: 16pter-16qter

C:Superfamily: trypsin; serine proteinase; zymogen

C:Keywords: hydrolase; signal sequence #status predicted <SIG>

F:1-21/Domain: activation sequence #status predicted <ACT>

F:22-30/Domain: signal sequence #status predicted <ACT>

F:31-275/Product: trypsin I #status predicted <MAT>

F:31-267/Domain: trypsin homology <TRY>

F:74,121,224/Active site: His, Asp, Ser #status predicted

Query Match 98.2%; Score 1368; DB 2; Length 275;

Best Local Similarity 99.6%; Pred. No. 1.1e-119;

Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IVGGQAPRSKWPQVSLRVHGFVWVHFCGSLHFPQVLTAAACVGPVKDIAALRVQL 64

|||||

```

Db      31  IVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWLTAACVGPDKDLAALRVQL 90
QY      65  REQLHYQDQLLPVSRIVVHPOFYTAQIGADIALLELEPVSQSHVHTVTLPPASETFP 124
Db      91  REQLHYQDQLLPVSRIVVHPOFYTAQIGADIALLELEPVSQSHVHTVTLPPASETFP 150
QY     125  PMPFCWVTGWGVDNDRERLPPFPFLKQVKVPIMENHI CDKAYHLGAYTGGDVRIVRDDML 184
Db     151  PMPFCWVTGWGVDNDRERLPPFPFLKQVKVPIMENHI CDKAYHLGAYTGGDVRIVRDDML 210
QY     185  CAGNTRRDS CGDSGGPLVCKVNGTWLQAGVVSWECAQPNRPGIYTRVTVYLDWIHHY 244
Db     211  CAGNTRRDS CGDSGGPLVCKVNGTWLQAGVVSWECAQPNRPGIYTRVTVYLDWIHHY 270
QY     245  VPKKP 249
Db     271  VPKKP 275

RESULT 2
A35863
tryptase (EC 3.4.21.59) I precursor - human
C:Species: Homo sapiens (man)
C:Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 21-Jul-2000
C:Accession: A35863; A60939; A39326
R:Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, G.
Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
A:Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine pr
A:Reference number: A35863; MUID:90251647; PMID:2187193
A:Accession: A35863
A:Molecule type: DNA
A:Residues: 1-275 <VA>
A:Cross-references: GB:M33494; NID:g3927804; PIDN:AAC83172.1; PID:g3339977
A:Accession: D35863
A:Molecule type: mRNA
A:Residues: 1-275 <VA2>
A:Cross-references: GB:M33491
R:Butterfield, J.H.; Weiler, D.A.; Hunt, L.W.; Wynn, S.R.; Roche, P.C.
J. Leukoc. Biol. 47, 409-419, 1990
A:Title: Purification of tryptase from a human mast cell line.
A:Reference number: A60939; MUID:90244210; PMID:2110591
A:Accession: A60939
A:Molecule type: protein
A:Residues: 31-38, 'P', 40-41, 'X', 43, 'T', 45-48, 'X', 50 <BUT>
A:Experimental source: mast cell
A:Note: 44-Gly was also found
R:Cromlish, J.A.; Seidah, N.G.; Marcinkiewicz, M.; Hamelin, J.; Johnson, D.A.; Chretien,
J. Biol. Chem. 262, 1363-1373, 1987
A:Title: Human pituitary tryptase: molecular forms, NH-2-terminal sequence, immunocytoch
A:Reference number: A39326; MUID:87109258; PMID:3543004
A:Accession: A39326
A:Molecule type: protein
A:Residues: 31-38 <CRO>
A:Experimental source: pituitary
C:Genetics:
A:Introns: 21/1; 78/2; 177/1; 221/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase; zymogen
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-30/Domain: activation peptide #status predicted <ACT>
F:31-275/Product: trypsin I #status experimental <MAT>
F:31-267/Domain: trypsin homology <TRY>
F:74,121,224/Active site: His, Asp, Ser #status predicted

Query Match      97.8%; Score 1363; DB 2; Length 275;
Best Local Similarity 99.2%; Pred. No. 3.2e-119;
Matches 243; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5  IVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWLTAACVGPDKDLAALRVQL 64
Db      31  IVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWLTAACVGPDKDLAALRVQL 90
QY     65  REQLHYQDQLLPVSRIVVHPOFYTAQIGADIALLELEPVSQSHVHTVTLPPASETFP 124
Db      91  REQLHYQDQLLPVSRIVVHPOFYTAQIGADIALLELEPVSQSHVHTVTLPPASETFP 150
QY     125  PMPFCWVTGWGVDNDRERLPPFPFLKQVKVPIMENHI CDKAYHLGAYTGGDVRIVRDDML 184
Db     151  PMPFCWVTGWGVDNDRERLPPFPFLKQVKVPIMENHI CDKAYHLGAYTGGDVRIVRDDML 210
QY     185  CAGNTRRDS CGDSGGPLVCKVNGTWLQAGVVSWECAQPNRPGIYTRVTVYLDWIHHY 244
Db     211  CAGNTRRDS CGDSGGPLVCKVNGTWLQAGVVSWECAQPNRPGIYTRVTVYLDWIHHY 270
QY     245  VPKKP 249
Db     271  VPKKP 275

```

```

Db      91  REQLHYQDQLLPVSRIVVHPOFYTAQIGADIALLELEPVSQSHVHTVTLPPASETFP 150
QY     125  PMPFCWVTGWGVDNDRERLPPFPFLKQVKVPIMENHI CDKAYHLGAYTGGDVRIVRDDML 184
Db     151  PMPFCWVTGWGVDNDRERLPPFPFLKQVKVPIMENHI CDKAYHLGAYTGGDVRIVRDDML 210
QY     185  CAGNTRRDS CGDSGGPLVCKVNGTWLQAGVVSWECAQPNRPGIYTRVTVYLDWIHHY 244
Db     211  CAGNTRRDS CGDSGGPLVCKVNGTWLQAGVVSWECAQPNRPGIYTRVTVYLDWIHHY 270
QY     245  VPKKP 249
Db     271  VPKKP 275

RESULT 3
C35863
tryptase (EC 3.4.21.59) III precursor - human
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-Mar-2003
C:Accession: C35863; A38893
R:Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, G.
Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
A:Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine pr
A:Reference number: A35863; MUID:90251647; PMID:2187193
A:Accession: C35863
A:Molecule type: mRNA
A:Residues: 9-275 <VA>
A:Accession: E35863
A:Molecule type: DNA
A:Residues: 1-9 <VA2>
A:Cross-references: GB:M33494; NID:g3927804; PIDN:AAC83172.1; PID:g3339977
A:Note: the first nine residues of this sequence are inferred from genomic DNA of tryptase
R:Vanderslice, P.
submitted to GenBank, April 1990
A:Reference number: A38893
A:Accession: A38893
A:Molecule type: mRNA
A:Residues: 9-131, 'K', 132-275 <VA3>
A:Cross-references: GB:M33493; NID:g339984; PIDN:AAA36780.1; PID:g3339985
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase; zymogen
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-30/Domain: activation peptide #status predicted <ACT>
F:31-275/Product: trypsin I #status predicted <MAT>
F:31-267/Domain: trypsin homology <TRY>
F:74,121,224/Active site: His, Asp, Ser #status predicted

Query Match      96.1%; Score 1339; DB 2; Length 275;
Best Local Similarity 98.0%; Pred. No. 5.4e-117;
Matches 240; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      5  IVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWLTAACVGPDKDLAALRVQL 64
Db      31  IVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWLTAACVGPDKDLAALRVQL 90
QY     65  REQLHYQDQLLPVSRIVVHPOFYTAQIGADIALLELEPVSQSHVHTVTLPPASETFP 124
Db      91  REQLHYQDQLLPVSRIVVHPOFYTAQIGADIALLELEPVSQSHVHTVTLPPASETFP 150
QY     125  PMPFCWVTGWGVDNDRERLPPFPFLKQVKVPIMENHI CDKAYHLGAYTGGDVRIVRDDML 184
Db     151  PMPFCWVTGWGVDNDRERLPPFPFLKQVKVPIMENHI CDKAYHLGAYTGGDVRIVRDDML 210
QY     185  CAGNTRRDS CGDSGGPLVCKVNGTWLQAGVVSWECAQPNRPGIYTRVTVYLDWIHHY 244
Db     211  CAGNTRRDS CGDSGGPLVCKVNGTWLQAGVVSWECAQPNRPGIYTRVTVYLDWIHHY 270
QY     245  VPKKP 249
Db     271  VPKKP 275

```

RESULT 4

A45754
 trypsinase (EC 3.4.21.59) alpha precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 08-Sep-1997
 C:Accession: A45754; B37193
 R:Miller, J.S.; Westin, E.H.; Schwartz, L.B.
 J. Clin. Invest. 84, 1188-1195, 1989
 A:Title: Cloning and characterization of complementary DNA for human trypsinase.
 A:Reference number: A45754; MUID:90009311; PMID:2677049
 A:Accession: A45754
 A:Molecule type: mRNA
 A:Residues: 1-274 <MIL>
 A:Cross-references: GB:M30038
 R:Miller, J.S.; Moxley, G.; Schwartz, L.B.
 J. Clin. Invest. 86, 864-870, 1990
 A:Title: Cloning and characterization of a second complementary DNA for human trypsinase.
 A:Reference number: A37193; MUID:90369005; PMID:2203827
 A:Accession: B37193
 A:Molecule type: mRNA
 A:Residues: 1-274 <MI2>
 A:Cross-references: GB:M30038
 A:Note: the sequence from Fig. 4 is inconsistent with that from Fig. 2 in having 205-Pro
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: hydrolase; serine proteinase; zymogen
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-30/Domain: activation peptide #status predicted <ACT>
 F:31-274/Product: trypsinase I #status predicted <MAT>
 F:31-266/Domain: trypsin homology <TRY>
 F:74,120,223/Active site: His, Asp, Ser #status predicted

Query Match	88.5%;	Score 1232.5;	DB 2;	Length 274;
Best Local Similarity	89.8%;	Pred No. 4.4e-107;		
Matches	220;	Conservative	7;	Mismatches 17; Indels 1; Gaps 1;

Qy	5	IVGQEPAPRKWPQVSLRVHGPYMMHFCGSLIHPQVWLTAACVGPDPVKDLAALRVQL	64
Db	31	IVGQEPAPRKWPQVSLRVHGPYMMHFCGSLIHPQVWLTAACVGPDPVKDLAALRVQL	89
Qy	65	REQLHYQDQLLPVSRIRIIVHPQFYTAQIGADIALLEELPEPVKSVSHVHTVILPPASETFP	124
Db	90	SGTHLYQDQLLPVSRIRIIVHPQFYTAQIGADIALLEELPEPVKSVSHVHTVILPPASETFP	149
Qy	125	PGMPCWVTGWDVNDRLPPFPPLKQVKVPIEMNHICDAKYLHGYATGDDVIRVDDML	184
Db	150	PGMPCWVTGWDVNDRLPPFPPLKQVKVPIEMNHICDAKYLHGYATGDDVIRVDDML	209
Qy	185	CAGNTRRDSQCGSGGLPLVCKVNGTWLQAGVVSWSGEGCAQPNRPGIYTRVYYLDWIHY	244
Db	210	CAGNSQRDSCKGSDGGLPLVCKVNGTWLQAGVVSWSGEGCAQPNRPGIYTRVYYLDWIHY	269
Qy	245	VPKKP 249	
Db	270	VPKKP 274	

RESULT 5

A38654
 mast cell proteinase 6 (EC 3.4.21.-) precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 21-Feb-1992 #sequence_revision 17-Feb-1994 #text_change 22-Jun-1999
 C:Accession: A38654; D35646; I59478
 R:Reynolds, D.S.; Gurley, D.S.; Austen, K.F.; Serafin, W.E.
 J. Biol. Chem. 266, 3847-3853, 1991
 A:Title: Cloning of the cDNA and gene of mouse mast cell protease-6. Transcription by pu
 A:Reference number: A38654; MUID:91139682; PMID:1995638
 A:Accession: A38654
 A:Molecule type: DNA
 A:Residues: 1-276 <REY>
 A:Cross-references: GB:M57625; NID:g200506; PIDN:AAA39987.1; PID:g200507
 A:Note: the authors translated the codon CGC for residue 24 as Ala, GAG for residue 37 a
 s Gly, GAG for residue 148 as Gly, GAG for residue 168 as Gly, and GAA for 185 as Gly

A:Accession: B38654
 A:Molecule type: mRNA
 A:Residues: 1-276 <RE2>
 A:Cross-references: GB:M57626; NID:g200508; PIDN:AAA39988.1; PID:g200509
 R:Reynolds, D.S.; Stevens, R.L.; Lane, W.S.; Carr, M.H.; Austen, K.F.; Serafin, W.E.
 Proc. Natl. Acad. Sci. U.S.A. 87, 3230-3234, 1990
 A:Title: Different mouse mast cell populations express various combinations of at least 8
 A:Reference number: A35646; MUID:90222202; PMID:2326280
 A:Accession: D35646
 A:Molecule type: protein
 A:Residues: 32-54 <RE3>
 R:Huang, R.; Abrink, M.; Gobl, A.E.; Nilsson, G.; Aveskogh, M.; Larsson, L.G.; Nilsson, E
 Scand. J. Immunol. 38, 359-367, 1993
 A:Title: Expression of a mast cell trypsinase in the human monocytic cell lines U-937 and n
 A:Reference number: I59478; MUID:94023807; PMID:8210998
 A:Accession: I59478
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-276 <RES>
 A:Cross-references: GB:L31853; NID:g473480; PIDN:AAA39725.1; PID:g473481
 C:Genetics:
 A:Gene: MMCP-6

A:Introns: 24/1; 79/2; 168/1; 222/3
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: hydrolase; serine proteinase; zymogen
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-31/Domain: activation peptide #status predicted <ACT>
 F:32-276/Product: mast cell proteinase 6 #status experimental <MAT>
 F:32-268/Domain: trypsin homology <TRY>
 F:75,122,225/Active site: His, Asp, Ser #status predicted

Query Match	78.3%;	Score 1091;	DB 2;	Length 276;
Best Local Similarity	78.2%;	Pred. No. 6.6e-94;		
Matches	190;	Conservative	19;	Mismatches 34; Indels 0; Gaps 0;

Qy	5	IVGQEPAPRKWPQVSLRVHGPYMMHFCGSLIHPQVWLTAACVGPDPVKDLAALRVQL	64
Db	32	IVGQEPAPRKWPQVSLRVHGPYMMHFCGSLIHPQVWLTAACVGPDPVKDLAALRVQL	91
Qy	65	REQLHYQDQLLPVSRIRIIVHPQFYTAQIGADIALLEELPEPVKSVSHVHTVILPPASETFP	124
Db	92	REQLHYQDQLLPVSRIRIIVHPQFYTAQIGADIALLEELPEPVKSVSHVHTVILPPASETFP	151
Qy	125	PGMPCWVTGWDVNDRLPPFPPLKQVKVPIEMNHICDAKYLHGYATGDDVIRVDDML	184
Db	152	PGTSCWVTGWDVNDRLPPFPPLKQVKVPIEMNHICDAKYLHGYATGDDVIRVDDML	211
Qy	185	CAGNTRRDSQCGSGGLPLVCKVNGTWLQAGVVSWSGEGCAQPNRPGIYTRVYYLDWIHY	244
Db	212	CAGNTRRDSQCGSGGLPLVCKVNGTWLQAGVVSWSGEGCAQPNRPGIYTRVYYLDWIHY	271
Qy	245	VPK 247	
Db	272	VPE 274	

RESULT 6

A32410
 trypsinase (EC 3.4.21.59) precursor - dog
 C:Species: Canis lupus familiaris (dog)
 C:Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 22-Jun-1999
 C:Accession: A32410
 R:Vanderslice, P.; Craik, C.S.; Nadel, J.A.; Caughey, G.H.
 Biochemistry 28, 4148-4155, 1989
 A:Title: Molecular cloning of dog mast cell trypsinase and a related protease: structural
 A:Reference number: A32410; MUID:89352460; PMID:2504277
 A:Accession: A32410
 A:Molecule type: mRNA
 A:Residues: 1-275 <VAN>
 A:Cross-references: GB:M24664; NID:g163982; PIDN:AAA30854.1; PID:g163983; GB:J02862
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: hydrolase; serine proteinase; zymogen
 F:1-21/Domain: signal sequence #status predicted <SIG>

F;22-30/Domain: activation peptide #status predicted <ACT>
F;31-275/Product: trypsin #status predicted <MAT>
F;31-267/Domain: trypsin homology <TRY>
F;74,121,224/Active site: His, Asp, Ser #status predicted

Query Match 77.3%; Score 1077; DB 2; Length 275;
Best Local Similarity 77.1%; Pred. No. 1.3e-92;

Matches 189; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

```
QY 5 IVGQEARPRSKWQVSLRVHGPYMHFCGSLIHPQWVLTAAACVGPDPVKDLAALRVQL 64
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 31 IVGQEARPGSKWQVSLRVHGPYMHFCGSLIHPQWVLTAAACVGPDPVKDLAALRVQL 90
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 65 REQLHYQDQLLPVSRITVHPQFYTAQIGADIALLELEPEPVKVSSSHVHTVTLPPASETFP 124
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 91 REQLHYQDQLLPVSRITVHPQFYTAQIGADIALLELEPEPVKVSSSHVHTVTLPPASETFP 150
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 125 PGMPCTWTGWDVNDRLPPPLKQVKVPIIMENHICDAKYHLGAYTGDDVIRVDDML 184
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 151 TGTPTCWVTGWDVHSGTLPPLPPPLKQVKVPIIMENHICDAKYHLGAYTGDDVIRVDDML 210
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 185 CAGNTRDSCQDGGGGLVCKVNGTWLQAGVWSWEGCAQPNRPGIYTRVYLDWIHY 244
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 211 CAGNTRDSCQDGGGGLVCKVNGTWLQAGVWSWEGCAQPNRPGIYTRVYLDWIHY 270
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 245 VPKP 249
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 271 VPKP 275
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 7

S56160
mast cell trypsin precursor - Mongolian jird
C;Species: Meriones unguiculatus (Mongolian jird)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000
C;Accession: S56160
R;Murakumo, Y.; Ide, H.; Itoh, H.; Tomita, M.; Kobayashi, T.; Maruyama, H.; Horii, Y.; N
Biochem. J. 309, 921-926, 1995
A;Title: Cloning of the cDNA encoding mast cell trypsin of Mongolian gerbil, Meriones u
A;Reference number: S56160; MUID:95366971; PMID:7639711
A;Accession: S56160
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-270 <MUR>
A;Cross-references: EMBL:D31789; NID:9517122; PIDN:BAA06598.1; PID:9517123
C;Superfamily: trypsin; trypsin homology
F;26-262/Domain: trypsin homology <TRY>

Query Match 77.2%; Score 1075; DB 2; Length 270;
Best Local Similarity 77.4%; Pred. No. 2e-92;

Matches 188; Conservative 18; Mismatches 37; Indels 0; Gaps 0;

```
QY 5 IVGQEARPRSKWQVSLRVHGPYMHFCGSLIHPQWVLTAAACVGPDPVKDLAALRVQL 64
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 26 IVGQEARPGSKWQVSLRVHGPYMHFCGSLIHPQWVLTAAACVGPDPVKDLAALRVQL 85
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 65 REQLHYQDQLLPVSRITVHPQFYTAQIGADIALLELEPEPVKVSSSHVHTVTLPPASETFP 124
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 86 RKQLYYHDLHLLAVSRITVHPQFYTAQIGADIALLELEPEPVKVSSSHVHTVTLPPASETFP 145
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 125 PGMPCTWTGWDVNDRLPPPLKQVKVPIIMENHICDAKYHLGAYTGDDVIRVDDML 184
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 146 SGTLCWTGWDVNDRLPPPLKQVKVPIIMENHICDAKYHLGAYTGDDVIRVDDML 205
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 185 CAGNTRDSCQDGGGGLVCKVNGTWLQAGVWSWEGCAQPNRPGIYTRVYLDWIHY 244
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 206 CAGNTRDSCQDGGGGLVCKVNGTWLQAGVWSWEGCAQPNRPGIYTRVYLDWIHY 265
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 245 VPK 247
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 266 VPK 268
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 8

A47246
trypsin (EC 3.4.21.59) 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A47246
R;McNeill, H.P.; Reynolds, D.S.; Schiller, V.; Ghildyal, N.; Gurley, D.S.; Austen, K.F.; S
Proc. Natl. Acad. Sci. U.S.A. 89, 11174-11178, 1992
A;Title: Isolation, characterization, and transcription of the gene encoding mouse mast
A;Reference number: A47246; MUID:93087489; PMID:1454796
A;Accession: A47246
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-273 <MCN>
A;Cross-references: GB:L00653; NID:9200518; PIDN:AAA39992.1; PID:g200519
A;Note: sequence extracted from NCBI backbone (NCBIN:119745, NCBIPI:119746)
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;29-265/Domain: trypsin homology <TRY>

Query Match 75.7%; Score 1054; DB 2; Length 273;
Best Local Similarity 76.5%; Pred. No. 1.0e-90;

Matches 186; Conservative 17; Mismatches 40; Indels 0; Gaps 0;

```
QY 5 IVGQEARPRSKWQVSLRVHGPYMHFCGSLIHPQWVLTAAACVGPDPVKDLAALRVQL 64
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 29 IVGQEARHGNKWPQVSLRVHGPYMHFCGSLIHPQWVLTAAACVGPDPVKDLAALRVQL 88
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 65 REQLHYQDQLLPVSRITVHPQFYTAQIGADIALLELEPEPVKVSSSHVHTVTLPPASETFP 124
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 89 RKQLYYHDLHLLAVSRITVHPQFYTAQIGADIALLELEPEPVKVSSSHVHTVTLPPASETFP 148
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 125 PGMPCTWTGWDVNDRLPPPLKQVKVPIIMENHICDAKYHLGAYTGDDVIRVDDML 184
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 149 SGTLCWTGWDVNDRLPPPLKQVKVPIIMENHICDAKYHLGAYTGDDVIRVDDML 208
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 185 CAGNTRDSCQDGGGGLVCKVNGTWLQAGVWSWEGCAQPNRPGIYTRVYLDWIHY 244
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 209 CAGNTRDSCQDGGGGLVCKVNGTWLQAGVWSWEGCAQPNRPGIYTRVYLDWIHY 268
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 245 VPK 247
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 269 VPK 271
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 9

JC4171
trypsin (EC 3.4.21.59) precursor - rat
N;Alternate names: mast cell trypsinase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Aug-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000
C;Accession: JC4171
R;Ide, H.; Itoh, H.; Tomita, M.; Murakumo, Y.; Kobayashi, T.; Maruyama, H.; Osada, Y.; Na
J. Biochem. 118, 210-215, 1995
A;Title: cDNA sequencing and expression of rat mast cell trypsinase.
A;Reference number: JC4171; MUID:96015171; PMID:8537314
A;Accession: JC4171
A;Molecule type: mRNA
A;Residues: 1-274 <IDE>
A;Cross-references: DDBJ:D38455; NID:9556555; PIDN:BAA07486.1; PID:9556556
C;Comment: This enzyme is basically specific for a connective tissue mast cell, it is up
eases inhibitors.

C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; mast cell; serine proteinase; zymogen
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-29/Domain: activation peptide #status predicted <ACT>
F;30-274/Product: mast cell trypsinase #status predicted <MAT>
F;30-266/Domain: trypsin homology <TRY>
F;73,120,223/Active site: His, Asp, Ser #status predicted
F;7131/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 75.4%; Score 1051; DB 2; Length 274;
Best Local Similarity 75.8%; Pred. No. 3.4e-90;


```
Db 198 IKQDMLCAGESEGHDSQMDSGGFLVCRWKCTWLIQGVSWGCGGY-NLPGVVARVTSYV 256
QY 239 DWTHVVPKPK 249
Db 257 SWIHQHPLSP 267

RESULT 13
A57014
proctasin (EC 3.4.21.-) precursor - human
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 21-Apr-2003
C:Accession: A57014; A54866
R;Yu, J.X.; Chao, L.; Chao, J.
J. Biol. Chem. 270, 13483-13489, 1995
A:Title: Molecular cloning, tissue-specific expression, and cellular localization of hum
A:Reference number: A57014; MUID:95286644; PMID:7768952
A:Accession: A57014
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-343 <RES>
A:Cross-references: GB:I41351; NID:9862304; PIDN:AA41759.1; PID:9862305
A:Experimental source: prostate
A>Note: parts of this sequence were determined by protein sequencing
R;Yu, J.X.; Chao, L.; Chao, J.
J. Biol. Chem. 269, 18843-18848, 1994
A:Title: Proctasin is a novel human serine proteinase from seminal fluid. Purification,
A:Reference number: A54866; MUID:94308140; PMID:8034638
A:Accession: A54866
A:Molecule type: protein
A:Residues: 45-64 <YUA>
C:Genetics:
A:Gene: GDB:PRSS8
A:Cross-references: GDB:676446; OMIM:600823
A:Map position: 16p11.2-16p11.2
C:Superfamily: trypsin; trypsin homology
C:Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-44, 45-343/Product: proctasin #status predicted <MAT>
F;33-44/Domain: proctasin light chain #status predicted <CHL>
F;45-343/Domain: proctasin heavy chain #status predicted <CHH>
F;45-281/Domain: trypsin homology <TRY>
F;323-341/Domain: transmembrane #status predicted <TM1>
F;37-154, 70-86, 168-244, 201-223, 234-262/Disulfide bonds: #status predicted
F;85, 134, 238/Active site: His, Asp, Ser #status predicted
F;159/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 36.8%; Score 512; DB 1; Length 343;
Best Local Similarity 41.4%; Pred. No. 6.7e-40;
Matches 103; Conservative 39; Mismatches 97; Indels 10; Gaps 6;

QY 2 EKRTVGQAPRSKWPQVSLRVHGPYWMHFCGSLHPQWLTAACVGPDKDLAALR 61
Db 42 QARITGSSAVAGWPQVSVITYEG---VHVCGSLVSEQWLAAHCF-PSEHHKAYE 97
QY 62 VQLEQHL--YYQD-QLLPVSRITVHPQFYTAQIAGADIALLEPEPVKVVSHVHTLPP 118
Db 98 VKLGAHQLDYSDEAKVSTLKDIIHPHSYLGQSGQDIALQLSRPTFSRYIRPICLA 157
QY 119 ASETFPFGMPCTWTGWDGNDERLPPFPFLKQVKVPIMENHICDAKYLGAFTGDDVRI 178
Db 158 ANASFPNGLHCTVTGWGHWAPSVSLTTPKPLQQLQLEVLPLISRETNCNLYNIDA-KPEEPHF 216
QY 179 VRDMLCAGNTR--RDSQCGSGGGLCKVNGTWLQAGVSWGCGCAQPNRPGYLVTRY 236
Db 217 VQEDMVCAGYVEGKDAQCGDGGGLSCPVBGLWYLTVIGVSWGDACGARNRPGVITLASS 276
QY 237 YLDWIHHYV 245
Db 277 YASMIQSKV 285
```

```
RESULT 14
KPHU1
coagulation factor Xla (EC 3.4.21.27) precursor [validated] - human
N;Alternate names: antihemophilic factor C; plasma thromboplastin antecedent
C:Species: Homo sapiens (man)
C:Date: 13-Aug-1986 #sequence_revision 26-May-1994 #text_change 08-Dec-2000
C:Accession: A27431; A00920; A37940
R;Asakai, R.; Davie, E.W.; Chung, D.W.
Biochemistry 26, 7221-7228, 1987
A:Title: Organization of the gene for human factor XI.
A:Reference number: A27431; MUID:88107663; PMID:2827746
A:Accession: A27431
A:Molecule type: DNA
A:Residues: 1-625 <ASA>
A:Cross-references: GB:M18295
A>Note: the sequence shown follows the authors' translation
R;Fujikawa, K.; Chung, D.W.; Hendrickson, L.E.; Davie, E.W.
Biochemistry 25, 2417-2424, 1986
A:Title: Amino acid sequence of human factor XI, a blood coagulation factor with four tar
A:Reference number: A00920; MUID:86243360; PMID:3636155
A:Accession: A00920
A:Molecule type: mRNA
A:Residues: 1-625 <FUJ>
A:Cross-references: GB:M13142; NID:9182832; PIDN:AAA52487.1; PID:9182833
R;McMullen, B.A.; Fujikawa, K.; Davie, E.W.
Biochemistry 30, 2056-2060, 1991
A:Title: Location of the disulfide bonds in human coagulation factor XI: the presence of
A:Reference number: A37940; MUID:91152017; PMID:1998667
A:Accession: A37940
A:Molecule type: protein
A:Residues: 28-33;35-49, X', 51-55, X', 57-63;70-75, X', 77-79;107-109, X', 111-112;132-139, X';
;280-282, X', 284;285-297;313-316, X', 318-319;320-326, X', 328-330, X', 347-349;373, X', 375;
C:Comment: The proenzyme consists of two identical chains linked by one or more disulfide
he active site, and a heavy chain, which associates with high molecular weight (HMW) kin
C:Genetics:
A:Gene: GDB:F11
A:Cross-references: GDB:1119891; OMIM:264900
A:Map position: 4q35-4q35
A:Introns: 19/1; 73/2; 109/1; 162/2; 199/1; 252/2; 289/1; 343/2; 379/1; 435/2; 494/1; 52
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor IX
A:Pathway: blood coagulation intrinsic pathway
C:Superfamily: coagulation factor XI; trypsin homology
C:Keywords: blood coagulation; duplication; glycoprotein; hemophilia C; homodimer; hydro
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-387/Product: coagulation factor Xla heavy chain #status experimental <HCH>
F;19-108/Domain: apple repeat <AP1>
F;109-198/Domain: apple repeat <AP2>
F;199-288/Domain: apple repeat <AP4>
F;290-379/Domain: apple repeat <AP4>
F;388-618/Domain: trypsin homology <TRY>
F;388-618/Domain: trypsin homology <TRY>
F;20-103, 514-581, 571-599/Disulfide bonds: #status predicted
F;29/Disulfide bonds: interchain #status experimental
F;46-76, 50-56, 110-193, 136-165, 140-146, 200-283, 226-255, 230-236, 291-374, 317-346, 321-327, 380
F;90, 126, 353, 450/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;339/Disulfide bonds: interchain #status predicted
F;387-388/Cleavage site: Arg-ile (coagulation factor XIa) #status experimental
F;431, 480, 575/Active site: His, Asp, Ser #status predicted
F;491/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 33.5%; Score 467; DB 1; Length 625;
Best Local Similarity 39.3%; Pred. No. 2.2e-35;
Matches 99; Conservative 31; Mismatches 94; Indels 28; Gaps 6;

QY 1 LEKRTVGQAPRSKWPQVSLRVHGPYWMHFCGSLHPQWLTAACVGPDKDLAAL 60
Db 384 IKPRIVGGTASVGEWPMQVTLTSTPTQRHLCGSLIGNQWILTAAHCF-YGVESPXIL 442
QY 61 RVQ---LREQHLYYQDQLLPVSRITVHPQFYTAQIAGADIALLEPEPVKVVSHVHTLPP 117
Db 443 RYSGILNQSEIKEDTSFFGVQEIHHQYKMAESGYDIALKLETTVNTYDTSQRPICLP 502
```

```
QY 118 PASFTFPGMPCWVTGWS-----DVDNDRLEPPFPPLKQVKVPIMENHI CDAYHLGAY 171
Db 503 SKGDRNVIYTDCTWVTGMYRKLQKIQN-----TIQAKIPLVTNEECQKRYRGHKI 554
QY 172 TGDVRIVRDDMLCAGNTR--RDSGCGSGGGLVCKVNGTWTLOAGVVSWGEGCAQPNRPG 229
Db 555 T-----HKMIGAGYREGGDKGSGGGLSKHNEVHLVIGTISWGEGCAQRRPG 606
QY 230 IYTRVTYVLDWI 241
Db 607 VYTNVEYVDWI 618

RESULT 15
KQHUP
plasma kallikrein (EC 3.4.21.34) precursor - human
N:Alternate names: kininogenin; plasma prekallikrein
C:Species: Homo sapiens (man)
C>Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 18-Jun-1999
C:Accession: A00921; A37939
R:Chung, D.W.; Fujikawa, K.; McMullen, B.A.; Davie, E.W.
Biochemistry 25, 2410-2417, 1986
A:Title: Human plasma prekallikrein, a zymogen to a serine protease that contains four
A:Reference number: A00921; MUID:86243359; PMID:3521732
A:Accession: A00921
A:Molecule type: mRNA
A:Residues: 1-638 <CHU>
A:Cross-references: GB:M13143; NID:g190262; PIDN:AAA60153.1; PID:g190263
R:McMullen, B.A.; Fujikawa, K.; Davie, E.W.
Biochemistry 30, 2050-2056, 1991
A:Title: Location of the disulfide bonds in human plasma prekallikrein: the presence of
A:Reference number: A37939; MUID:91152016; PMID:1998666
A:Accession: A37939
A:Molecule type: protein
A:Residues: 20-27,40-46, 'X', 48, 'H', 50, 'X', 52-70, 'H', 75-76, 'X', 78-80, 103-113, 131-140, 141-
260-283, 'X', 285, 287-291, 'X', 293-295, 314-317, 'X', 319-320, 321-324, 'X', 329-333, 334-339, 'X',
525, 538-551, 562, 'X', 564-567, 573, 'X', 575-576, 578-583, 'X', 585, 592-604 <MCW>
C:Comment: This protein, synthesized in the liver, circulates as a noncovalent complex w
are linked by one or more disulfide bonds.
C:Comment: The zymogen is activated by factor XIIa, which cleaves the molecule into a li
C:Comment: The enzyme cleaves Lys-Arg and Arg-Ser bonds. It activates, in a reciprocal r
inogen and may also play a role in the renin-angiotensin system by converting prorenin i
C:Genetics:
A:Gene: GDB:KLLK3
A:Cross-references: GDB:127575; OMIM:229000
A:Map position: 4q35-4q35
C:Superfamily: coagulation factor XI; trypsin homology
F:1-19/Domain: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; infla
F:21-19/Domain: signal sequence #status predicted <SIG>
F:20-638/Product: plasma kallikrein #status predicted <MAT>
F:20-390/Domain: plasma kallikrein heavy chain #status predicted <HCH>
F:20-109/Domain: apple repeat <AP1>
F:110-199/Domain: apple repeat <AP2>
F:200-289/Domain: apple repeat <AP3>
F:291-380/Domain: apple repeat <AP4>
F:391-638/Domain: plasma kallikrein light chain #status predicted <LCH>
F:391-621/Domain: trypsin homology <TRY>
F:21-104, 47-77, 51-57, 111-194, 137-166, 141-147, 201-284, 227-256, 231-237, 292-375, 322-328, 383
F:127, 308, 396, 453, 494/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:318-347, 340-345/Disulfide bonds: #status predicted
F:390-391/Cleavage site: Arg-Ile (coagulation factor XIIa) #status predicted
F:434, 483, 578/Active site: His, Asp, Ser #status predicted

Query Match 32.4%; Score 451; DB 1; Length 638;
Best Local Similarity 38.4%; Pred. No. 6.9e-34;
Matches 96; Conservative 40; Mismatches 84; Indels 30; Gaps 8;

QY 4 RIVGGQEPAPRSKPQVSLRVHGPYVWVHFCGSLHPQWVLTAAACV-GPDVKDLAALRV 62
Db 390 RIVGGTSSWGGEWVQVSLQVLTQARHLCGSLIGHQWVLTAAHCPDGLPQDV--WRI 447
QY 63 Q---LRQHLHYQDQLLPVSRVHVIHPQFYTAQIGADIALLELEPEPVKVSVHVHTVTLPPA 119
```

```
Db 448 YSGILNLSDTKOTPFQSIKEIIIIHQNVKVSSEGNHDIALIKLQAPLVNTEFQKPICLPSK 507
QY 120 SETFPFGMPCWVTGW-----GDVNDRLPPPPPLKQVKVPIMENHI CDAYHLGAYTG 173
Db 508 GDTSTIYTNCWVTGWFSGFSGKEGIQN-----ILOKVNIPLVNTEECQKRY----- 552
QY 174 DDVRIVRDDMLCAGNTR--RDSGCGSGGGLVCKVNGTWTLOAGVVSWGEGCAQPNRPGIY 231
Db 553 QDYKITQ-RMVCAGYKEGGKDGSGGGLVCKHNGWRLVIGTISWGEGCARREQPGVY 611
QY 232 TRVTYVLDWI 241
Db 612 TKVAEYMDWI 621
```

Search completed: July 22, 2004, 15:26:16
Job time : 57 secs

This Page Blank (uspto)

US-09-598-	62	VQUREOHLXYQDOLLPSVRIIVHQPFTQAGIADIALLEEPVNVSSHVHTVTLPPASET
US-09-598-	62	VQUREOHLXYQDOLLPSVRIIVHQPFTQAGIADIALLEEPVNVSSHVHTVTLPPASET
US-09-598-	62	VQUREOHLXYQDOLLPSVRIIVHQPFTQAGIADIALLEEPVNVSSHVHTVTLPPASET
US-09-598-	62	VQUREOHLXYQDOLLPSVRIIVHQPFTQAGIADIALLEEPVNVSSHVHTVTLPPASET
US-09-598-✓	62	VQUREOHLXYQDOLLPSVRIIVHQPFTQAGIADIALLEEPVNVSSHVHTVTLPPASET

US-09-598-	62	VQLREQLHYQDQLLPVSR	II	VH	PFQVTA	IGAD	IA	ALLEEE	EPKVSSHV	HTVTL	PPAS	SET		
US-09-598-	62	VQLREQLHYQDQLLPVSR	II	VH	PFQVTA	IGAD	IA	ALLEEE	EPKVSSHV	HTVTL	PPAS	SET		
US-09-598-	62	VQLREQLHYQDQLLPVSR	II	VH	PFQVTA	IGAD	IA	ALLEEE	EPKVSSHV	HTVTL	PPAS	SET		
US-09-598-	62	VQLREQLHYQDQLLPVSR	II	VH	PFQVTA	IGAD	IA	ALLEEE	EPKVSSHV	HTVTL	PPAS	SET		
US-09-598-	62	VQLREQLHYQDQLLPVSR	II	VH	PFQVTA	IGAD	IA	ALLEEE	EPKVSSHV	HTVTL	PPAS	SET		
US-09-598-	58	VQLREQLHYQDQLLPVSR	II	VH	PFQVTA	IGAD	IA	ALLEEE	EPKVSSHV	HTVTL	PPAS	SET		
consensus		VQLREQLHYQDQLLPVSR	II	VH	PFQVTA	IGAD	IA	ALLEEE	EPKVSSHV	HTVTL	PPAS	SET		
US-09-598-	123	FPFGMPCWVTGWDVNDER	L	PP	PF	LK	OV	KV	PIMEN	HI	CD	AKYHLGAYTGDDVR	IVR	
US-09-598-	123	FPFGMPCWVTGWDVNDER	L	PP	PF	LK	OV	KV	PIMEN	HI	CD	AKYHLGAYTGDDVR	IVR	
US-09-598-	123	FPFGMPCWVTGWDVNDER	L	PP	PF	LK	OV	KV	PIMEN	HI	CD	AKYHLGAYTGDDVR	IVR	
US-09-598-	123	FPFGMPCWVTGWDVNDER	L	PP	PF	LK	OV	KV	PIMEN	HI	CD	AKYHLGAYTGDDVR	IVR	
US-09-598-	123	FPFGMPCWVTGWDVNDER	L	PP	PF	LK	OV	KV	PIMEN	HI	CD	AKYHLGAYTGDDVR	IVR	
US-09-598-	123	FPFGMPCWVTGWDVNDER	L	PP	PF	LK	OV	KV	PIMEN	HI	CD	AKYHLGAYTGDDVR	IVR	
US-09-598-	123	FPFGMPCWVTGWDVNDER	L	PP	PF	LK	OV	KV	PIMEN	HI	CD	AKYHLGAYTGDDVR	IVR	
US-09-598-	123	FPFGMPCWVTGWDVNDER	L	PP	PF	LK	OV	KV	PIMEN	HI	CD	AKYHLGAYTGDDVR	IVR	
US-09-598-	123	FPFGMPCWVTGWDVNDER	L	PP	PF	LK	OV	KV	PIMEN	HI	CD	AKYHLGAYTGDDVR	IVR	
US-09-598-	123	FPFGMPCWVTGWDVNDER	L	PP	PF	LK	OV	KV	PIMEN	HI	CD	AKYHLGAYTGDDVR	IVR	
US-09-598-	119	FPFGMPCWVTGWDVNDER	L	PP	PF	LK	OV	KV	PIMEN	HI	CD	AKYHLGAYTGDDVR	IVR	
consensus		FPFGMPCWVTGWDVNDER	L	PP	PF	LK	OV	KV	PIMEN	HI	CD	AKYHLGAYTGDDVR	IVR	
US-09-598-	184	LCAGNTRRDS	CO	GD	AG	GLV	CK	NG	TW	LQ	AG	VV	SWGEGCAQPNR	PGIYTRV
US-09-598-	184	LCAGNTRRDS	CO	GD	AG	GLV	CK	NG	TW	LQ	AG	VV	SWGEGCAQPNR	PGIYTRV
US-09-598-	184	LCAGNTRRDS	CO	GD	AG	GLV	CK	NG	TW	LQ	AG	VV	SWGEGCAQPNR	PGIYTRV
US-09-598-	184	LCAGNTRRDS	CO	GD	AG	GLV	CK	NG	TW	LQ	AG	VV	SWGEGCAQPNR	PGIYTRV
US-09-598-	184	LCAGNTRRDS	CO	GD	AG	GLV	CK	NG	TW	LQ	AG	VV	SWGEGCAQPNR	PGIYTRV
US-09-598-	184	LCAGNTRRDS	CO	GD	AG	GLV	CK	NG	TW	LQ	AG	VV	SWGEGCAQPNR	PGIYTRV
US-09-598-	184	LCAGNTRRDS	CO	GD	AG	GLV	CK	NG	TW	LQ	AG	VV	SWGEGCAQPNR	PGIYTRV
US-09-598-	184	LCAGNTRRDS	CO	GD	AG	GLV	CK	NG	TW	LQ	AG	VV	SWGEGCAQPNR	PGIYTRV
US-09-598-	184	LCAGNTRRDS	CO	GD	AG	GLV	CK	NG	TW	LQ	AG	VV	SWGEGCAQPNR	PGIYTRV
US-09-598-	184	LCAGNTRRDS	CO	GD	AG	GLV	CK	NG	TW	LQ	AG	VV	SWGEGCAQPNR	PGIYTRV
US-09-598-	180	LCAGNTRRDS	CO	GD	AG	GLV	CK	NG	TW	LQ	AG	VV	SWGEGCAQPNR	PGIYTRV
consensus		LCAGNTRRDS	CO	GD	AG	GLV	CK	NG	TW	LQ	AG	VV	SWGEGCAQPNR	PGIYTRV
US-09-598-	245	VPKKP												

US-09-598- 245 VPKKP
 |||||
 US-09-598- 245 VPKKP
 |||||
 US-09-598- 241 VPKKP
 |||||
 consensus VPKKP

Alignment score = 2213.00

Scoring matrix:

	3	4	5	6	7	8	13	14	15	16
3		225	248	248	248	248	247	247	247	247
4			224	224	224	224	223	223	223	223
5				247	247	247	248	246	246	246
6					247	247	246	248	246	246
7						249	246	246	248	248
8							246	246	248	248
13								247	247	247
14									247	247
15										249
16										

US-09-598-	62	AGTGAGCCTGAGAGTCCACGGGCCCATACTGGATGCACTTCTGCGGGGCTCCCTCATCCA
US-09-598-	62	AGTGAGCCTGAGAGTCCACGGGCCCATACTGGATGCACTTCTGCGGGGCTCCCTCATCCA
US-09-598-	62	AGTGAGCCTGAGAGTCCACGGGCCCATACTGGATGCACTTCTGCGGGGCTCCCTCATCCA
US-09-598-	62	AGTGAGCCTGAGAGTCCACGGGCCCATACTGGATGCACTTCTGCGGGGCTCCCTCATCCA
US-09-598-	62	AGTGAGCCTGAGAGTCCACGGGCCCATACTGGATGCACTTCTGCGGGGCTCCCTCATCCA

[illegible]

1
2
3
4
5
6
7
8

consensus CACTATGTCTCCCAAAAGCCGtgaagcgggcgcgcgtcgt

Scoring matrix:

[illegible]

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: July 23, 2004, 08:23:52 ; Search time 0.001 Seconds
(without alignments)
383.958 Million cell updates/sec
Title: US-09-598-982-9
Perfect score: 1397
Sequence: 1 LEKRVGQEPARKPWQV.....IYTRVTYLDWIHHVVKPK 249

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1 seqs, 771 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=soft -Q=Pending Patents AA_Main.US-09-598-982-9
-DB=Pending Patents NA_Main.US-09-598-982-8 -SURFIX=pto -OUT=align9_8
-MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1
-MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=1 -DOCLIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -NCPV=6 -NO_XLPXY -NEG SCORES=0
-LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10
-YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending Patents NA_Main.US-09-598-982-8
1: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-8
2: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-8
3: /cgn2_6/ptodata/2/pna/US098A COMB.seq:US-09-598-982-8
4: /cgn2_6/ptodata/2/pna/US098B COMB.seq:US-09-598-982-8
5: /cgn2_6/ptodata/2/pna/US098C COMB.seq:US-09-598-982-8
6: /cgn2_6/ptodata/2/pna/US098D COMB.seq:US-09-598-982-8
7: /cgn2_6/ptodata/2/pna/US098E COMB.seq:US-09-598-982-8
8: /cgn2_6/ptodata/2/pna/US098F COMB.seq:US-09-598-982-8
9: /cgn2_6/ptodata/2/pna/US098G COMB.seq:US-09-598-982-8
10: /cgn2_6/ptodata/2/pna/US098H COMB.seq:US-09-598-982-8
11: /cgn2_6/ptodata/2/pna/US098I COMB.seq:US-09-598-982-8
12: /cgn2_6/ptodata/2/pna/US098J COMB.seq:US-09-598-982-8
13: /cgn2_6/ptodata/2/pna/US098K COMB.seq:US-09-598-982-8
14: /cgn2_6/ptodata/2/pna/US098L COMB.seq:US-09-598-982-8
15: /cgn2_6/ptodata/2/pna/US098M COMB.seq:US-09-598-982-8
16: /cgn2_6/ptodata/2/pna/US098N COMB.seq:US-09-598-982-8
17: /cgn2_6/ptodata/2/pna/US098O COMB.seq:US-09-598-982-8
18: /cgn2_6/ptodata/2/pna/US098P COMB.seq:US-09-598-982-8
19: /cgn2_6/ptodata/2/pna/US098Q COMB.seq:US-09-598-982-8
20: /cgn2_6/ptodata/2/pna/US098R COMB.seq:US-09-598-982-8
21: /cgn2_6/ptodata/2/pna/US098S COMB.seq:US-09-598-982-8
22: /cgn2_6/ptodata/2/pna/US098T COMB.seq:US-09-598-982-8
23: /cgn2_6/ptodata/2/pna/US098U COMB.seq:US-09-598-982-8
24: /cgn2_6/ptodata/2/pna/US098V COMB.seq:US-09-598-982-8
25: /cgn2_6/ptodata/2/pna/US098W COMB.seq:US-09-598-982-8
26: /cgn2_6/ptodata/2/pna/US098X COMB.seq:US-09-598-982-8
27: /cgn2_6/ptodata/2/pna/US098Y COMB.seq:US-09-598-982-8
28: /cgn2_6/ptodata/2/pna/US098Z COMB.seq:US-09-598-982-8
29: /cgn2_6/ptodata/2/pna/US098A COMB.seq:US-09-598-982-8
30: /cgn2_6/ptodata/2/pna/US098B COMB.seq:US-09-598-982-8

31: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-8
32: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-8
33: /cgn2_6/ptodata/2/pna/US098A COMB.seq:US-09-598-982-8
34: /cgn2_6/ptodata/2/pna/US098B COMB.seq:US-09-598-982-8
35: /cgn2_6/ptodata/2/pna/US098C COMB.seq:US-09-598-982-8
36: /cgn2_6/ptodata/2/pna/US098D COMB.seq:US-09-598-982-8
37: /cgn2_6/ptodata/2/pna/US098E COMB.seq:US-09-598-982-8
38: /cgn2_6/ptodata/2/pna/US098F COMB.seq:US-09-598-982-8
39: /cgn2_6/ptodata/2/pna/US098G COMB.seq:US-09-598-982-8
40: /cgn2_6/ptodata/2/pna/US098H COMB.seq:US-09-598-982-8
41: /cgn2_6/ptodata/2/pna/US098I COMB.seq:US-09-598-982-8
42: /cgn2_6/ptodata/2/pna/US098J COMB.seq:US-09-598-982-8
43: /cgn2_6/ptodata/2/pna/US098K COMB.seq:US-09-598-982-8
44: /cgn2_6/ptodata/2/pna/US098L COMB.seq:US-09-598-982-8
45: /cgn2_6/ptodata/2/pna/US098M COMB.seq:US-09-598-982-8
46: /cgn2_6/ptodata/2/pna/US098N COMB.seq:US-09-598-982-8
47: /cgn2_6/ptodata/2/pna/US098O COMB.seq:US-09-598-982-8
48: /cgn2_6/ptodata/2/pna/US098P COMB.seq:US-09-598-982-8
49: /cgn2_6/ptodata/2/pna/US098Q COMB.seq:US-09-598-982-8
50: /cgn2_6/ptodata/2/pna/US098R COMB.seq:US-09-598-982-8
51: /cgn2_6/ptodata/2/pna/US098S COMB.seq:US-09-598-982-8
52: /cgn2_6/ptodata/2/pna/US098T COMB.seq:US-09-598-982-8
53: /cgn2_6/ptodata/2/pna/US098U COMB.seq:US-09-598-982-8
54: /cgn2_6/ptodata/2/pna/US098V COMB.seq:US-09-598-982-8
55: /cgn2_6/ptodata/2/pna/US098W COMB.seq:US-09-598-982-8
56: /cgn2_6/ptodata/2/pna/US098X COMB.seq:US-09-598-982-8
57: /cgn2_6/ptodata/2/pna/US098Y COMB.seq:US-09-598-982-8
58: /cgn2_6/ptodata/2/pna/US098Z COMB.seq:US-09-598-982-8
59: /cgn2_6/ptodata/2/pna/US098A COMB.seq:US-09-598-982-8
60: /cgn2_6/ptodata/2/pna/US098B COMB.seq:US-09-598-982-8
61: /cgn2_6/ptodata/2/pna/US098C COMB.seq:US-09-598-982-8
62: /cgn2_6/ptodata/2/pna/US098D COMB.seq:US-09-598-982-8
63: /cgn2_6/ptodata/2/pna/US098E COMB.seq:US-09-598-982-8
64: /cgn2_6/ptodata/2/pna/US098F COMB.seq:US-09-598-982-8
65: /cgn2_6/ptodata/2/pna/US098G COMB.seq:US-09-598-982-8
66: /cgn2_6/ptodata/2/pna/US098H COMB.seq:US-09-598-982-8
67: /cgn2_6/ptodata/2/pna/US098I COMB.seq:US-09-598-982-8
68: /cgn2_6/ptodata/2/pna/US098J COMB.seq:US-09-598-982-8
69: /cgn2_6/ptodata/2/pna/US098K COMB.seq:US-09-598-982-8
70: /cgn2_6/ptodata/2/pna/US098L COMB.seq:US-09-598-982-8
71: /cgn2_6/ptodata/2/pna/US098M COMB.seq:US-09-598-982-8
72: /cgn2_6/ptodata/2/pna/US098N COMB.seq:US-09-598-982-8
73: /cgn2_6/ptodata/2/pna/US098O COMB.seq:US-09-598-982-8
74: /cgn2_6/ptodata/2/pna/US098P COMB.seq:US-09-598-982-8
75: /cgn2_6/ptodata/2/pna/US098Q COMB.seq:US-09-598-982-8
76: /cgn2_6/ptodata/2/pna/US098R COMB.seq:US-09-598-982-8
77: /cgn2_6/ptodata/2/pna/US098S COMB.seq:US-09-598-982-8
78: /cgn2_6/ptodata/2/pna/US098T COMB.seq:US-09-598-982-8
79: /cgn2_6/ptodata/2/pna/US098U COMB.seq:US-09-598-982-8
80: /cgn2_6/ptodata/2/pna/US098V COMB.seq:US-09-598-982-8
81: /cgn2_6/ptodata/2/pna/US098W COMB.seq:US-09-598-982-8
82: /cgn2_6/ptodata/2/pna/US098X COMB.seq:US-09-598-982-8
83: /cgn2_6/ptodata/2/pna/US098Y COMB.seq:US-09-598-982-8
84: /cgn2_6/ptodata/2/pna/US098Z COMB.seq:US-09-598-982-8
85: /cgn2_6/ptodata/2/pna/US098A COMB.seq:US-09-598-982-8
86: /cgn2_6/ptodata/2/pna/US098B COMB.seq:US-09-598-982-8
87: /cgn2_6/ptodata/2/pna/US098C COMB.seq:US-09-598-982-8
88: /cgn2_6/ptodata/2/pna/US098D COMB.seq:US-09-598-982-8
89: /cgn2_6/ptodata/2/pna/US098E COMB.seq:US-09-598-982-8
90: /cgn2_6/ptodata/2/pna/US098F COMB.seq:US-09-598-982-8
91: /cgn2_6/ptodata/2/pna/US098G COMB.seq:US-09-598-982-8
92: /cgn2_6/ptodata/2/pna/US098H COMB.seq:US-09-598-982-8
93: /cgn2_6/ptodata/2/pna/US098I COMB.seq:US-09-598-982-8
94: /cgn2_6/ptodata/2/pna/US098J COMB.seq:US-09-598-982-8
95: /cgn2_6/ptodata/2/pna/US098K COMB.seq:US-09-598-982-8
96: /cgn2_6/ptodata/2/pna/US098L COMB.seq:US-09-598-982-8
97: /cgn2_6/ptodata/2/pna/US098M COMB.seq:US-09-598-982-8
98: /cgn2_6/ptodata/2/pna/US098N COMB.seq:US-09-598-982-8
99: /cgn2_6/ptodata/2/pna/US098O COMB.seq:US-09-598-982-8
100: /cgn2_6/ptodata/2/pna/US098P COMB.seq:US-09-598-982-8
101: /cgn2_6/ptodata/2/pna/US098Q COMB.seq:US-09-598-982-8
102: /cgn2_6/ptodata/2/pna/US098R COMB.seq:US-09-598-982-8
103: /cgn2_6/ptodata/2/pna/US098S COMB.seq:US-09-598-982-8

104: /cgn2_6/ptodata/2/pna/US6047_COMB.seq:US-09-598-982-8
 105: /cgn2_6/ptodata/2/pna/US6048_COMB.seq:US-09-598-982-8
 106: /cgn2_6/ptodata/2/pna/US6049_COMB.seq:US-09-598-982-8
 107: /cgn2_6/ptodata/2/pna/US6050_COMB.seq:US-09-598-982-8
 108: /cgn2_6/ptodata/2/pna/US6051_COMB.seq:US-09-598-982-8
 109: /cgn2_6/ptodata/2/pna/US6052_COMB.seq:US-09-598-982-8
 110: /cgn2_6/ptodata/2/pna/US6053_COMB.seq:US-09-598-982-8

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1397	100.0	771	24	US-09-598-982-8 Sequence 8, App.1

ALIGNMENTS

RESULT 1

US-09-598-982-8
 ; Sequence 8, Application US/09598982
 ; GENERAL INFORMATION:
 ; APPLICANT: NILES, ANDREW L
 ; APPLICANT: MAFFITT, MARK A
 ; APPLICANT: HAAS-FRENDSCHO, MARY
 ; TITLE OF INVENTION: RECOMBINANT PROTEOLYTIC TYPTASES, ACTIVE SITE MUTANTS
 ; TITLE OF INVENTION: THEREOF, AND METHODS OF MAKING SAME
 ; FILE REFERENCE: CIP TRYPTASE
 ; CURRENT APPLICATION NUMBER: US/09/598,982
 ; CURRENT FILING DATE: 2000-06-21
 ; PRIOR FILING DATE: 09/079,970
 ; PRIOR FILING DATE: 1998-04-15
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 771
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (7)..(753)
 US-09-598-982-8

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
0	1397.00	771	249
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-598-982-9 (1-249) x US-09-598-982-8 (1-771)

Qy	1	LeuGluLysArgGlyLeuValGlyGlnGluAlaProArgSerLysTyrProTyrGlnVal	20
Db	7	CTCAGAGAAAGATCGTCGGGGGTCAGGAGCCCGGAGCAAGTGGCCCTGGCAGGTG	66
Qy	21	SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro	40
Db	67	AGCCTGAGAGTCCACGGCCCATCTGGATGCATCTCTCGGGGGTCCCTCATCCACCC	126
Qy	41	GlnTrpValLeuThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaLeu	60
Db	127	CAGTGGGTGCTGACCGGAGCGACATCGCTGGGACCGGAGCAAGATCTGGCCGCCCTC	186
Qy	61	ArgValGlnLeuArgGluGlnHisLeuTyrTrpGlnAspGlnLeuLeuProValSerArg	80
Db	187	AGGGTGCAACTGCGGGGAGCAGCACCTCTACTACAGGACCGAGTCTGCGCGTCAGCAGG	246

Qy	81	IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu	100
Db	247	ATCATGTCACCCACACAGTTCTACACCGCCAGATCGGAGCGGACATCGCCCTGCTGGAG	306
Qy	101	LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer	120
Db	307	CTGGAGAGCCGGTGAAGGTCTCCAGCCACGTCACACCGTCAACCCTGCCCTGCTCTCA	366
Qy	121	GluThrPheProProGlyMetProCysTyrTyrValThrGlyTyrGlyAspValAspAsnAsp	140
Db	367	GAGACCTTCCCCCGGGGATGCCGTCTGGGTCACTGGCTGGGGCCGATGGGACAATGAT	426
Qy	141	GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis	160
Db	427	GAGCGCTCCACCGCCATTTCCTCTGAAGCAGGTGAAGTCCCCCATATATGAAAAACAC	486
Qy	161	IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspValAlaGlyLeuValArg	180
Db	487	ATTGTGACGCAAAATACCACTTGGCGCTACACGGAGACGACGTCCGCTGCTCGCT	546
Qy	181	AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly	200
Db	547	GACGACATGCTGTGTCGGGGAACACCCGAGGAGCTCATGCCAGGGCGACTCCGGAGGG	606
Qy	201	ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu	220
Db	607	CCCTGCTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGCGTGTGTGCTGGGGCGAG	666
Qy	221	GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTyr	240
Db	667	GGCTGTGCCAGCCCAACCGGCTGGCATCTACACCGGTGTACCTACTTACTTGGACTGG	726
Qy	241	IleHisHisTyrValProLysLysPro	249
Db	727	ATCCACCACTATGTCCCAAAAAGCCG	753

Search completed: July 23, 2004, 08:23:53

Job time : 0.001 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 23, 2004, 08:25:03 ; Search time 1 Seconds

(without alignments)

0.360 Million cell updates/sec

Title: US-09-598-982-11

Perfect score: 1378

Sequence: 1 IVGQEPKSRKMPQVSLRV.....IYRTVYILDWIRHVVKP 245

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 1 segs, 735 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=soft -Q=Pending Patents_AA_Main:US-09-598-982-11
-DB=Pending Patents_AA_Main:US-09-598-982-10 -Suffix=pto -OUT=align11_10
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -DOCLIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO_XLPXY -NEG SCORES=0
-LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10
-YGAPEXT=0.5 -DELOP=6 -DLEXT=7

Database : Pending Patents NA Main:US-09-598-982-10

1: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-10
2: /cgn2_6/ptodata/2/pna/US06 COMB.seq:US-09-598-982-10
3: /cgn2_6/ptodata/2/pna/US07 COMB.seq:US-09-598-982-10
4: /cgn2_6/ptodata/2/pna/US080 COMB.seq:US-09-598-982-10
5: /cgn2_6/ptodata/2/pna/US081 COMB.seq:US-09-598-982-10
6: /cgn2_6/ptodata/2/pna/US082 COMB.seq:US-09-598-982-10
7: /cgn2_6/ptodata/2/pna/US083 COMB.seq:US-09-598-982-10
8: /cgn2_6/ptodata/2/pna/US084 COMB.seq:US-09-598-982-10
9: /cgn2_6/ptodata/2/pna/US085 COMB.seq:US-09-598-982-10
10: /cgn2_6/ptodata/2/pna/US086 COMB.seq:US-09-598-982-10
11: /cgn2_6/ptodata/2/pna/US087 COMB.seq:US-09-598-982-10
12: /cgn2_6/ptodata/2/pna/US088 COMB.seq:US-09-598-982-10
13: /cgn2_6/ptodata/2/pna/US089 COMB.seq:US-09-598-982-10
14: /cgn2_6/ptodata/2/pna/US090 COMB.seq:US-09-598-982-10
15: /cgn2_6/ptodata/2/pna/US091 COMB.seq:US-09-598-982-10
16: /cgn2_6/ptodata/2/pna/US092A COMB.seq:US-09-598-982-10
17: /cgn2_6/ptodata/2/pna/US092B COMB.seq:US-09-598-982-10
18: /cgn2_6/ptodata/2/pna/US093A COMB.seq:US-09-598-982-10
19: /cgn2_6/ptodata/2/pna/US093B COMB.seq:US-09-598-982-10
20: /cgn2_6/ptodata/2/pna/US094 COMB.seq:US-09-598-982-10
21: /cgn2_6/ptodata/2/pna/US095A COMB.seq:US-09-598-982-10
22: /cgn2_6/ptodata/2/pna/US095B COMB.seq:US-09-598-982-10
23: /cgn2_6/ptodata/2/pna/US095C COMB.seq:US-09-598-982-10
24: /cgn2_6/ptodata/2/pna/US095D COMB.seq:US-09-598-982-10
25: /cgn2_6/ptodata/2/pna/US096A COMB.seq:US-09-598-982-10
26: /cgn2_6/ptodata/2/pna/US096B COMB.seq:US-09-598-982-10
27: /cgn2_6/ptodata/2/pna/US096C COMB.seq:US-09-598-982-10
28: /cgn2_6/ptodata/2/pna/US096D COMB.seq:US-09-598-982-10
29: /cgn2_6/ptodata/2/pna/US096E COMB.seq:US-09-598-982-10
30: /cgn2_6/ptodata/2/pna/US097A COMB.seq:US-09-598-982-10

104: /cgn2_6/ptodata/2/pna/US6047_COMB.seq:US-09-598-982-10
 105: /cgn2_6/ptodata/2/pna/US6048_COMB.seq:US-09-598-982-10
 106: /cgn2_6/ptodata/2/pna/US6049_COMB.seq:US-09-598-982-10
 107: /cgn2_6/ptodata/2/pna/US6050_COMB.seq:US-09-598-982-10
 108: /cgn2_6/ptodata/2/pna/US6051_COMB.seq:US-09-598-982-10
 109: /cgn2_6/ptodata/2/pna/US6052_COMB.seq:US-09-598-982-10
 110: /cgn2_6/ptodata/2/pna/US6053_COMB.seq:US-09-598-982-10

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1378	100.0	735	24	US-09-598-982-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1
 US-09-598-982-10
 ; Sequence 10, Application US/09598982
 ; GENERAL INFORMATION:
 ; APPLICANT: NILES, ANDREW L
 ; APPLICANT: MAFFITT, MARK A
 ; APPLICANT: HAAK-FRENDSCHO, MARY
 ; TITLE OF INVENTION: RECOMBINANT PROTEOLYTIC TYPTASES, ACTIVE SITE MUTANTS
 ; FILE OF INVENTION: THEREOF, AND METHODS OF MAKING SAME
 ; FILE REFERENCE: CIP TRYPTASE
 ; CURRENT APPLICATION NUMBER: US/09/598,982
 ; CURRENT FILING DATE: 2000-06-21
 ; PRIOR APPLICATION NUMBER: 09/079,970
 ; PRIOR FILING DATE: 1998-04-15
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 735
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(735)
 ; US-09-598-982-10

Alignment Scores:
 Pred. No.: 0 Length: 735
 Score: 1378.00 Matches: 245
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-09-598-982-11 (1-245) x US-09-598-982-10 (1-735)

Qy	1	IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal	20
Db	1	ATCGTGGGGGTCTAGGAGGCCCCGAGGACGAGTGGCCCTGGCAGGTGAGCTGAGAGTC	60
Qy	21	HisGlyProTyrTrpMetHisPheCysGlySerLeuIleHisProGlnTrpValLeu	40
Db	61	CACGGCCCATACTCGATGCACTTCTCGGGGGCTCCCTCATCCACCCCGAGTGGGTGCTG	120
Qy	41	ThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaLeuArgValGlnLeu	60
Db	121	ACCGAGCGCACTCGTGGGACCGGACGTCAGGATCTGGCCGCTCCAGGGTGCAACTG	180
Qy	61	ArgGluGlnHisLeuTyrTrpGlnAspGlnLeuProValSerArgIleIleValHis	80
Db	181	CGGAGGACGACCTCTACTACAGGACGAGTGTGCGGGTCAGCAGGATCATCGTGAC	240

Search completed: July 23, 2004, 08:25:04

Job time : 1 secs

Qy	81	ProGlnPheTyrTrpAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluPro	100
Db	241	CCACAGTTCTACACCGCCCGAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGAGCCG	300
Qy	101	ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro	120
Db	301	GTGAAGGTCTCCAGCCACGTCACACGCTCACCGGTCACTCCCTGCTCAGAGACCTTCCCC	360
Qy	121	ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluAtrLeuPro	140
Db	361	CCGGGGATGCGGTCTGGGTCACTGGGTGGGGCGATGTGGACAAATGATGAGCGGCTCCCCA	420
Qy	141	ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla	160
Db	421	CCGCCATTTCTCTGAAGCAGGTGAAGTCCCCCATATATGAAACCAACATTTGTGACGCA	480
Qy	161	LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspAspMetLeu	180
Db	481	AAATACCACCTTGGCGCTTACACGGGAGACGACGTCGCGCATCGTCCGTGACGACATGCTG	540
Qy	181	CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys	200
Db	541	TGTGCCGGGAACACCCCGAGGGACTCATGCCAGGGCGACTCCGGAGGGGCCCTGCTGTGTC	600
Qy	201	LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln	220
Db	601	AAGGTGAATGGACCTGGCTGCAGCGGGCGTGGTCACTGGGGCGAGGGCTGTGCCAG	660
Qy	221	ProAsnArgProGlyIleTyrThrArgValThrTyrTrpLeuAspTrpIleHisHisTyr	240
Db	661	CCCAACCGGCTGGCATCTACCCCGTGTCACTTACTTGGACTGGATCCACCACTAT	720
Qy	241	ValProLysLysPro	245
Db	721	GTCCCCAAAAGCCG	735

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 23, 2004, 08:27:03 ; Search time 1 Seconds
(without alignments)
0.384 Million cell updates/sec

Title: US-09-598-982-21

Perfect score: 1393

Sequence: 1 LEKRVGQAPRSKWPQV.....IYTRVTYLDWIHHVVKPK 249

Scoring table: BLOSUM62

Xgapop 10.0 ,	Xgapext 0.5
Ygapop 10.0 ,	Ygapext 0.5
Fgapop 6.0 ,	Fgapext 7.0
Delop 6.0 ,	Delext 7.0

Searched: 1 seqs, 771 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=soft -Q=Pending Patents AA.Main.US-09-598-982-21
-DB=Pending Patents NA.Main.US-09-598-982-20 -SUFFIX=pto -OUT=align21_20
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -DOCALLIGN=100 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO_XLPXY -NEG SCORES=0
-LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10
-YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending Patents NA.Main.US-09-598-982-20

1:	/cgn2_6/ptodata/2/pna/US097B	COMB	seq:US-09-598-982-20
2:	/cgn2_6/ptodata/2/pna/US06	COMB	seq:US-09-598-982-20
3:	/cgn2_6/ptodata/2/pna/US07	COMB	seq:US-09-598-982-20
4:	/cgn2_6/ptodata/2/pna/US080	COMB	seq:US-09-598-982-20
5:	/cgn2_6/ptodata/2/pna/US081	COMB	seq:US-09-598-982-20
6:	/cgn2_6/ptodata/2/pna/US082	COMB	seq:US-09-598-982-20
7:	/cgn2_6/ptodata/2/pna/US083	COMB	seq:US-09-598-982-20
8:	/cgn2_6/ptodata/2/pna/US084	COMB	seq:US-09-598-982-20
9:	/cgn2_6/ptodata/2/pna/US085	COMB	seq:US-09-598-982-20
10:	/cgn2_6/ptodata/2/pna/US086	COMB	seq:US-09-598-982-20
11:	/cgn2_6/ptodata/2/pna/US087	COMB	seq:US-09-598-982-20
12:	/cgn2_6/ptodata/2/pna/US088	COMB	seq:US-09-598-982-20
13:	/cgn2_6/ptodata/2/pna/US089	COMB	seq:US-09-598-982-20
14:	/cgn2_6/ptodata/2/pna/US090	COMB	seq:US-09-598-982-20
15:	/cgn2_6/ptodata/2/pna/US091	COMB	seq:US-09-598-982-20
16:	/cgn2_6/ptodata/2/pna/US092A	COMB	seq:US-09-598-982-20
17:	/cgn2_6/ptodata/2/pna/US092B	COMB	seq:US-09-598-982-20
18:	/cgn2_6/ptodata/2/pna/US093A	COMB	seq:US-09-598-982-20
19:	/cgn2_6/ptodata/2/pna/US093B	COMB	seq:US-09-598-982-20
20:	/cgn2_6/ptodata/2/pna/US094	COMB	seq:US-09-598-982-20
21:	/cgn2_6/ptodata/2/pna/US095A	COMB	seq:US-09-598-982-20
22:	/cgn2_6/ptodata/2/pna/US095B	COMB	seq:US-09-598-982-20
23:	/cgn2_6/ptodata/2/pna/US095C	COMB	seq:US-09-598-982-20
24:	/cgn2_6/ptodata/2/pna/US095D	COMB	seq:US-09-598-982-20
25:	/cgn2_6/ptodata/2/pna/US096A	COMB	seq:US-09-598-982-20
26:	/cgn2_6/ptodata/2/pna/US096B	COMB	seq:US-09-598-982-20
27:	/cgn2_6/ptodata/2/pna/US096C	COMB	seq:US-09-598-982-20
28:	/cgn2_6/ptodata/2/pna/US096D	COMB	seq:US-09-598-982-20
29:	/cgn2_6/ptodata/2/pna/US096E	COMB	seq:US-09-598-982-20
30:	/cgn2_6/ptodata/2/pna/US097A	COMB	seq:US-09-598-982-20

104: /cgn2_6/ptodata/2/pna/US6047_COMB.seq:US-09-598-982-20
 105: /cgn2_6/ptodata/2/pna/US6048_COMB.seq:US-09-598-982-20
 106: /cgn2_6/ptodata/2/pna/US6049_COMB.seq:US-09-598-982-20
 107: /cgn2_6/ptodata/2/pna/US6050_COMB.seq:US-09-598-982-20
 108: /cgn2_6/ptodata/2/pna/US6051_COMB.seq:US-09-598-982-20
 109: /cgn2_6/ptodata/2/pna/US6052_COMB.seq:US-09-598-982-20
 110: /cgn2_6/ptodata/2/pna/US6053_COMB.seq:US-09-598-982-20

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
1	1393	100.0	771 24	US-09-598-982-20 Sequence 20, Appl

ALIGNMENTS

RESULT 1
 US-09-598-982-20
 ; Sequence 20, Application US/09598982
 ; GENERAL INFORMATION:
 ; APPLICANT: NILES, ANDREW L
 ; APPLICANT: MAFFITT, MARK A
 ; APPLICANT: HAAK-FRENDSCHO, MARY
 ; TITLE OF INVENTION: RECOMBINANT PROTEOLYTIC TYPTASES, ACTIVE SITE MUTANTS
 ; FILE OF INVENTION: THEREOF, AND METHODS OF MAKING SAME
 ; FILE REFERENCE: CIP TRYPTASE
 ; CURRENT APPLICATION NUMBER: US/09/598,982
 ; CURRENT FILING DATE: 2000-06-21
 ; PRIOR APPLICATION NUMBER: 09/079,970
 ; PRIOR FILING DATE: 1998-04-15
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 20
 ; LENGTH: 771
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (7)...(753)
 US-09-598-982-20

Alignment Scores:
 Pred. No.: 0 Length: 771
 Score: 1393.00 Matches: 249
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-09-598-982-21 (1-249) x US-09-598-982-20 (1-771)

Qy	1	LeuGluLysArgIleValGlyGlnGluAlaProArgSerLysTrpProTlpGlnVal	20
Db	7	CTCGAAGAAAGATCTCGGGGTCAGGAGCCCCCAGGACCAAGTGGCCCTGCAGGTG	66
Qy	21	SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro	40
Db	67	AGCCTGAGAGTCCACGGGCCATCTGGATGCATCTTCGCGGGGCTCCCTCATCCACCC	126
Qy	41	GlnTrpValLeuThrAlaAlaCysValGlyProAspValLysAspLeuAlaLeu	60
Db	127	CAGTGGGTGCTGACCGCGCGCGTGGACCGGACGTCAGGATCTGGCCGCCCTC	186
Qy	61	ArgValGlnLeuArgGluGlnHisLeuTyrTrpGlnAspGlnLeuLeuProValSerArg	80
Db	187	AGGCTGCAACTGCGGGAGCAGCACCTCTACTACCGAGACCAGCTGCTGCCGCTCAGCAGG	246

Qy	81	IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu	100
Db	247	ATCATCTGTGACCCACAGTTCTACACGCCCCAGATCGAGGGGACATCGCCCTGCTGGAG	306
Qy	101	LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer	120
Db	307	CTGAGGAGCGCGGTGAAGGTCTCCAGCCAGGTCCACACGGGTACCCCTGCCCCCTGCCTCA	366
Qy	121	GluThrPheProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp	140
Db	367	GAGACCTTCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGGATGTGGACAAATGAT	426
Qy	141	GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis	160
Db	427	GAGCGCTCCACCGCCATTTCCTCTGAAGCAGGTGAAGTCCCCCATATGGAACACAC	486
Qy	161	IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArg	180
Db	487	ATTGTGACGCAAAATACCACTTGGCGCCTTACACGGGAGACGACGTCCGCATCGTCCGT	546
Qy	181	AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly	200
Db	547	GACGACATGTGTGTCGGGACACCCCGAGGACTCATGCCAGGGGACTCCGGAGGG	606
Qy	201	ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu	220
Db	607	CCCTGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGCGTGGTCACTGGGGGCGAG	666
Qy	221	GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTrpLeuAspTrp	240
Db	667	GGCTGTGCCAGGCCCAACCGGCTGGCATCTACACCGGTGTACCTACTACTTGGACTGG	726
Qy	241	IleHisHisTyrValProLysLysPro	249
Db	727	ATCCACCACCTATGTCCCCCAAAAGCCG	753

Search completed: July 23, 2004, 08:27:04

Job time : 1 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 23, 2004, 08:28:04 ; Search time 1 Seconds
(without alignments)
0.384 Million cell updates/sec

Title: US-09-598-982-23

Perfect score: 1395

Sequence: 1 LEKRVGGQAPRSKMPQV.....IYRTVYLLDWHVVPKKP 249

Scoring table: BLOSUM62

Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5
Fgapop 6.0	Fgapext 7.0
Delop 6.0	Delext 7.0

Searched: 1 seqs, 771 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=soft -O=Pending Patents AA_Main:US-09-598-982-23
-DB=Pending Patents NA_Main:US-09-598-982-22 -SUFFIX=pto -OUT=align23_22
-MINMATCH=0.1 -LOOFCIL=0 -LOOPEXT=1 -UNITIS-bits -START=1 -END=-1
-MATRIX=BIOSUM62 -TRANS=human40.cdi -LIST=1 -DOCLIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO XLPXY -NEG SCORES=0
-LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10
-YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Pending Patents NA_Main:US-09-598-982-22

1:	/cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-22
2:	/cgn2_6/ptodata/2/pna/US06 COMB.seq:US-09-598-982-22
3:	/cgn2_6/ptodata/2/pna/US07 COMB.seq:US-09-598-982-22
4:	/cgn2_6/ptodata/2/pna/US08 COMB.seq:US-09-598-982-22
5:	/cgn2_6/ptodata/2/pna/US081 COMB.seq:US-09-598-982-22
6:	/cgn2_6/ptodata/2/pna/US082 COMB.seq:US-09-598-982-22
7:	/cgn2_6/ptodata/2/pna/US083 COMB.seq:US-09-598-982-22
8:	/cgn2_6/ptodata/2/pna/US084 COMB.seq:US-09-598-982-22
9:	/cgn2_6/ptodata/2/pna/US085 COMB.seq:US-09-598-982-22
10:	/cgn2_6/ptodata/2/pna/US086 COMB.seq:US-09-598-982-22
11:	/cgn2_6/ptodata/2/pna/US087 COMB.seq:US-09-598-982-22
12:	/cgn2_6/ptodata/2/pna/US088 COMB.seq:US-09-598-982-22
13:	/cgn2_6/ptodata/2/pna/US089 COMB.seq:US-09-598-982-22
14:	/cgn2_6/ptodata/2/pna/US090 COMB.seq:US-09-598-982-22
15:	/cgn2_6/ptodata/2/pna/US091 COMB.seq:US-09-598-982-22
16:	/cgn2_6/ptodata/2/pna/US092 COMB.seq:US-09-598-982-22
17:	/cgn2_6/ptodata/2/pna/US093 COMB.seq:US-09-598-982-22
18:	/cgn2_6/ptodata/2/pna/US094 COMB.seq:US-09-598-982-22
19:	/cgn2_6/ptodata/2/pna/US095 COMB.seq:US-09-598-982-22
20:	/cgn2_6/ptodata/2/pna/US096 COMB.seq:US-09-598-982-22
21:	/cgn2_6/ptodata/2/pna/US097 COMB.seq:US-09-598-982-22
22:	/cgn2_6/ptodata/2/pna/US098 COMB.seq:US-09-598-982-22
23:	/cgn2_6/ptodata/2/pna/US099 COMB.seq:US-09-598-982-22
24:	/cgn2_6/ptodata/2/pna/US100 COMB.seq:US-09-598-982-22
25:	/cgn2_6/ptodata/2/pna/US101 COMB.seq:US-09-598-982-22
26:	/cgn2_6/ptodata/2/pna/US102 COMB.seq:US-09-598-982-22
27:	/cgn2_6/ptodata/2/pna/US103 COMB.seq:US-09-598-982-22
28:	/cgn2_6/ptodata/2/pna/US104 COMB.seq:US-09-598-982-22
29:	/cgn2_6/ptodata/2/pna/US105 COMB.seq:US-09-598-982-22
30:	/cgn2_6/ptodata/2/pna/US106 COMB.seq:US-09-598-982-22

31:	/cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-22
32:	/cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-22
33:	/cgn2_6/ptodata/2/pna/US098A COMB.seq:US-09-598-982-22
34:	/cgn2_6/ptodata/2/pna/US098B COMB.seq:US-09-598-982-22
35:	/cgn2_6/ptodata/2/pna/US098C COMB.seq:US-09-598-982-22
36:	/cgn2_6/ptodata/2/pna/US098D COMB.seq:US-09-598-982-22
37:	/cgn2_6/ptodata/2/pna/US099A COMB.seq:US-09-598-982-22
38:	/cgn2_6/ptodata/2/pna/US099B COMB.seq:US-09-598-982-22
39:	/cgn2_6/ptodata/2/pna/US099C COMB.seq:US-09-598-982-22
40:	/cgn2_6/ptodata/2/pna/US099D COMB.seq:US-09-598-982-22
41:	/cgn2_6/ptodata/2/pna/US099E COMB.seq:US-09-598-982-22
42:	/cgn2_6/ptodata/2/pna/US099F COMB.seq:US-09-598-982-22
43:	/cgn2_6/ptodata/2/pna/US100A COMB.seq:US-09-598-982-22
44:	/cgn2_6/ptodata/2/pna/US100B COMB.seq:US-09-598-982-22
45:	/cgn2_6/ptodata/2/pna/US101A COMB.seq:US-09-598-982-22
46:	/cgn2_6/ptodata/2/pna/US101B COMB.seq:US-09-598-982-22
47:	/cgn2_6/ptodata/2/pna/US102A COMB.seq:US-09-598-982-22
48:	/cgn2_6/ptodata/2/pna/US102B COMB.seq:US-09-598-982-22
49:	/cgn2_6/ptodata/2/pna/US103A COMB.seq:US-09-598-982-22
50:	/cgn2_6/ptodata/2/pna/US103B COMB.seq:US-09-598-982-22
51:	/cgn2_6/ptodata/2/pna/US104A COMB.seq:US-09-598-982-22
52:	/cgn2_6/ptodata/2/pna/US104B COMB.seq:US-09-598-982-22
53:	/cgn2_6/ptodata/2/pna/US106 COMB.seq:US-09-598-982-22
54:	/cgn2_6/ptodata/2/pna/US107A COMB.seq:US-09-598-982-22
55:	/cgn2_6/ptodata/2/pna/US107B COMB.seq:US-09-598-982-22
56:	/cgn2_6/ptodata/2/pna/US6000 COMB.seq:US-09-598-982-22
57:	/cgn2_6/ptodata/2/pna/US6001 COMB.seq:US-09-598-982-22
58:	/cgn2_6/ptodata/2/pna/US6002 COMB.seq:US-09-598-982-22
59:	/cgn2_6/ptodata/2/pna/US6003 COMB.seq:US-09-598-982-22
60:	/cgn2_6/ptodata/2/pna/US6004 COMB.seq:US-09-598-982-22
61:	/cgn2_6/ptodata/2/pna/US6005 COMB.seq:US-09-598-982-22
62:	/cgn2_6/ptodata/2/pna/US6006 COMB.seq:US-09-598-982-22
63:	/cgn2_6/ptodata/2/pna/US6007 COMB.seq:US-09-598-982-22
64:	/cgn2_6/ptodata/2/pna/US6008 COMB.seq:US-09-598-982-22
65:	/cgn2_6/ptodata/2/pna/US6009 COMB.seq:US-09-598-982-22
66:	/cgn2_6/ptodata/2/pna/US6010 COMB.seq:US-09-598-982-22
67:	/cgn2_6/ptodata/2/pna/US6011 COMB.seq:US-09-598-982-22
68:	/cgn2_6/ptodata/2/pna/US6012 COMB.seq:US-09-598-982-22
69:	/cgn2_6/ptodata/2/pna/US6013 COMB.seq:US-09-598-982-22
70:	/cgn2_6/ptodata/2/pna/US6014 COMB.seq:US-09-598-982-22
71:	/cgn2_6/ptodata/2/pna/US6015 COMB.seq:US-09-598-982-22
72:	/cgn2_6/ptodata/2/pna/US6016 COMB.seq:US-09-598-982-22
73:	/cgn2_6/ptodata/2/pna/US6017 COMB.seq:US-09-598-982-22
74:	/cgn2_6/ptodata/2/pna/US6018 COMB.seq:US-09-598-982-22
75:	/cgn2_6/ptodata/2/pna/US6019 COMB.seq:US-09-598-982-22
76:	/cgn2_6/ptodata/2/pna/US6020 COMB.seq:US-09-598-982-22
77:	/cgn2_6/ptodata/2/pna/US6021 COMB.seq:US-09-598-982-22
78:	/cgn2_6/ptodata/2/pna/US6022 COMB.seq:US-09-598-982-22
79:	/cgn2_6/ptodata/2/pna/US6023 COMB.seq:US-09-598-982-22
80:	/cgn2_6/ptodata/2/pna/US6024 COMB.seq:US-09-598-982-22
81:	/cgn2_6/ptodata/2/pna/US6025 COMB.seq:US-09-598-982-22
82:	/cgn2_6/ptodata/2/pna/US6026 COMB.seq:US-09-598-982-22
83:	/cgn2_6/ptodata/2/pna/US6027 COMB.seq:US-09-598-982-22
84:	/cgn2_6/ptodata/2/pna/US6028 COMB.seq:US-09-598-982-22
85:	/cgn2_6/ptodata/2/pna/US6029 COMB.seq:US-09-598-982-22
86:	/cgn2_6/ptodata/2/pna/US6030 COMB.seq:US-09-598-982-22
87:	/cgn2_6/ptodata/2/pna/US6031 COMB.seq:US-09-598-982-22
88:	/cgn2_6/ptodata/2/pna/US6032 COMB.seq:US-09-598-982-22
89:	/cgn2_6/ptodata/2/pna/US6033 COMB.seq:US-09-598-982-22
90:	/cgn2_6/ptodata/2/pna/US6034 COMB.seq:US-09-598-982-22
91:	/cgn2_6/ptodata/2/pna/US6035 COMB.seq:US-09-598-982-22
92:	/cgn2_6/ptodata/2/pna/US6036 COMB.seq:US-09-598-982-22
93:	/cgn2_6/ptodata/2/pna/US6037 COMB.seq:US-09-598-982-22
94:	/cgn2_6/ptodata/2/pna/US6038 COMB.seq:US-09-598-982-22
95:	/cgn2_6/ptodata/2/pna/US6039 COMB.seq:US-09-598-982-22
96:	/cgn2_6/ptodata/2/pna/US6040 COMB.seq:US-09-598-982-22
97:	/cgn2_6/ptodata/2/pna/US6041 COMB.seq:US-09-598-982-22
98:	/cgn2_6/ptodata/2/pna/US6042 COMB.seq:US-09-598-982-22
99:	/cgn2_6/ptodata/2/pna/US6043 COMB.seq:US-09-598-982-22
100:	/cgn2_6/ptodata/2/pna/US6044 COMB.seq:US-09-598-982-22
101:	/cgn2_6/ptodata/2/pna/US6045 COMB.seq:US-09-598-982-22
102:	/cgn2_6/ptodata/2/pna/US6046 COMB.seq:US-09-598-982-22
103:	/cgn2_6/ptodata/2/pna/US6047 COMB.seq:US-09-598-982-22

104: /cgn2_6/ptodata/2/pna/US6047_COMB.seq:US-09-598-982-22
 105: /cgn2_6/ptodata/2/pna/US6048_COMB.seq:US-09-598-982-22
 106: /cgn2_6/ptodata/2/pna/US6049_COMB.seq:US-09-598-982-22
 107: /cgn2_6/ptodata/2/pna/US6050_COMB.seq:US-09-598-982-22
 108: /cgn2_6/ptodata/2/pna/US6051_COMB.seq:US-09-598-982-22
 109: /cgn2_6/ptodata/2/pna/US6052_COMB.seq:US-09-598-982-22
 110: /cgn2_6/ptodata/2/pna/US6053_COMB.seq:US-09-598-982-22

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1395	100.0	771	24	US-09-598-982-22 Sequence 22, Appl

ALIGNMENTS

RESULT 1
 US-09-598-982-22
 ; Sequence 22, Application US/09598982
 ; GENERAL INFORMATION:
 ; APPLICANT: NILES, ANDREW L
 ; APPLICANT: MAFFITT, MARK A
 ; APPLICANT: HAAK-FRENDSCHO, MARY
 ; TITLE OF INVENTION: RECOMBINANT PROTEOLYTIC TYPTASES, ACTIVE SITE MUTANTS
 ; TITLE OF INVENTION: THEREOF, AND METHODS OF MAKING SAME
 ; FILE REFERENCE: CIP TRYPTASE
 ; CURRENT APPLICATION NUMBER: US/09/598,982
 ; CURRENT FILING DATE: 2000-06-21
 ; PRIOR APPLICATION NUMBER: 09/079,970
 ; PRIOR FILING DATE: 1998-04-15
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 22
 ; LENGTH: 771
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (7)..(753)
 US-09-598-982-22

Alignment Scores:	Pred. No.:	Score:	Length:
Percent Similarity:	0	1395.00	771
Best Local Similarity:	100.00%	Conservative:	249
Query Match:	100.00%	Mismatches:	0
DB:	24	Indels:	0
		Gaps:	0

US-09-598-982-23 (1-249) x US-09-598-982-22 (1-771)

Qy	Db	Score	Length	Description
1	LeuGluLysArgIleValGlyGlnGluAlaProArgSerLysTrpProTribGlnVal	20		
7	CTCGAAGAAAGATCGTGGGGGTGAGAGGCCGCCAGAGCAAGTGGCCCTGGCAGGTG	66		
21	SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro	40		
67	AGCCTGAGAGTCCACGGGCCCATCTGATGCACTTCTCGGGGGGTGCTCATCCGCC	126		
41	GlnTrpValLeuThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaLeu	60		
127	CAGTGGGTGCTGACCGCAGCGCACGTCGGGACCGGACGTCAGGATCTGGCCGCCCTC	186		
61	ArgValGlnLeuArgGluGlnHisLeuTyrTrpGlnAspGlnLeuLeuProValSerArg	80		
187	AGGTTGCACTGCGGGAGCAGCACCTCTACTACAGGACCAGCTGCTGCCGGTCAGCAGG	246		

Qy	Db	Score	Length	Description
81	IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAlaIleLeuLeuGlu	100		
247	ATCATGTCGACCCACACAGTTCTACACGCCCCAGATCGAGCGGCAATCGCCCTGCTGGAG	306		
101	LeuGluGlnProValLysValSerSerHisValHisThrValThrLeuProAlaSer	120		
307	CTGGAGAGCGCGGTGAAGGTCTCCAGCCACGTCCACACGGTCAACCCCTGCCCTCA	366		
121	GluThrPheProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp	140		
367	GAGACCTTCCCGCGGATGCCGTGTGGGTCACTGGCTGGGGCGATGTGGACAATGAT	426		
141	GluArgLeuProPropheProLeuLysGlnValLysValProIleMetGluAsnHis	160		
427	GAGCGCTCCACCGCCATTTCTCTGAAGCAGGTGAAGGTCCCCATAATGAAAAACCCAC	486		
161	IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArg	180		
487	ATTGTGACGCAAAATACCACTTGGCGCCTTACACGGGAGACGACGTCCTCGTCCGT	546		
181	AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly	200		
547	GACGACATGCTGTGCGCGGAACACCCGGAGGAGTCTATGCCAGGGCGACTCCCGAGGG	606		
201	ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu	220		
607	CCCTGGTGTCAAGGTGAATGGCACCTGGCTGGCGGGCGTGTGTCAGTGGGGCGAG	666		
221	GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp	240		
667	GGCTGTGCCAGCCCAACCGGCTGGCATCTACACCCGTCACCTACTACTTGGACTGG	726		
241	IleHisHisTyrValProLysLysPro	249		
727	ATCCACCACTATGTCCCCAAAAAGCCG	753		

Search completed: July 23, 2004, 08:28:05
 Job time : 1 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 23, 2004, 08:29:03 ; Search time 0.001 Seconds
(without alignments)

383.958 Million cell updates/sec

Title: US-09-598-982-25

Perfect score: 1397

Sequence: 1 LKRIIVGGQAPRSKWPQV.....IYTRVTYILDIIHHYVKKP 249

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1 segs, 771 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Command line parameters:

-MODEL=frame_plus_p2n.model -DEV=soft -Q=Pending_Patents_AA.Main.US-09-598-982-25
-DB=Pending_Patents_AA.Main.US-09-598-982-24 -SUFFIX=pto -OUT=align25_24
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1
-MATRIX=biosum62 -TRANS=human40.cdi -LIST=1 -DOCALIGN=200 -THR_SCORE=ptc
-THR_MAX=100 -THR_MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HRAFSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO_XLPXY -NEG_SCORES=0
-LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPEXT=10
-YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending Patents NA Main:US-09-598-982-24

1: /cgn2_6/ptodata/2/pna/pctus COMB.seq:US-09-598-982-24
2: /cgn2_6/ptodata/2/pna/US06 COMB.seq:US-09-598-982-24
3: /cgn2_6/ptodata/2/pna/US07 COMB.seq:US-09-598-982-24
4: /cgn2_6/ptodata/2/pna/US080 COMB.seq:US-09-598-982-24
5: /cgn2_6/ptodata/2/pna/US081 COMB.seq:US-09-598-982-24
6: /cgn2_6/ptodata/2/pna/US082 COMB.seq:US-09-598-982-24
7: /cgn2_6/ptodata/2/pna/US083 COMB.seq:US-09-598-982-24
8: /cgn2_6/ptodata/2/pna/US084 COMB.seq:US-09-598-982-24
9: /cgn2_6/ptodata/2/pna/US085 COMB.seq:US-09-598-982-24
10: /cgn2_6/ptodata/2/pna/US086 COMB.seq:US-09-598-982-24
11: /cgn2_6/ptodata/2/pna/US087 COMB.seq:US-09-598-982-24
12: /cgn2_6/ptodata/2/pna/US088 COMB.seq:US-09-598-982-24
13: /cgn2_6/ptodata/2/pna/US089 COMB.seq:US-09-598-982-24
14: /cgn2_6/ptodata/2/pna/US090 COMB.seq:US-09-598-982-24
15: /cgn2_6/ptodata/2/pna/US091 COMB.seq:US-09-598-982-24
16: /cgn2_6/ptodata/2/pna/US092A COMB.seq:US-09-598-982-24
17: /cgn2_6/ptodata/2/pna/US092B COMB.seq:US-09-598-982-24
18: /cgn2_6/ptodata/2/pna/US093A COMB.seq:US-09-598-982-24
19: /cgn2_6/ptodata/2/pna/US093B COMB.seq:US-09-598-982-24
20: /cgn2_6/ptodata/2/pna/US094 COMB.seq:US-09-598-982-24
21: /cgn2_6/ptodata/2/pna/US095A COMB.seq:US-09-598-982-24
22: /cgn2_6/ptodata/2/pna/US095B COMB.seq:US-09-598-982-24
23: /cgn2_6/ptodata/2/pna/US095C COMB.seq:US-09-598-982-24
24: /cgn2_6/ptodata/2/pna/US096 COMB.seq:US-09-598-982-24
25: /cgn2_6/ptodata/2/pna/US096A COMB.seq:US-09-598-982-24
26: /cgn2_6/ptodata/2/pna/US096B COMB.seq:US-09-598-982-24
27: /cgn2_6/ptodata/2/pna/US096C COMB.seq:US-09-598-982-24
28: /cgn2_6/ptodata/2/pna/US096D COMB.seq:US-09-598-982-24
29: /cgn2_6/ptodata/2/pna/US096E COMB.seq:US-09-598-982-24
30: /cgn2_6/ptodata/2/pna/US097A COMB.seq:US-09-598-982-24

31: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-24
32: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-24
33: /cgn2_6/ptodata/2/pna/US098A COMB.seq:US-09-598-982-24
34: /cgn2_6/ptodata/2/pna/US098B COMB.seq:US-09-598-982-24
35: /cgn2_6/ptodata/2/pna/US098C COMB.seq:US-09-598-982-24
36: /cgn2_6/ptodata/2/pna/US098D COMB.seq:US-09-598-982-24
37: /cgn2_6/ptodata/2/pna/US099A COMB.seq:US-09-598-982-24
38: /cgn2_6/ptodata/2/pna/US099B COMB.seq:US-09-598-982-24
39: /cgn2_6/ptodata/2/pna/US099C COMB.seq:US-09-598-982-24
40: /cgn2_6/ptodata/2/pna/US099D COMB.seq:US-09-598-982-24
41: /cgn2_6/ptodata/2/pna/US099E COMB.seq:US-09-598-982-24
42: /cgn2_6/ptodata/2/pna/US099F COMB.seq:US-09-598-982-24
43: /cgn2_6/ptodata/2/pna/US100A COMB.seq:US-09-598-982-24
44: /cgn2_6/ptodata/2/pna/US100B COMB.seq:US-09-598-982-24
45: /cgn2_6/ptodata/2/pna/US101A COMB.seq:US-09-598-982-24
46: /cgn2_6/ptodata/2/pna/US101B COMB.seq:US-09-598-982-24
47: /cgn2_6/ptodata/2/pna/US102A COMB.seq:US-09-598-982-24
48: /cgn2_6/ptodata/2/pna/US102B COMB.seq:US-09-598-982-24
49: /cgn2_6/ptodata/2/pna/US103A COMB.seq:US-09-598-982-24
50: /cgn2_6/ptodata/2/pna/US103B COMB.seq:US-09-598-982-24
51: /cgn2_6/ptodata/2/pna/US104A COMB.seq:US-09-598-982-24
52: /cgn2_6/ptodata/2/pna/US104B COMB.seq:US-09-598-982-24
53: /cgn2_6/ptodata/2/pna/US106 COMB.seq:US-09-598-982-24
54: /cgn2_6/ptodata/2/pna/US107A COMB.seq:US-09-598-982-24
55: /cgn2_6/ptodata/2/pna/US107B COMB.seq:US-09-598-982-24
56: /cgn2_6/ptodata/2/pna/US6000 COMB.seq:US-09-598-982-24
57: /cgn2_6/ptodata/2/pna/US6001 COMB.seq:US-09-598-982-24
58: /cgn2_6/ptodata/2/pna/US6002 COMB.seq:US-09-598-982-24
59: /cgn2_6/ptodata/2/pna/US6003 COMB.seq:US-09-598-982-24
60: /cgn2_6/ptodata/2/pna/US6004 COMB.seq:US-09-598-982-24
61: /cgn2_6/ptodata/2/pna/US6005 COMB.seq:US-09-598-982-24
62: /cgn2_6/ptodata/2/pna/US6006 COMB.seq:US-09-598-982-24
63: /cgn2_6/ptodata/2/pna/US6007 COMB.seq:US-09-598-982-24
64: /cgn2_6/ptodata/2/pna/US6008 COMB.seq:US-09-598-982-24
65: /cgn2_6/ptodata/2/pna/US6009 COMB.seq:US-09-598-982-24
66: /cgn2_6/ptodata/2/pna/US6010 COMB.seq:US-09-598-982-24
67: /cgn2_6/ptodata/2/pna/US6011 COMB.seq:US-09-598-982-24
68: /cgn2_6/ptodata/2/pna/US6012 COMB.seq:US-09-598-982-24
69: /cgn2_6/ptodata/2/pna/US6013 COMB.seq:US-09-598-982-24
70: /cgn2_6/ptodata/2/pna/US6014 COMB.seq:US-09-598-982-24
71: /cgn2_6/ptodata/2/pna/US6015 COMB.seq:US-09-598-982-24
72: /cgn2_6/ptodata/2/pna/US6016 COMB.seq:US-09-598-982-24
73: /cgn2_6/ptodata/2/pna/US6017 COMB.seq:US-09-598-982-24
74: /cgn2_6/ptodata/2/pna/US6018 COMB.seq:US-09-598-982-24
75: /cgn2_6/ptodata/2/pna/US6019 COMB.seq:US-09-598-982-24
76: /cgn2_6/ptodata/2/pna/US6020 COMB.seq:US-09-598-982-24
77: /cgn2_6/ptodata/2/pna/US6021 COMB.seq:US-09-598-982-24
78: /cgn2_6/ptodata/2/pna/US6022 COMB.seq:US-09-598-982-24
79: /cgn2_6/ptodata/2/pna/US6023A COMB.seq:US-09-598-982-24
80: /cgn2_6/ptodata/2/pna/US6023B COMB.seq:US-09-598-982-24
81: /cgn2_6/ptodata/2/pna/US6024 COMB.seq:US-09-598-982-24
82: /cgn2_6/ptodata/2/pna/US6025 COMB.seq:US-09-598-982-24
83: /cgn2_6/ptodata/2/pna/US6026 COMB.seq:US-09-598-982-24
84: /cgn2_6/ptodata/2/pna/US6027 COMB.seq:US-09-598-982-24
85: /cgn2_6/ptodata/2/pna/US6028 COMB.seq:US-09-598-982-24
86: /cgn2_6/ptodata/2/pna/US6029 COMB.seq:US-09-598-982-24
87: /cgn2_6/ptodata/2/pna/US6030 COMB.seq:US-09-598-982-24
88: /cgn2_6/ptodata/2/pna/US6031 COMB.seq:US-09-598-982-24
89: /cgn2_6/ptodata/2/pna/US6032 COMB.seq:US-09-598-982-24
90: /cgn2_6/ptodata/2/pna/US6033 COMB.seq:US-09-598-982-24
91: /cgn2_6/ptodata/2/pna/US6034 COMB.seq:US-09-598-982-24
92: /cgn2_6/ptodata/2/pna/US6035 COMB.seq:US-09-598-982-24
93: /cgn2_6/ptodata/2/pna/US6036 COMB.seq:US-09-598-982-24
94: /cgn2_6/ptodata/2/pna/US6037 COMB.seq:US-09-598-982-24
95: /cgn2_6/ptodata/2/pna/US6038 COMB.seq:US-09-598-982-24
96: /cgn2_6/ptodata/2/pna/US6039 COMB.seq:US-09-598-982-24
97: /cgn2_6/ptodata/2/pna/US6040 COMB.seq:US-09-598-982-24
98: /cgn2_6/ptodata/2/pna/US6041 COMB.seq:US-09-598-982-24
99: /cgn2_6/ptodata/2/pna/US6042 COMB.seq:US-09-598-982-24
100: /cgn2_6/ptodata/2/pna/US6043 COMB.seq:US-09-598-982-24
101: /cgn2_6/ptodata/2/pna/US6044 COMB.seq:US-09-598-982-24
102: /cgn2_6/ptodata/2/pna/US6045 COMB.seq:US-09-598-982-24
103: /cgn2_6/ptodata/2/pna/US6046 COMB.seq:US-09-598-982-24

104: /cgn2_6/ptodata/2/pna/US6047_COMB.seq:US-09-598-982-24
105: /cgn2_6/ptodata/2/pna/US6048_COMB.seq:US-09-598-982-24
106: /cgn2_6/ptodata/2/pna/US6049_COMB.seq:US-09-598-982-24
107: /cgn2_6/ptodata/2/pna/US6050_COMB.seq:US-09-598-982-24
108: /cgn2_6/ptodata/2/pna/US6051_COMB.seq:US-09-598-982-24
109: /cgn2_6/ptodata/2/pna/US6052_COMB.seq:US-09-598-982-24
110: /cgn2_6/ptodata/2/pna/US6053_COMB.seq:US-09-598-982-24

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1397	100.0	771	24	US-09-598-982-24 Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-598-982-24
; Sequence 24, Application US/09598982
; GENERAL INFORMATION:
; APPLICANT: NILES, ANDREW L
; APPLICANT: MAFFITT, MARK A
; APPLICANT: HAAK-FRENDSCHO, MARY
; TITLE OF INVENTION: RECOMBINANT PROTEOLYTIC TYPTASES, ACTIVE SITE MUTANTS
; FILE REFERENCE: CIP TRYPTASE
; CURRENT APPLICATION NUMBER: US/09/598,982
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 09/079,970
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(753)
US-09-598-982-24

Alignment Scores:
Pred. No.: 0 Length: 771
Score: 1397.00 Matches: 249
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0

US-09-598-982-25 (1-249) x US-09-598-982-24 (1-771)

Qy	1	LeuGluysArgIleValGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal	20
Db	7	CTCGAAGAAAGATCGTCGGGGTTCAGAGAGCCCCAGGAGCAAGTGGCCCTGGCAGGTG	66
Qy	21	SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro	40
Db	67	AGCCTGAGAGTCCACGCCCATCTCGATGCACTTCTGCGGGGGCTCCCTCATCCACCC	126
Qy	41	GlnTrpValLeuThrAlaHisCysValGlyProAspValLysAspLeuAlaLeu	60
Db	127	CAGTGGGTGTCGACCGAGCGCACTGCGTGGGACCGAGACGTCAAGGATCGGCCGCCCTC	186
Qy	61	ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg	80
Db	187	AGGGTGCNACTGCGGAGCAGCACCTCTACTACAGGACCAGCTGCTGCCGGTCAGCAGG	246

Qy	81	IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu	100
Db	247	ATCATGTGCACCCACAGTTCTACACGCCCCACATCGGAGCGACATCGCCCTGCTGGAG	306
Qy	101	LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProAlaSer	120
Db	307	CTGGAGGAGCGGTGAAGGTCTCCAGCCACGTCCACACGGTCAACCTGCCCTGGCTCA	366
Qy	121	GluThrPheProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp	140
Db	367	GAGACCTTCCCCCGGGGATGCGTGTGGGTCACTGGCTGGGGCGATGGACAATGAT	426
Qy	141	GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis	160
Db	427	GAGCGCTCCACCGCCATTTCCTCTGAAGCAGGTGAAGTCCCCATAATGGAACAC	486
Qy	161	IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArg	180
Db	487	ATTGTGACGCAAAATACCACTTGGCGCTTACACGGGAGACACGTCCGCATCGTCCGT	546
Qy	181	AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspAlaGlyGly	200
Db	547	GACGACATGCTGTGTCGGGAAACACCCGGAGGAGCTCATGTCAAGCGACGCCGCGGA	606
Qy	201	ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu	220
Db	607	CCTCTGGTGTGCAAGGTGAATGGCACCTGGCTGACGGCGGGCGTGTGTCAGCTGGGCGAG	666
Qy	221	GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp	240
Db	667	GGCTGTGCCAGCCCAACCGGCTGGCATCTACACCCGTGTACCTACTACTTGGACTGG	726
Qy	241	IleHisHisTyrValProLysLysPro	249
Db	727	ATCCACCACTATGTCCCCCAAAAGCCG	753

Search completed: July 23, 2004, 08:29:04
Job time : 0.001 secs

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:      July 23, 2004, 08:29:57 ; Search time 1 Seconds
           (without alignments)
           0.384 Million cell updates/sec

Title:
Perfect score: 1397
Sequence: 1 LEXRIVGGQAPRSKMPQV.....IYTRVTYVLDWIHHVFKKP 249

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched:      1 seqs, 771 residues

Total number of hits satisfying chosen parameters:      2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Command line parameters:
-MODEL=frame+ p2n.model DEV=soft -Q=Pending_Patents_AA_Main:US-09-598-982-27
-DB=Pending_Patents_AA_Main:US-09-598-982-26 -SUFFIX=pro -OUT=align27_26
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -DOCLIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=ptc -NORM=NEG
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO_XLPXY -NEG SCORES=0
-LOGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10
-YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: /cgn2_6/ptodata/2/pna/US097A COMB.seq:US-09-598-982-26
2: /cgn2_6/ptodata/2/pna/US06 COMB.seq:US-09-598-982-26
3: /cgn2_6/ptodata/2/pna/US098A COMB.seq:US-09-598-982-26
4: /cgn2_6/ptodata/2/pna/US080 COMB.seq:US-09-598-982-26
5: /cgn2_6/ptodata/2/pna/US081 COMB.seq:US-09-598-982-26
6: /cgn2_6/ptodata/2/pna/US082 COMB.seq:US-09-598-982-26
7: /cgn2_6/ptodata/2/pna/US083 COMB.seq:US-09-598-982-26
8: /cgn2_6/ptodata/2/pna/US084 COMB.seq:US-09-598-982-26
9: /cgn2_6/ptodata/2/pna/US085 COMB.seq:US-09-598-982-26
10: /cgn2_6/ptodata/2/pna/US086 COMB.seq:US-09-598-982-26
11: /cgn2_6/ptodata/2/pna/US087 COMB.seq:US-09-598-982-26
12: /cgn2_6/ptodata/2/pna/US088 COMB.seq:US-09-598-982-26
13: /cgn2_6/ptodata/2/pna/US089 COMB.seq:US-09-598-982-26
14: /cgn2_6/ptodata/2/pna/US090 COMB.seq:US-09-598-982-26
15: /cgn2_6/ptodata/2/pna/US091 COMB.seq:US-09-598-982-26
16: /cgn2_6/ptodata/2/pna/US092A COMB.seq:US-09-598-982-26
17: /cgn2_6/ptodata/2/pna/US092B COMB.seq:US-09-598-982-26
18: /cgn2_6/ptodata/2/pna/US093A COMB.seq:US-09-598-982-26
19: /cgn2_6/ptodata/2/pna/US093B COMB.seq:US-09-598-982-26
20: /cgn2_6/ptodata/2/pna/US094 COMB.seq:US-09-598-982-26
21: /cgn2_6/ptodata/2/pna/US095A COMB.seq:US-09-598-982-26
22: /cgn2_6/ptodata/2/pna/US095B COMB.seq:US-09-598-982-26
23: /cgn2_6/ptodata/2/pna/US095C COMB.seq:US-09-598-982-26
24: /cgn2_6/ptodata/2/pna/US095D COMB.seq:US-09-598-982-26
25: /cgn2_6/ptodata/2/pna/US096A COMB.seq:US-09-598-982-26
26: /cgn2_6/ptodata/2/pna/US096B COMB.seq:US-09-598-982-26
27: /cgn2_6/ptodata/2/pna/US096C COMB.seq:US-09-598-982-26
28: /cgn2_6/ptodata/2/pna/US096D COMB.seq:US-09-598-982-26
29: /cgn2_6/ptodata/2/pna/US096E COMB.seq:US-09-598-982-26
30: /cgn2_6/ptodata/2/pna/US097A COMB.seq:US-09-598-982-26
31: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-26
32: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-26
33: /cgn2_6/ptodata/2/pna/US098A COMB.seq:US-09-598-982-26
34: /cgn2_6/ptodata/2/pna/US098B COMB.seq:US-09-598-982-26
35: /cgn2_6/ptodata/2/pna/US098C COMB.seq:US-09-598-982-26
36: /cgn2_6/ptodata/2/pna/US098D COMB.seq:US-09-598-982-26
37: /cgn2_6/ptodata/2/pna/US099A COMB.seq:US-09-598-982-26
38: /cgn2_6/ptodata/2/pna/US099B COMB.seq:US-09-598-982-26
39: /cgn2_6/ptodata/2/pna/US099C COMB.seq:US-09-598-982-26
40: /cgn2_6/ptodata/2/pna/US099D COMB.seq:US-09-598-982-26
41: /cgn2_6/ptodata/2/pna/US099E COMB.seq:US-09-598-982-26
42: /cgn2_6/ptodata/2/pna/US099F COMB.seq:US-09-598-982-26
43: /cgn2_6/ptodata/2/pna/US100A COMB.seq:US-09-598-982-26
44: /cgn2_6/ptodata/2/pna/US100B COMB.seq:US-09-598-982-26
45: /cgn2_6/ptodata/2/pna/US101A COMB.seq:US-09-598-982-26
46: /cgn2_6/ptodata/2/pna/US101B COMB.seq:US-09-598-982-26
47: /cgn2_6/ptodata/2/pna/US102A COMB.seq:US-09-598-982-26
48: /cgn2_6/ptodata/2/pna/US102B COMB.seq:US-09-598-982-26
49: /cgn2_6/ptodata/2/pna/US103A COMB.seq:US-09-598-982-26
50: /cgn2_6/ptodata/2/pna/US103B COMB.seq:US-09-598-982-26
51: /cgn2_6/ptodata/2/pna/US104A COMB.seq:US-09-598-982-26
52: /cgn2_6/ptodata/2/pna/US104B COMB.seq:US-09-598-982-26
53: /cgn2_6/ptodata/2/pna/US106 COMB.seq:US-09-598-982-26
54: /cgn2_6/ptodata/2/pna/US107A COMB.seq:US-09-598-982-26
55: /cgn2_6/ptodata/2/pna/US107B COMB.seq:US-09-598-982-26
56: /cgn2_6/ptodata/2/pna/US6000 COMB.seq:US-09-598-982-26
57: /cgn2_6/ptodata/2/pna/US6001 COMB.seq:US-09-598-982-26
58: /cgn2_6/ptodata/2/pna/US6002 COMB.seq:US-09-598-982-26
59: /cgn2_6/ptodata/2/pna/US6003 COMB.seq:US-09-598-982-26
60: /cgn2_6/ptodata/2/pna/US6004 COMB.seq:US-09-598-982-26
61: /cgn2_6/ptodata/2/pna/US6005 COMB.seq:US-09-598-982-26
62: /cgn2_6/ptodata/2/pna/US6006 COMB.seq:US-09-598-982-26
63: /cgn2_6/ptodata/2/pna/US6007 COMB.seq:US-09-598-982-26
64: /cgn2_6/ptodata/2/pna/US6008 COMB.seq:US-09-598-982-26
65: /cgn2_6/ptodata/2/pna/US6009 COMB.seq:US-09-598-982-26
66: /cgn2_6/ptodata/2/pna/US6010 COMB.seq:US-09-598-982-26
67: /cgn2_6/ptodata/2/pna/US6011 COMB.seq:US-09-598-982-26
68: /cgn2_6/ptodata/2/pna/US6012 COMB.seq:US-09-598-982-26
69: /cgn2_6/ptodata/2/pna/US6013 COMB.seq:US-09-598-982-26
70: /cgn2_6/ptodata/2/pna/US6014 COMB.seq:US-09-598-982-26
71: /cgn2_6/ptodata/2/pna/US6015 COMB.seq:US-09-598-982-26
72: /cgn2_6/ptodata/2/pna/US6016 COMB.seq:US-09-598-982-26
73: /cgn2_6/ptodata/2/pna/US6017 COMB.seq:US-09-598-982-26
74: /cgn2_6/ptodata/2/pna/US6018 COMB.seq:US-09-598-982-26
75: /cgn2_6/ptodata/2/pna/US6019 COMB.seq:US-09-598-982-26
76: /cgn2_6/ptodata/2/pna/US6020 COMB.seq:US-09-598-982-26
77: /cgn2_6/ptodata/2/pna/US6021 COMB.seq:US-09-598-982-26
78: /cgn2_6/ptodata/2/pna/US6022 COMB.seq:US-09-598-982-26
79: /cgn2_6/ptodata/2/pna/US6023A COMB.seq:US-09-598-982-26
80: /cgn2_6/ptodata/2/pna/US6023B COMB.seq:US-09-598-982-26
81: /cgn2_6/ptodata/2/pna/US6024 COMB.seq:US-09-598-982-26
82: /cgn2_6/ptodata/2/pna/US6025 COMB.seq:US-09-598-982-26
83: /cgn2_6/ptodata/2/pna/US6026 COMB.seq:US-09-598-982-26
84: /cgn2_6/ptodata/2/pna/US6027 COMB.seq:US-09-598-982-26
85: /cgn2_6/ptodata/2/pna/US6028 COMB.seq:US-09-598-982-26
86: /cgn2_6/ptodata/2/pna/US6029 COMB.seq:US-09-598-982-26
87: /cgn2_6/ptodata/2/pna/US6030 COMB.seq:US-09-598-982-26
88: /cgn2_6/ptodata/2/pna/US6031 COMB.seq:US-09-598-982-26
89: /cgn2_6/ptodata/2/pna/US6032 COMB.seq:US-09-598-982-26
90: /cgn2_6/ptodata/2/pna/US6033 COMB.seq:US-09-598-982-26
91: /cgn2_6/ptodata/2/pna/US6034 COMB.seq:US-09-598-982-26
92: /cgn2_6/ptodata/2/pna/US6035 COMB.seq:US-09-598-982-26
93: /cgn2_6/ptodata/2/pna/US6036 COMB.seq:US-09-598-982-26
94: /cgn2_6/ptodata/2/pna/US6037 COMB.seq:US-09-598-982-26
95: /cgn2_6/ptodata/2/pna/US6038 COMB.seq:US-09-598-982-26
96: /cgn2_6/ptodata/2/pna/US6039 COMB.seq:US-09-598-982-26
97: /cgn2_6/ptodata/2/pna/US6040 COMB.seq:US-09-598-982-26
98: /cgn2_6/ptodata/2/pna/US6041 COMB.seq:US-09-598-982-26
99: /cgn2_6/ptodata/2/pna/US6042 COMB.seq:US-09-598-982-26
100: /cgn2_6/ptodata/2/pna/US6043 COMB.seq:US-09-598-982-26
101: /cgn2_6/ptodata/2/pna/US6044 COMB.seq:US-09-598-982-26
102: /cgn2_6/ptodata/2/pna/US6045 COMB.seq:US-09-598-982-26
103: /cgn2_6/ptodata/2/pna/US6046 COMB.seq:US-09-598-982-26
```


104: /cgn2_6/ptodata/2/pna/US6047_COMB.seq:US-09-598-982-26
 105: /cgn2_6/ptodata/2/pna/US6048_COMB.seq:US-09-598-982-26
 106: /cgn2_6/ptodata/2/pna/US6049_COMB.seq:US-09-598-982-26
 107: /cgn2_6/ptodata/2/pna/US6050_COMB.seq:US-09-598-982-26
 108: /cgn2_6/ptodata/2/pna/US6051_COMB.seq:US-09-598-982-26
 109: /cgn2_6/ptodata/2/pna/US6052_COMB.seq:US-09-598-982-26
 110: /cgn2_6/ptodata/2/pna/US6053_COMB.seq:US-09-598-982-26

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
1	1397	100.0	771	24	US-09-598-982-26		Sequence 26, Appl

ALIGNMENTS

RESULT 1
 US-09-598-982-26
 ; Sequence 26, Application US/09598982
 ; GENERAL INFORMATION:
 ; APPLICANT: NILES, ANDREW L
 ; APPLICANT: MAFFITT, MARK A
 ; APPLICANT: HAARK-FRENDSCHO, MARY
 ; TITLE OF INVENTION: RECOMBINANT PROTEOLYTIC TYPTASES, ACTIVE SITE MUTANTS
 ; FILE REFERENCE: THEREOF, AND METHODS OF MAKING SAME
 ; CURRENT APPLICATION NUMBER: US/09/598,982
 ; CURRENT FILING DATE: 2000-06-21
 ; PRIOR APPLICATION NUMBER: 09/079,970
 ; PRIOR FILING DATE: 1998-04-15
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 26
 ; LENGTH: 771
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (7)..(753)
 ; US-09-598-982-26

Alignment Scores:
 Pred. No.: 0 Length: 771
 Score: 1397.00 Matches: 249
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-09-598-982-27 (1-249) x US-09-598-982-26 (1-771)

Qy	1	LeuGluLysArgIleValGlyGlyGlnAlaProArgSerLysTrpProTyrGlnVal	20
Db	7	CTCGAGAAAGATCGTCGGGGGTGAGAGAGCCCCAGGAGCAAGTGGCCCTGGCAGGTG	66
Qy	21	SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro	40
Db	67	AGCCTGAGAGTCCACGGCCCATATCGATGCACTTCTGCGGGGGCTCCCTCATCCACCC	126
Qy	41	GlnTrpValLeuThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaLeu	60
Db	127	CAGTGGTGTGACCGCAGCGCACTGCGTGGAGCCGACGTCAGGATCGGGCGCCCTC	186
Qy	61	ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg	80
Db	187	AGGGTGCAACTGCGGGAGCAGCACCTCTACTACAGGACCAGCTGCTGCGGGTCAGCAGG	246

Qy	81	IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu	100
Db	247	ATCATCTGTGACCCACAGTTCTTACCCGCCAGATCGAGCGGACATCGCCCTCTGGAG	306
Qy	101	LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer	120
Db	307	CTGGAGGAGCGGTGAAGGTCTCCAGCCACGTCACACGCGTCCACCTGCCCTGCCTCA	366
Qy	121	GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp	140
Db	367	GAGACCTTCCCGCGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGAT	426
Qy	141	GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis	160
Db	427	GAGCGCCTCCACCGCCATTCTCTGAAGCAGGTGAAGTCCCCATATATGAAAAACAC	486
Qy	161	IleCysAspAlaLysTyrHisLeuGlyAlaLysThrGlyAspValArgIleValArg	180
Db	487	ATTTGTGACGCAAAATACCACTTGGCGCCTACACGGGAGACGACGTCGCTCCGT	546
Qy	181	AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspAlaGlyGly	200
Db	547	GAGACATGCTGTGTCGGGGAACACCGGAGGACTCATGCCAAGGAGAGCGCGCGGA	606
Qy	201	ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu	220
Db	607	CCACTGGTGTGCAAGGTGAATGGACCTGGCTGCAGCGCGGGTGGTCAGCTGGGGCGAG	666
Qy	221	GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp	240
Db	667	GGCTGTGCCAGCCCAACCGGCGCTGGCATCTACACCGGTGTACCTACTACTTTGGACTGG	726
Qy	241	IleHisHisTyrValProLysLysPro	249
Db	727	ATCCACCACTATGTCCCCAAAAAGCCG	753

Search completed: July 23, 2004, 08:29:58

Job time : 1 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 23, 2004, 08:34:09 ; Search time 1 Seconds
(without alignments)
0.384 Million cell updates/sec

Title: US-09-598-982-37

Perfect score: 1394

Sequence: 1 LKRRVGGQAPRSKMPQV.....IYTRVTYLDWIHHYVKKP 249

Scoring table: BLOSUM62

Xgapop 10.0 ,	Xgapext 0.5
Ygapop 10.0 ,	Ygapext 0.5
Fgapop 6.0 ,	Fgapext 7.0
Delop 6.0 ,	Delext 7.0

Searched: 1 seqs, 771 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=soft -Q=Pending_Patents_AA_Main:US-09-598-982-37
-DB=Pending_Patents_NA_Main:US-09-598-982-36 -SUFFIX=pro -OUT=align37_36
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -DOCLIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pro -NORM=ext
-HEPESIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO_XLPXY -NEG SCORES=0
-LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10
-YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-36
2: /cgn2_6/ptodata/2/pna/US06 COMB.seq:US-09-598-982-36
3: /cgn2_6/ptodata/2/pna/US07 COMB.seq:US-09-598-982-36
4: /cgn2_6/ptodata/2/pna/US080 COMB.seq:US-09-598-982-36
5: /cgn2_6/ptodata/2/pna/US081 COMB.seq:US-09-598-982-36
6: /cgn2_6/ptodata/2/pna/US082 COMB.seq:US-09-598-982-36
7: /cgn2_6/ptodata/2/pna/US083 COMB.seq:US-09-598-982-36
8: /cgn2_6/ptodata/2/pna/US084 COMB.seq:US-09-598-982-36
9: /cgn2_6/ptodata/2/pna/US085 COMB.seq:US-09-598-982-36
10: /cgn2_6/ptodata/2/pna/US086 COMB.seq:US-09-598-982-36
11: /cgn2_6/ptodata/2/pna/US087 COMB.seq:US-09-598-982-36
12: /cgn2_6/ptodata/2/pna/US088 COMB.seq:US-09-598-982-36
13: /cgn2_6/ptodata/2/pna/US089 COMB.seq:US-09-598-982-36
14: /cgn2_6/ptodata/2/pna/US090 COMB.seq:US-09-598-982-36
15: /cgn2_6/ptodata/2/pna/US091 COMB.seq:US-09-598-982-36
16: /cgn2_6/ptodata/2/pna/US092A COMB.seq:US-09-598-982-36
17: /cgn2_6/ptodata/2/pna/US092B COMB.seq:US-09-598-982-36
18: /cgn2_6/ptodata/2/pna/US093A COMB.seq:US-09-598-982-36
19: /cgn2_6/ptodata/2/pna/US093B COMB.seq:US-09-598-982-36
20: /cgn2_6/ptodata/2/pna/US094 COMB.seq:US-09-598-982-36
21: /cgn2_6/ptodata/2/pna/US095A COMB.seq:US-09-598-982-36
22: /cgn2_6/ptodata/2/pna/US095B COMB.seq:US-09-598-982-36
23: /cgn2_6/ptodata/2/pna/US095C COMB.seq:US-09-598-982-36
24: /cgn2_6/ptodata/2/pna/US095D COMB.seq:US-09-598-982-36
25: /cgn2_6/ptodata/2/pna/US096A COMB.seq:US-09-598-982-36
26: /cgn2_6/ptodata/2/pna/US096B COMB.seq:US-09-598-982-36
27: /cgn2_6/ptodata/2/pna/US096C COMB.seq:US-09-598-982-36
28: /cgn2_6/ptodata/2/pna/US096D COMB.seq:US-09-598-982-36
29: /cgn2_6/ptodata/2/pna/US096E COMB.seq:US-09-598-982-36
30: /cgn2_6/ptodata/2/pna/US097A COMB.seq:US-09-598-982-36

31: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-36
32: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-36
33: /cgn2_6/ptodata/2/pna/US098A COMB.seq:US-09-598-982-36
34: /cgn2_6/ptodata/2/pna/US098B COMB.seq:US-09-598-982-36
35: /cgn2_6/ptodata/2/pna/US098C COMB.seq:US-09-598-982-36
36: /cgn2_6/ptodata/2/pna/US098D COMB.seq:US-09-598-982-36
37: /cgn2_6/ptodata/2/pna/US099A COMB.seq:US-09-598-982-36
38: /cgn2_6/ptodata/2/pna/US099B COMB.seq:US-09-598-982-36
39: /cgn2_6/ptodata/2/pna/US099C COMB.seq:US-09-598-982-36
40: /cgn2_6/ptodata/2/pna/US099E COMB.seq:US-09-598-982-36
41: /cgn2_6/ptodata/2/pna/US099F COMB.seq:US-09-598-982-36
42: /cgn2_6/ptodata/2/pna/US099G COMB.seq:US-09-598-982-36
43: /cgn2_6/ptodata/2/pna/US100A COMB.seq:US-09-598-982-36
44: /cgn2_6/ptodata/2/pna/US100B COMB.seq:US-09-598-982-36
45: /cgn2_6/ptodata/2/pna/US101A COMB.seq:US-09-598-982-36
46: /cgn2_6/ptodata/2/pna/US101B COMB.seq:US-09-598-982-36
47: /cgn2_6/ptodata/2/pna/US102A COMB.seq:US-09-598-982-36
48: /cgn2_6/ptodata/2/pna/US102B COMB.seq:US-09-598-982-36
49: /cgn2_6/ptodata/2/pna/US103A COMB.seq:US-09-598-982-36
50: /cgn2_6/ptodata/2/pna/US103B COMB.seq:US-09-598-982-36
51: /cgn2_6/ptodata/2/pna/US104A COMB.seq:US-09-598-982-36
52: /cgn2_6/ptodata/2/pna/US104B COMB.seq:US-09-598-982-36
53: /cgn2_6/ptodata/2/pna/US106 COMB.seq:US-09-598-982-36
54: /cgn2_6/ptodata/2/pna/US107A COMB.seq:US-09-598-982-36
55: /cgn2_6/ptodata/2/pna/US107B COMB.seq:US-09-598-982-36
56: /cgn2_6/ptodata/2/pna/US6000 COMB.seq:US-09-598-982-36
57: /cgn2_6/ptodata/2/pna/US6001 COMB.seq:US-09-598-982-36
58: /cgn2_6/ptodata/2/pna/US6002 COMB.seq:US-09-598-982-36
59: /cgn2_6/ptodata/2/pna/US6003 COMB.seq:US-09-598-982-36
60: /cgn2_6/ptodata/2/pna/US6004 COMB.seq:US-09-598-982-36
61: /cgn2_6/ptodata/2/pna/US6005 COMB.seq:US-09-598-982-36
62: /cgn2_6/ptodata/2/pna/US6006 COMB.seq:US-09-598-982-36
63: /cgn2_6/ptodata/2/pna/US6007 COMB.seq:US-09-598-982-36
64: /cgn2_6/ptodata/2/pna/US6008 COMB.seq:US-09-598-982-36
65: /cgn2_6/ptodata/2/pna/US6009 COMB.seq:US-09-598-982-36
66: /cgn2_6/ptodata/2/pna/US6010 COMB.seq:US-09-598-982-36
67: /cgn2_6/ptodata/2/pna/US6011 COMB.seq:US-09-598-982-36
68: /cgn2_6/ptodata/2/pna/US6012 COMB.seq:US-09-598-982-36
69: /cgn2_6/ptodata/2/pna/US6013 COMB.seq:US-09-598-982-36
70: /cgn2_6/ptodata/2/pna/US6014 COMB.seq:US-09-598-982-36
71: /cgn2_6/ptodata/2/pna/US6015 COMB.seq:US-09-598-982-36
72: /cgn2_6/ptodata/2/pna/US6016 COMB.seq:US-09-598-982-36
73: /cgn2_6/ptodata/2/pna/US6017 COMB.seq:US-09-598-982-36
74: /cgn2_6/ptodata/2/pna/US6018 COMB.seq:US-09-598-982-36
75: /cgn2_6/ptodata/2/pna/US6019 COMB.seq:US-09-598-982-36
76: /cgn2_6/ptodata/2/pna/US6020 COMB.seq:US-09-598-982-36
77: /cgn2_6/ptodata/2/pna/US6021 COMB.seq:US-09-598-982-36
78: /cgn2_6/ptodata/2/pna/US6022 COMB.seq:US-09-598-982-36
79: /cgn2_6/ptodata/2/pna/US6023A COMB.seq:US-09-598-982-36
80: /cgn2_6/ptodata/2/pna/US6023B COMB.seq:US-09-598-982-36
81: /cgn2_6/ptodata/2/pna/US6024 COMB.seq:US-09-598-982-36
82: /cgn2_6/ptodata/2/pna/US6025 COMB.seq:US-09-598-982-36
83: /cgn2_6/ptodata/2/pna/US6026 COMB.seq:US-09-598-982-36
84: /cgn2_6/ptodata/2/pna/US6027 COMB.seq:US-09-598-982-36
85: /cgn2_6/ptodata/2/pna/US6028 COMB.seq:US-09-598-982-36
86: /cgn2_6/ptodata/2/pna/US6029 COMB.seq:US-09-598-982-36
87: /cgn2_6/ptodata/2/pna/US6030 COMB.seq:US-09-598-982-36
88: /cgn2_6/ptodata/2/pna/US6031 COMB.seq:US-09-598-982-36
89: /cgn2_6/ptodata/2/pna/US6032 COMB.seq:US-09-598-982-36
90: /cgn2_6/ptodata/2/pna/US6033 COMB.seq:US-09-598-982-36
91: /cgn2_6/ptodata/2/pna/US6034 COMB.seq:US-09-598-982-36
92: /cgn2_6/ptodata/2/pna/US6035 COMB.seq:US-09-598-982-36
93: /cgn2_6/ptodata/2/pna/US6036 COMB.seq:US-09-598-982-36
94: /cgn2_6/ptodata/2/pna/US6037 COMB.seq:US-09-598-982-36
95: /cgn2_6/ptodata/2/pna/US6038 COMB.seq:US-09-598-982-36
96: /cgn2_6/ptodata/2/pna/US6039 COMB.seq:US-09-598-982-36
97: /cgn2_6/ptodata/2/pna/US6040 COMB.seq:US-09-598-982-36
98: /cgn2_6/ptodata/2/pna/US6041 COMB.seq:US-09-598-982-36
99: /cgn2_6/ptodata/2/pna/US6042 COMB.seq:US-09-598-982-36
100: /cgn2_6/ptodata/2/pna/US6043 COMB.seq:US-09-598-982-36
101: /cgn2_6/ptodata/2/pna/US6044 COMB.seq:US-09-598-982-36
102: /cgn2_6/ptodata/2/pna/US6045 COMB.seq:US-09-598-982-36
103: /cgn2_6/ptodata/2/pna/US6046 COMB.seq:US-09-598-982-36

104: /cgn2_6/ptodata/2/pna/US6047_COMB.seq:US-09-598-982-36
105: /cgn2_6/ptodata/2/pna/US6048_COMB.seq:US-09-598-982-36
106: /cgn2_6/ptodata/2/pna/US6049_COMB.seq:US-09-598-982-36
107: /cgn2_6/ptodata/2/pna/US6050_COMB.seq:US-09-598-982-36
108: /cgn2_6/ptodata/2/pna/US6051_COMB.seq:US-09-598-982-36
109: /cgn2_6/ptodata/2/pna/US6052_COMB.seq:US-09-598-982-36
110: /cgn2_6/ptodata/2/pna/US6053_COMB.seq:US-09-598-982-36

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1394	100.0	771	24	US-09-598-982-36

ALIGNMENTS

RESULT 1
US-09-598-982-36
; Sequence 36, Application US/09598982
; GENERAL INFORMATION:
; APPLICANT: NILES, ANDREW L
; APPLICANT: MAFFITT, MARK A
; APPLICANT: HAAK-FRENDSCHO, MARY
; TITLE OF INVENTION: RECOMBINANT PROTEOLYTIC TYPTASES, ACTIVE SITE MUTANTS
; FILE REFERENCE: CIP TRYPTASE
; CURRENT APPLICATION NUMBER: US/09/598,982
; CURRENT FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 09/079,970
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(753)
US-09-598-982-36

Alignment Scores:

Pred. No.:	0	Length:	771
Score:	1394.00	Matches:	249
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-598-982-37 (1-249) x US-09-598-982-36 (1-771)

Qy	1	LeuGluHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu	20
Db	7	CTCGAGAAAAGATCGTCGGGGGTTCAGAGAGCCCGCCAGGAGCAAGTGGCCCTGGCAGGTG	66
Qy	21	SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro	40
Db	67	AGCCTGAGAGTCCACGCCCCATCTGGATGCACCTTCGCGGGGCTCCCTCATCCACCC	126
Qy	41	GlnTrpValLeuThrAlaAlaCysValGlyProAspValIysAspLeuAlaLeu	60
Db	127	CAGTGGGTGTGACCCCGCGCGGTGCTGGAGCCGACGTCAGAGATCGGCCCTC	186
Qy	61	ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuProValSerArg	80
Db	187	AGGGTGCAACTGGGGGAGCAGCACCTCTACTACAGGACCAGGTGCTGCCGGTCAGCAGG	246

Qy	81	IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu	100
Db	247	ATCATCTGTGACCCACACAGTTCTACACGCCCCAGATCGGAGCGGACATCGCCCTGCTGGAG	306
Qy	101	LeuGluGluProValAsnValSerSerHisValHisThrValThrLeuProProAlaSer	120
Db	307	CTGGAGGAGCGGGTGAACGTCTCCAGCCAGCTCCACACGGGTCAACCTGCCCTGCCCTCA	366
Qy	121	GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp	140
Db	367	GAGACCTTCCCGCGGGATGCCGTGCTGGGTCACTGGCTGGCGGATGGACAAATGAT	426
Qy	141	GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis	160
Db	427	GAGCGCTCCACCGCCATTTCTCTGAGCAGGTGAAGTCCCCATAATGGAACACAC	486
Qy	161	IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArg	180
Db	487	ATTTGTGACGCAAAATACCACTTGGCGCCTACACGGGAGACGACGTCCGTCCTCGT	546
Qy	181	AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly	200
Db	547	GACGACATGTGTGTGCCGGGACACCCGAGGACTCATGCCAGGCGGACTCCGGAGGG	606
Qy	201	ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu	220
Db	607	CCCTGTGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCTGGTCAGCTGGGGCGAG	666
Qy	221	GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp	240
Db	667	GGCTGTGCCAGGCCCAACCGCGCTGGCATCTACACCGGTGTACACCTACTACTTGGACTGG	726
Qy	241	IleHisHisTyrValProLysLysPro	249
Db	727	ATCCACCACTATGTCCCCAAAAAGCCG	753

Search completed: July 23, 2004, 08:34:10

Job time : 1 secs

```

OM protein - nucleic search, using frame_plus_p2n model

Run on:      July 23, 2004, 08:35:02 ; Search time 0.001 Seconds
            (without alignments)
            383.958 Million cell updates/sec

Title:
Perfect score: 1396
Sequence: 1 LEXRIVGGQAPRSKWPQV.....IYRTVTYLDIHHYVKKP 249

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched:      1 segs, 771 residues

Total number of hits satisfying chosen parameters:      2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=soft -Q=Pending Patents_AA_Main:US-09-598-982-39
-DB=Pending Patents_NA_Main:US-09-598-982-38 -SUFFIX=pto -OUT=align39_38
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -DOCLIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEADING=500 -MINLEN=0 -MAXLEN=200000000 -NCPY=6 -NO_XLPXY -NEG SCORES=0
-LOGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10
-YGAPEXT=0.5 -DELOP=6 -DLEXT=7

Database :      Pending Patents_NA_Main:US-09-598-982-38
1: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
2: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
3: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
4: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
5: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
6: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
7: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
8: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
9: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
10: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
11: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
12: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
13: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
14: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
15: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
16: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
17: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
18: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
19: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
20: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
21: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
22: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
23: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
24: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
25: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
26: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
27: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
28: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
29: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
30: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-38
31: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
32: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
33: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
34: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
35: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
36: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
37: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
38: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
39: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
40: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
41: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
42: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
43: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
44: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
45: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
46: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
47: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
48: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
49: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
50: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
51: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
52: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
53: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
54: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
55: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
56: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
57: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
58: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
59: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
60: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
61: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
62: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
63: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
64: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
65: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
66: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
67: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
68: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
69: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
70: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
71: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
72: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
73: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
74: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
75: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
76: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
77: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
78: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
79: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
80: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
81: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
82: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
83: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
84: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
85: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
86: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
87: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
88: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
89: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
90: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
91: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
92: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
93: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
94: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
95: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
96: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
97: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
98: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
99: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
100: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
101: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
102: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38
103: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-38

```

104: /cgn2_6/ptodata/2/pna/US6047 COMB. seq: US-09-598-982-38
 105: /cgn2_6/ptodata/2/pna/US6048 COMB. seq: US-09-598-982-38
 106: /cgn2_6/ptodata/2/pna/US6049 COMB. seq: US-09-598-982-38
 107: /cgn2_6/ptodata/2/pna/US6050 COMB. seq: US-09-598-982-38
 108: /cgn2_6/ptodata/2/pna/US6051 COMB. seq: US-09-598-982-38
 109: /cgn2_6/ptodata/2/pna/US6052 COMB. seq: US-09-598-982-38
 110: /cgn2_6/ptodata/2/pna/US6053 COMB. seq: US-09-598-982-38

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1396	100.0	771	24	US-09-598-982-38 Sequence 38, Appl

ALIGNMENTS

RESULT 1

US-09-598-982-38

```

; Sequence 38 Application US/09598982
; GENERAL INFORMATION:
; APPLICANT: NILES, ANDREW L
; APPLICANT: MAFFITT, MARK A
; APPLICANT: HAAK-FRENDSCHO, MARY
; TITLE OF INVENTION: RECOMBINANT PROTEOLYTIC TYPTASES, ACTIVE SITE MUTANTS
; TITLE OF INVENTION: THEREOF, AND METHODS OF MAKING SAME
; FILE REFERENCE: CIP TRYPTASE
; CURRENT APPLICATION NUMBER: US/09/598, 982
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 09/079,970
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (7)..(753)
US-09-598-982-38

```

Alignment Scores:

Pred. No.:	Score:	Length:
0	1396.00	771
1	100.00%	249
Best Local Similarity:	100.00%	0
Query Match:	100.00%	0
DB:	24	0

US-09-598-982-39 (1-249) x US-09-598-982-38 (1-771)

QY	Db	QY	Db	QY	Db	QY	Db	QY	Db
1	LeuGluLysArgIleValGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal	20							
7	CTCAGAAAAGAAATCGTCGGGGGTACGAGAGCCCGGAGAGAGTGGCCCTGCAGGTG	66							
21	SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlySerLeuIleHisPro	40							
67	AGCCTGAGAGTCCAGCGCCCATCTGGATCACTTCGCGGGGCTCCCTCATCCACCCC	126							
41	GlnTrpValLeuThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaLeu	60							
127	CAGTGGGTGCTGACCGCAGCGCACTGCTGGACCGACGTCAGGATCTGGCCGCCCTC	186							
61	ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuProValSerArg	80							
187	AGGGTGCACTGGGGAGCAGCACCTCTACTACAGACCAAGCTGCTGCGGTGACGAGG	246							

QY	Db	QY	Db	QY	Db	QY	Db	QY	Db
81	IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAlaIleAlaLeuLeuGlu	100							
247	ATCATCTGTGACCCACAGTTCTACACGCCCCAGATCGGAGCGCAATCGCCCTGCTGGAG	306							
101	LeuGluGluProValAsnValSerSerHisValHisThrValThrLeuProProAlaSer	120							
307	CTGGAGGAGCGGTGAACGCTCTCCAGCCACGCTCCACACGGTCAACCTGCCCTCCCTCA	366							
121	GlnThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp	140							
367	GAGACCTTCCCGGCGGATGCGGTGCTGGGTCACTGGCTGGGCGATGTGACAAATGAT	426							
141	GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis	160							
427	GAGCGCTCCACCGCCATTTCTCTGAGCAGGTGAAGTCCCATTAATGGAACCCAC	486							
161	IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArg	180							
487	ATTGTGACGCAAAATACCACTTGGCGCTTACACGGGAGACGACGTCGTCGTCGCT	546							
181	AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly	200							
547	GACGACATGCTGTGTCGGGAAACCCCGAGGAGCTCATGCCAGGGGCTCCGGAGGG	606							
201	ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu	220							
607	CCCTGTGTGCAAGGTGAATGGCACTGCTGCAGCGCGGCGTGGTCACTGCGGGCGAG	666							
221	GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp	240							
667	GGCTGTGCCAGCCCAACCGCGCTGGCATCTACACCGCTGTCACTACTACTTGGACTGG	726							
241	IleHisHisTyrValProLysLysPro	249							
727	ATCCACCACTATGTCCCCAAAAAGCCG	753							

Search completed: July 23, 2004, 08:35:03

Job time : 0.001 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 23, 2004, 08:35:57 ; Search time 0.001 Seconds
(without alignments)

383.958 Million cell updates/sec

Title: US-09-598-982-41

Perfect score: 1398

Sequence: 1 LEKRIVGGQAPRSKPWQV.....IYTRVYVYLDIIHHYVKKP 249

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1 seqs, 771 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Command line parameters:

-MODEL=frame_plus_p2n.model -DEV=soft -Q=Pending_Patents_AA_Main:US-09-598-982-41
-DB=Pending Patents NA_Main:US-09-598-982-40 -SUFFIX=pro -OUT=align41_40
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -DOCALLIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pro -NORM=ext
-HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO_XLPXY -NEG SCORES=0
-LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10
-YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending Patents NA_Main:US-09-598-982-40

1: /cgn2_6/ptodata/2/pna/US097B	COMB.seq:US-09-598-982-40
2: /cgn2_6/ptodata/2/pna/US06	COMB.seq:US-09-598-982-40
3: /cgn2_6/ptodata/2/pna/US07	COMB.seq:US-09-598-982-40
4: /cgn2_6/ptodata/2/pna/US080	COMB.seq:US-09-598-982-40
5: /cgn2_6/ptodata/2/pna/US081	COMB.seq:US-09-598-982-40
6: /cgn2_6/ptodata/2/pna/US082	COMB.seq:US-09-598-982-40
7: /cgn2_6/ptodata/2/pna/US083	COMB.seq:US-09-598-982-40
8: /cgn2_6/ptodata/2/pna/US084	COMB.seq:US-09-598-982-40
9: /cgn2_6/ptodata/2/pna/US085	COMB.seq:US-09-598-982-40
10: /cgn2_6/ptodata/2/pna/US086	COMB.seq:US-09-598-982-40
11: /cgn2_6/ptodata/2/pna/US087	COMB.seq:US-09-598-982-40
12: /cgn2_6/ptodata/2/pna/US088	COMB.seq:US-09-598-982-40
13: /cgn2_6/ptodata/2/pna/US089	COMB.seq:US-09-598-982-40
14: /cgn2_6/ptodata/2/pna/US090	COMB.seq:US-09-598-982-40
15: /cgn2_6/ptodata/2/pna/US091	COMB.seq:US-09-598-982-40
16: /cgn2_6/ptodata/2/pna/US092A	COMB.seq:US-09-598-982-40
17: /cgn2_6/ptodata/2/pna/US092B	COMB.seq:US-09-598-982-40
18: /cgn2_6/ptodata/2/pna/US093A	COMB.seq:US-09-598-982-40
19: /cgn2_6/ptodata/2/pna/US093B	COMB.seq:US-09-598-982-40
20: /cgn2_6/ptodata/2/pna/US094	COMB.seq:US-09-598-982-40
21: /cgn2_6/ptodata/2/pna/US095A	COMB.seq:US-09-598-982-40
22: /cgn2_6/ptodata/2/pna/US095B	COMB.seq:US-09-598-982-40
23: /cgn2_6/ptodata/2/pna/US095C	COMB.seq:US-09-598-982-40
24: /cgn2_6/ptodata/2/pna/US095D	COMB.seq:US-09-598-982-40
25: /cgn2_6/ptodata/2/pna/US096A	COMB.seq:US-09-598-982-40
26: /cgn2_6/ptodata/2/pna/US096B	COMB.seq:US-09-598-982-40
27: /cgn2_6/ptodata/2/pna/US096C	COMB.seq:US-09-598-982-40
28: /cgn2_6/ptodata/2/pna/US096D	COMB.seq:US-09-598-982-40
29: /cgn2_6/ptodata/2/pna/US096E	COMB.seq:US-09-598-982-40
30: /cgn2_6/ptodata/2/pna/US097A	COMB.seq:US-09-598-982-40

31: /cgn2_6/ptodata/2/pna/US097B	COMB.seq:US-09-598-982-40
32: /cgn2_6/ptodata/2/pna/US097C	COMB.seq:US-09-598-982-40
33: /cgn2_6/ptodata/2/pna/US098A	COMB.seq:US-09-598-982-40
34: /cgn2_6/ptodata/2/pna/US098B	COMB.seq:US-09-598-982-40
35: /cgn2_6/ptodata/2/pna/US098C	COMB.seq:US-09-598-982-40
36: /cgn2_6/ptodata/2/pna/US098D	COMB.seq:US-09-598-982-40
37: /cgn2_6/ptodata/2/pna/US099A	COMB.seq:US-09-598-982-40
38: /cgn2_6/ptodata/2/pna/US099B	COMB.seq:US-09-598-982-40
39: /cgn2_6/ptodata/2/pna/US099C	COMB.seq:US-09-598-982-40
40: /cgn2_6/ptodata/2/pna/US099D	COMB.seq:US-09-598-982-40
41: /cgn2_6/ptodata/2/pna/US099E	COMB.seq:US-09-598-982-40
42: /cgn2_6/ptodata/2/pna/US099F	COMB.seq:US-09-598-982-40
43: /cgn2_6/ptodata/2/pna/US100A	COMB.seq:US-09-598-982-40
44: /cgn2_6/ptodata/2/pna/US100B	COMB.seq:US-09-598-982-40
45: /cgn2_6/ptodata/2/pna/US101A	COMB.seq:US-09-598-982-40
46: /cgn2_6/ptodata/2/pna/US101B	COMB.seq:US-09-598-982-40
47: /cgn2_6/ptodata/2/pna/US102A	COMB.seq:US-09-598-982-40
48: /cgn2_6/ptodata/2/pna/US102B	COMB.seq:US-09-598-982-40
49: /cgn2_6/ptodata/2/pna/US103A	COMB.seq:US-09-598-982-40
50: /cgn2_6/ptodata/2/pna/US103B	COMB.seq:US-09-598-982-40
51: /cgn2_6/ptodata/2/pna/US104A	COMB.seq:US-09-598-982-40
52: /cgn2_6/ptodata/2/pna/US104B	COMB.seq:US-09-598-982-40
53: /cgn2_6/ptodata/2/pna/US106	COMB.seq:US-09-598-982-40
54: /cgn2_6/ptodata/2/pna/US107A	COMB.seq:US-09-598-982-40
55: /cgn2_6/ptodata/2/pna/US107B	COMB.seq:US-09-598-982-40
56: /cgn2_6/ptodata/2/pna/US6000	COMB.seq:US-09-598-982-40
57: /cgn2_6/ptodata/2/pna/US6001	COMB.seq:US-09-598-982-40
58: /cgn2_6/ptodata/2/pna/US6002	COMB.seq:US-09-598-982-40
59: /cgn2_6/ptodata/2/pna/US6003	COMB.seq:US-09-598-982-40
60: /cgn2_6/ptodata/2/pna/US6004	COMB.seq:US-09-598-982-40
61: /cgn2_6/ptodata/2/pna/US6005	COMB.seq:US-09-598-982-40
62: /cgn2_6/ptodata/2/pna/US6006	COMB.seq:US-09-598-982-40
63: /cgn2_6/ptodata/2/pna/US6007	COMB.seq:US-09-598-982-40
64: /cgn2_6/ptodata/2/pna/US6008	COMB.seq:US-09-598-982-40
65: /cgn2_6/ptodata/2/pna/US6009	COMB.seq:US-09-598-982-40
66: /cgn2_6/ptodata/2/pna/US6010	COMB.seq:US-09-598-982-40
67: /cgn2_6/ptodata/2/pna/US6011	COMB.seq:US-09-598-982-40
68: /cgn2_6/ptodata/2/pna/US6012	COMB.seq:US-09-598-982-40
69: /cgn2_6/ptodata/2/pna/US6013	COMB.seq:US-09-598-982-40
70: /cgn2_6/ptodata/2/pna/US6014	COMB.seq:US-09-598-982-40
71: /cgn2_6/ptodata/2/pna/US6015	COMB.seq:US-09-598-982-40
72: /cgn2_6/ptodata/2/pna/US6016	COMB.seq:US-09-598-982-40
73: /cgn2_6/ptodata/2/pna/US6017	COMB.seq:US-09-598-982-40
74: /cgn2_6/ptodata/2/pna/US6018	COMB.seq:US-09-598-982-40
75: /cgn2_6/ptodata/2/pna/US6019	COMB.seq:US-09-598-982-40
76: /cgn2_6/ptodata/2/pna/US6020	COMB.seq:US-09-598-982-40
77: /cgn2_6/ptodata/2/pna/US6021	COMB.seq:US-09-598-982-40
78: /cgn2_6/ptodata/2/pna/US6022	COMB.seq:US-09-598-982-40
79: /cgn2_6/ptodata/2/pna/US6023A	COMB.seq:US-09-598-982-40
80: /cgn2_6/ptodata/2/pna/US6023B	COMB.seq:US-09-598-982-40
81: /cgn2_6/ptodata/2/pna/US6024	COMB.seq:US-09-598-982-40
82: /cgn2_6/ptodata/2/pna/US6025	COMB.seq:US-09-598-982-40
83: /cgn2_6/ptodata/2/pna/US6026	COMB.seq:US-09-598-982-40
84: /cgn2_6/ptodata/2/pna/US6027	COMB.seq:US-09-598-982-40
85: /cgn2_6/ptodata/2/pna/US6028	COMB.seq:US-09-598-982-40
86: /cgn2_6/ptodata/2/pna/US6029	COMB.seq:US-09-598-982-40
87: /cgn2_6/ptodata/2/pna/US6030	COMB.seq:US-09-598-982-40
88: /cgn2_6/ptodata/2/pna/US6031	COMB.seq:US-09-598-982-40
89: /cgn2_6/ptodata/2/pna/US6032	COMB.seq:US-09-598-982-40
90: /cgn2_6/ptodata/2/pna/US6033	COMB.seq:US-09-598-982-40
91: /cgn2_6/ptodata/2/pna/US6034	COMB.seq:US-09-598-982-40
92: /cgn2_6/ptodata/2/pna/US6035	COMB.seq:US-09-598-982-40
93: /cgn2_6/ptodata/2/pna/US6036	COMB.seq:US-09-598-982-40
94: /cgn2_6/ptodata/2/pna/US6037	COMB.seq:US-09-598-982-40
95: /cgn2_6/ptodata/2/pna/US6038	COMB.seq:US-09-598-982-40
96: /cgn2_6/ptodata/2/pna/US6039	COMB.seq:US-09-598-982-40
97: /cgn2_6/ptodata/2/pna/US6040	COMB.seq:US-09-598-982-40
98: /cgn2_6/ptodata/2/pna/US6041	COMB.seq:US-09-598-982-40
99: /cgn2_6/ptodata/2/pna/US6042	COMB.seq:US-09-598-982-40
100: /cgn2_6/ptodata/2/pna/US6043	COMB.seq:US-09-598-982-40
101: /cgn2_6/ptodata/2/pna/US6044	COMB.seq:US-09-598-982-40
102: /cgn2_6/ptodata/2/pna/US6045	COMB.seq:US-09-598-982-40
103: /cgn2_6/ptodata/2/pna/US6046	COMB.seq:US-09-598-982-40

104: /cgn2_6/ptodata/2/pna/US6047_COMB.seq:US-09-598-982-40
 105: /cgn2_6/ptodata/2/pna/US6048_COMB.seq:US-09-598-982-40
 106: /cgn2_6/ptodata/2/pna/US6049_COMB.seq:US-09-598-982-40
 107: /cgn2_6/ptodata/2/pna/US6050_COMB.seq:US-09-598-982-40
 108: /cgn2_6/ptodata/2/pna/US6051_COMB.seq:US-09-598-982-40
 109: /cgn2_6/ptodata/2/pna/US6052_COMB.seq:US-09-598-982-40
 110: /cgn2_6/ptodata/2/pna/US6053_COMB.seq:US-09-598-982-40

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Match	Length	ID	Description
1	1398	100.0	771	24	US-09-598-982-40 Sequence 40, Appl

ALIGNMENTS

RESULT 1

US-09-598-982-40
 ; Sequence 40, Application US/09598982
 ; GENERAL INFORMATION:
 ; APPLICANT: NILES, ANDREW L
 ; APPLICANT: MAFFITT, MARK A
 ; APPLICANT: HAAK-FRENDSCHO, MARY
 ; TITLE OF INVENTION: RECOMBINANT PROTEOLYTIC TYPTASES, ACTIVE SITE MUTANTS
 ; FILE REFERENCE: CIP TRYPTASE
 ; CURRENT FILING DATE: 2000-06-21
 ; PRIOR APPLICATION NUMBER: US/09/598,982
 ; PRIOR FILING DATE: 1998-04-15
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 40
 ; LENGTH: 771
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (7)..(753)
 US-09-598-982-40

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
0	1398.00	771	249
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-598-982-41 (1-249) x US-09-598-982-40 (1-771)

Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db
1	LeuGluLysArgIleValGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal	20							
7	CTCGAGAAAAGATCGTCGGGGTCAGGAGCCCCCAGAGCAAGTGGCCCTGGCAGGTG	66							
21	SeuLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro	40							
67	AGCCTGAGAGTCCACGCCCATCTCGATGCACTTCTGCGGGGGCTCCCTCATCCACCCC	126							
41	GlnTrpValLeuThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaLeu	60							
127	CAGTGGGTGTCACCGCAGCGCACTGCGTGGGACCGGACGTCAGGATCTGGCGGCCCTC	186							
61	ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg	80							
187	AGGGTGCAACTCGGGGAGCAGCACCTCTACTACAGGACCAGCTGCTGCCGGTCAGCAGG	246							

Search completed: July 23, 2004, 08:35:57

Job time : 0.001 secs

Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db
81	IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu	100							
247	ATCATGTGTGACCCACAGTTCTACCCGCCAGATCGGAGCGGACATCGCCCTGCTGGAG	306							
101	LeuGluGluProValAsnValSerSerHisValHisThrValThrLeuProProAlaSer	120							
307	CTGAGGAGCGCGGTGAACGCTCCACGACCGTCCACACGGGTACCCCTGCCCTGCCTCA	366							
121	GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp	140							
367	GAGACCTTCCTCCCGGGGATGCGGTGTCTGGGTCACTGCTGGGGCGATGTGGACATGAT	426							
141	GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis	160							
427	GAGGCTCTCCACCGCATTTCTCTGAAGCAGGTGAAGTCCCATATATGGAACACAC	486							
161	IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArg	180							
487	ATTGTGACGCAAAATACCACTTGGCGCTTACAGGGAGACGACGTCCGTCGTCGT	546							
181	AspAsoMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspAlaGlyGly	200							
547	GACGACATGCTGTGTCGGGAAACACCCGAGGACTCATGTCAAGCGCAGCGCGCGGA	606							
201	ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu	220							
607	CCTCTGGTGTGCAAGGTGANTGGACCTGGCTGACGGCGCGGTGGTCACTGGGGCGAG	666							
221	GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp	240							
667	GGCTGTGCCAGCCCAACCGGCTGGCATCTACACCGGTGTACCTACTACTTGGACTGG	726							
241	IleHisHisTyrValProLysLysPro	249							
727	ATCCACCACTATGTCCCCAAAAAGCCG	753							

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 23, 2004, 08:36:46 ; Search time 0.001 Seconds
(without alignments)

383.958 Million cell updates/sec

Title: US-09-598-982-43

Perfect score: 1398

Sequence: 1 LKRIIVGGQAPRSKWPQV.....IYTRVTYLDIHHYVFKP 249

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1 seqs, 771 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=soft -Q=Pending_Patents_AA_Main:US-09-598-982-43
-DB=Pending Patents NA_Main:US-09-598-982-42 -SUFFIX=pro -OUT=align43_42
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=pro -NORM=ext
-HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6 -NO_XLPXY -NEG SCORES=0
-LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10
-YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending Patents NA_Main:US-09-598-982-42

```

1: /cgn2_6/ptodata/2/pna/PCUTUS COMB.seq:US-09-598-982-42
2: /cgn2_6/ptodata/2/pna/US06 COMB.seq:US-09-598-982-42
3: /cgn2_6/ptodata/2/pna/US07 COMB.seq:US-09-598-982-42
4: /cgn2_6/ptodata/2/pna/US08 COMB.seq:US-09-598-982-42
5: /cgn2_6/ptodata/2/pna/US081 COMB.seq:US-09-598-982-42
6: /cgn2_6/ptodata/2/pna/US082 COMB.seq:US-09-598-982-42
7: /cgn2_6/ptodata/2/pna/US083 COMB.seq:US-09-598-982-42
8: /cgn2_6/ptodata/2/pna/US084 COMB.seq:US-09-598-982-42
9: /cgn2_6/ptodata/2/pna/US085 COMB.seq:US-09-598-982-42
10: /cgn2_6/ptodata/2/pna/US086 COMB.seq:US-09-598-982-42
11: /cgn2_6/ptodata/2/pna/US087 COMB.seq:US-09-598-982-42
12: /cgn2_6/ptodata/2/pna/US088 COMB.seq:US-09-598-982-42
13: /cgn2_6/ptodata/2/pna/US089 COMB.seq:US-09-598-982-42
14: /cgn2_6/ptodata/2/pna/US090 COMB.seq:US-09-598-982-42
15: /cgn2_6/ptodata/2/pna/US091 COMB.seq:US-09-598-982-42
16: /cgn2_6/ptodata/2/pna/US092A COMB.seq:US-09-598-982-42
17: /cgn2_6/ptodata/2/pna/US092B COMB.seq:US-09-598-982-42
18: /cgn2_6/ptodata/2/pna/US093A COMB.seq:US-09-598-982-42
19: /cgn2_6/ptodata/2/pna/US093B COMB.seq:US-09-598-982-42
20: /cgn2_6/ptodata/2/pna/US094 COMB.seq:US-09-598-982-42
21: /cgn2_6/ptodata/2/pna/US095A COMB.seq:US-09-598-982-42
22: /cgn2_6/ptodata/2/pna/US095B COMB.seq:US-09-598-982-42
23: /cgn2_6/ptodata/2/pna/US095C COMB.seq:US-09-598-982-42
24: /cgn2_6/ptodata/2/pna/US095D COMB.seq:US-09-598-982-42
25: /cgn2_6/ptodata/2/pna/US096A COMB.seq:US-09-598-982-42
26: /cgn2_6/ptodata/2/pna/US096B COMB.seq:US-09-598-982-42
27: /cgn2_6/ptodata/2/pna/US096C COMB.seq:US-09-598-982-42
28: /cgn2_6/ptodata/2/pna/US096D COMB.seq:US-09-598-982-42
29: /cgn2_6/ptodata/2/pna/US096E COMB.seq:US-09-598-982-42
30: /cgn2_6/ptodata/2/pna/US097A COMB.seq:US-09-598-982-42

```

```

31: /cgn2_6/ptodata/2/pna/US097B COMB.seq:US-09-598-982-42
32: /cgn2_6/ptodata/2/pna/US097C COMB.seq:US-09-598-982-42
33: /cgn2_6/ptodata/2/pna/US098A COMB.seq:US-09-598-982-42
34: /cgn2_6/ptodata/2/pna/US098B COMB.seq:US-09-598-982-42
35: /cgn2_6/ptodata/2/pna/US098C COMB.seq:US-09-598-982-42
36: /cgn2_6/ptodata/2/pna/US098D COMB.seq:US-09-598-982-42
37: /cgn2_6/ptodata/2/pna/US099A COMB.seq:US-09-598-982-42
38: /cgn2_6/ptodata/2/pna/US099B COMB.seq:US-09-598-982-42
39: /cgn2_6/ptodata/2/pna/US099C COMB.seq:US-09-598-982-42
40: /cgn2_6/ptodata/2/pna/US099D COMB.seq:US-09-598-982-42
41: /cgn2_6/ptodata/2/pna/US099E COMB.seq:US-09-598-982-42
42: /cgn2_6/ptodata/2/pna/US099F COMB.seq:US-09-598-982-42
43: /cgn2_6/ptodata/2/pna/US100A COMB.seq:US-09-598-982-42
44: /cgn2_6/ptodata/2/pna/US100B COMB.seq:US-09-598-982-42
45: /cgn2_6/ptodata/2/pna/US101A COMB.seq:US-09-598-982-42
46: /cgn2_6/ptodata/2/pna/US101B COMB.seq:US-09-598-982-42
47: /cgn2_6/ptodata/2/pna/US102A COMB.seq:US-09-598-982-42
48: /cgn2_6/ptodata/2/pna/US102B COMB.seq:US-09-598-982-42
49: /cgn2_6/ptodata/2/pna/US103A COMB.seq:US-09-598-982-42
50: /cgn2_6/ptodata/2/pna/US103B COMB.seq:US-09-598-982-42
51: /cgn2_6/ptodata/2/pna/US104A COMB.seq:US-09-598-982-42
52: /cgn2_6/ptodata/2/pna/US104B COMB.seq:US-09-598-982-42
53: /cgn2_6/ptodata/2/pna/US106 COMB.seq:US-09-598-982-42
54: /cgn2_6/ptodata/2/pna/US107A COMB.seq:US-09-598-982-42
55: /cgn2_6/ptodata/2/pna/US107B COMB.seq:US-09-598-982-42
56: /cgn2_6/ptodata/2/pna/US6000 COMB.seq:US-09-598-982-42
57: /cgn2_6/ptodata/2/pna/US6001 COMB.seq:US-09-598-982-42
58: /cgn2_6/ptodata/2/pna/US6002 COMB.seq:US-09-598-982-42
59: /cgn2_6/ptodata/2/pna/US6003 COMB.seq:US-09-598-982-42
60: /cgn2_6/ptodata/2/pna/US6004 COMB.seq:US-09-598-982-42
61: /cgn2_6/ptodata/2/pna/US6005 COMB.seq:US-09-598-982-42
62: /cgn2_6/ptodata/2/pna/US6006 COMB.seq:US-09-598-982-42
63: /cgn2_6/ptodata/2/pna/US6007 COMB.seq:US-09-598-982-42
64: /cgn2_6/ptodata/2/pna/US6008 COMB.seq:US-09-598-982-42
65: /cgn2_6/ptodata/2/pna/US6009 COMB.seq:US-09-598-982-42
66: /cgn2_6/ptodata/2/pna/US6010 COMB.seq:US-09-598-982-42
67: /cgn2_6/ptodata/2/pna/US6011 COMB.seq:US-09-598-982-42
68: /cgn2_6/ptodata/2/pna/US6012 COMB.seq:US-09-598-982-42
69: /cgn2_6/ptodata/2/pna/US6013 COMB.seq:US-09-598-982-42
70: /cgn2_6/ptodata/2/pna/US6014 COMB.seq:US-09-598-982-42
71: /cgn2_6/ptodata/2/pna/US6015 COMB.seq:US-09-598-982-42
72: /cgn2_6/ptodata/2/pna/US6016 COMB.seq:US-09-598-982-42
73: /cgn2_6/ptodata/2/pna/US6017 COMB.seq:US-09-598-982-42
74: /cgn2_6/ptodata/2/pna/US6018 COMB.seq:US-09-598-982-42
75: /cgn2_6/ptodata/2/pna/US6019 COMB.seq:US-09-598-982-42
76: /cgn2_6/ptodata/2/pna/US6020 COMB.seq:US-09-598-982-42
77: /cgn2_6/ptodata/2/pna/US6021 COMB.seq:US-09-598-982-42
78: /cgn2_6/ptodata/2/pna/US6022 COMB.seq:US-09-598-982-42
79: /cgn2_6/ptodata/2/pna/US6023A COMB.seq:US-09-598-982-42
80: /cgn2_6/ptodata/2/pna/US6023B COMB.seq:US-09-598-982-42
81: /cgn2_6/ptodata/2/pna/US6024 COMB.seq:US-09-598-982-42
82: /cgn2_6/ptodata/2/pna/US6025 COMB.seq:US-09-598-982-42
83: /cgn2_6/ptodata/2/pna/US6026 COMB.seq:US-09-598-982-42
84: /cgn2_6/ptodata/2/pna/US6027 COMB.seq:US-09-598-982-42
85: /cgn2_6/ptodata/2/pna/US6028 COMB.seq:US-09-598-982-42
86: /cgn2_6/ptodata/2/pna/US6029 COMB.seq:US-09-598-982-42
87: /cgn2_6/ptodata/2/pna/US6030 COMB.seq:US-09-598-982-42
88: /cgn2_6/ptodata/2/pna/US6031 COMB.seq:US-09-598-982-42
89: /cgn2_6/ptodata/2/pna/US6032 COMB.seq:US-09-598-982-42
90: /cgn2_6/ptodata/2/pna/US6033 COMB.seq:US-09-598-982-42
91: /cgn2_6/ptodata/2/pna/US6034 COMB.seq:US-09-598-982-42
92: /cgn2_6/ptodata/2/pna/US6035 COMB.seq:US-09-598-982-42
93: /cgn2_6/ptodata/2/pna/US6036 COMB.seq:US-09-598-982-42
94: /cgn2_6/ptodata/2/pna/US6037 COMB.seq:US-09-598-982-42
95: /cgn2_6/ptodata/2/pna/US6038 COMB.seq:US-09-598-982-42
96: /cgn2_6/ptodata/2/pna/US6039 COMB.seq:US-09-598-982-42
97: /cgn2_6/ptodata/2/pna/US6040 COMB.seq:US-09-598-982-42
98: /cgn2_6/ptodata/2/pna/US6041 COMB.seq:US-09-598-982-42
99: /cgn2_6/ptodata/2/pna/US6042 COMB.seq:US-09-598-982-42
100: /cgn2_6/ptodata/2/pna/US6043 COMB.seq:US-09-598-982-42
101: /cgn2_6/ptodata/2/pna/US6044 COMB.seq:US-09-598-982-42
102: /cgn2_6/ptodata/2/pna/US6045 COMB.seq:US-09-598-982-42
103: /cgn2_6/ptodata/2/pna/US6046 COMB.seq:US-09-598-982-42

```

104: /cgn2_6/ptodata/2/pna/US6047_COMB.seq:US-09-598-982-42
 105: /cgn2_6/ptodata/2/pna/US6048_COMB.seq:US-09-598-982-42
 106: /cgn2_6/ptodata/2/pna/US6049_COMB.seq:US-09-598-982-42
 107: /cgn2_6/ptodata/2/pna/US6050_COMB.seq:US-09-598-982-42
 108: /cgn2_6/ptodata/2/pna/US6051_COMB.seq:US-09-598-982-42
 109: /cgn2_6/ptodata/2/pna/US6052_COMB.seq:US-09-598-982-42
 110: /cgn2_6/ptodata/2/pna/US6053_COMB.seq:US-09-598-982-42

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1398	100.0	771	24	US-09-598-982-42

ALIGNMENTS

RESULT 1

US-09-598-982-42

; Sequence 42, Application US/09598982
 ; GENERAL INFORMATION:
 ; APPLICANT: NILES, ANDREW L
 ; APPLICANT: MAFFITT, MARK A
 ; APPLICANT: HAAK-FRENDSCO, MARY
 ; TITLE OF INVENTION: RECOMBINANT PROTEOLYTIC TYPTASES, ACTIVE SITE MUTANTS
 ; FILE REFERENCE: THEREOF, AND METHODS OF MAKING SAME
 ; CURRENT APPLICATION NUMBER: US/09/598,982
 ; PRIOR FILING DATE: 2000-06-21
 ; PRIOR APPLICATION NUMBER: 09/079,970
 ; PRIOR FILING DATE: 1998-04-15
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 42
 ; LENGTH: 771
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (7)..(753)
 US-09-598-982-42

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
0	1398.00	771	249
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-598-982-43 (1-249) x US-09-598-982-42 (1-771)

QY	1	LeuGluysArgIleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal	20
Db	7	CTCGAGAAAGATCGTCGGGGTCAGGAGCCCCCAGGAGCAAGTGGCCCTGGCAGGTG	66
QY	21	SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro	40
Db	67	AGCCTGAGAGTCCAGCGCCCATCTATGGATGCACTTCTGCGGGGCTCCCTCATCCACCCC	126
QY	41	GlnTrpValLeuThrAlaAlaHisCysValGlyProAspValLysAspLeuAlaLeu	60
Db	127	CAGTGGGTGTCACCGCAGCGCACTGCTGGACCGGACGTCGCAAGGATCTGGCCGCCCTC	186
QY	61	ArgValGlnLeuArgGluGlnHisLeuTyrTrpGlnAspGlnLeuLeuProValSerArg	80
Db	187	AGGGTCAACTGCGGGAGCAGCACCTCTACTACAGGACCAAGTCTGCTGCGGGTCAGCAGG	246

QY	81	IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu	100
Db	247	ATCATCGTGCACCAAGTTCTACACGCCCCAGATCGGAGCGGACATCGCCCTGCTGGAG	306
QY	101	LeuGluGluProValAsnValSerSerHisValHisThrValThrLeuProProAlaSer	120
Db	307	CTGAGAGCGCGGTGAACGTCTCCAGCCACGTCACACCGGTTCACCCCTGCCCTGCCTCA	366
QY	121	GluThrPheProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp	140
Db	367	GAGACCTTCCTCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGGACAATGAT	426
QY	141	GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis	160
Db	427	GAGCGCTCCACCGCCATTTCTCTGAAGCAGGTGAAGTCCCCATAATGGAAACACAC	486
QY	161	IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArg	180
Db	487	ATTTGTGACGCAAAATACCACTTGGCGCTACACGGGAGACGACGTCCGTCCTCGT	546
QY	181	AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspAlaGlyGly	200
Db	547	GACGACATGCTGTGTCGGGAAACCCCGAGGACTCATGCCAAGGAGACGCGCGGGA	606
QY	201	ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu	220
Db	607	CCACTGTGTGCAAGGTGAATGGACCTGGCTGCAGGCGGCGTGGTCACTGGGGCGAG	666
QY	221	GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp	240
Db	667	GGCTGTGCCAGGCCAACCGCGCTGGCATCTACACCGGTGTCACTACTACTTGGACTGG	726
QY	241	IleHisHisTyrValProLysLysPro	249
Db	727	ATCCACCACTATGTCCCCAAAAAGCCG	753

Search completed: July 23, 2004, 08:36:47

Job time : 1 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 22, 2004, 13:26:16 ; Search time 52 Seconds
(without alignments)
249.336 Million cell updates/sec

Title: US-09-598-982-21

Perfect score: 1393

Sequence: 1 LKRIVGQAEAPRSKWPQV.....IYTRVTYLDWIHHVVPKPK 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1368	98.2	275	1	TRB2_HUMAN
2	1363	97.8	275	1	TRB1_HUMAN
3	1282	92.0	275	1	TRYA_HUMAN
4	1091	78.3	276	1	MCT6_MOUSE
5	1077	77.3	275	1	TRYT_CANFA
6	1075	77.2	270	1	TRYT_MERIN
7	1054	75.7	273	1	MCT7_MOUSE
8	1051	75.4	273	1	MCT6_RAT
9	1037	74.4	273	1	MCT7_RAT
10	1030	73.9	273	1	TRYT_SHEEP
11	1006	72.2	275	1	TRYT_PIG
12	988	70.9	235	1	TRYD_HUMAN
13	684.5	49.1	269	1	TRYM_CANFA
14	605.5	43.5	311	1	TRYG_MOUSE
15	593.5	42.6	321	1	TRYG_HUMAN
16	563.5	40.5	290	1	PRZT_HUMAN
17	529	38.0	342	1	PSS8_RAT
18	526	37.8	342	1	PSS8_MOUSE
19	512	36.8	343	1	PSS8_HUMAN
20	501.5	36.0	317	1	BSS4_HUMAN
21	493.5	35.4	314	1	TEST_HUMAN
22	491	35.2	453	1	TMS5_MOUSE
23	488	35.0	455	1	TMS5_MOUSE
24	476	34.2	324	1	TEST_MOUSE
25	474.5	34.1	454	1	TMS3_HUMAN
26	467	33.5	625	1	PS7727_homo sapien
27	464.5	33.3	811	1	FAIL_HUMAN
28	463	33.2	306	1	TMS6_MOUSE
29	460.5	33.1	418	1	HATT_HUMAN
30	460.5	33.1	811	1	TMS6_HUMAN
31	457	32.8	457	1	TMS5_HUMAN
32	451	32.4	638	1	KAL_HUMAN
33	448	32.2	338	1	PLMN_HORSE

34	447	32.1	638	1	KAL_MOUSE
35	446.5	32.1	812	1	PLMN_BOVIN
36	445	31.9	638	1	PLMN_RAT
37	444.5	31.9	271	1	EL2_RAT
38	444	31.9	333	1	PLMN_CANFA
39	443	31.8	245	1	CTRB_BOVIN
40	441	31.7	343	1	PLMN_SHEEP
41	436.5	31.3	269	1	EL2A_HUMAN
42	434	31.2	490	1	TMS2_MOUSE
43	430.5	30.9	471	1	EL2_MOUSE
44	429	30.8	435	1	TMS4_MOUSE
45	429	30.8	810	1	PLMN_HUMAN

P26262	mus musculus
P05868	bos taurus
P14272	rattus norv
P00774	bos taurus
P80009	canis famil
P00767	bos taurus
P81286	ovis aries
P08217	homo sapien
Q9J1Q8	mus musculus
P05208	mus musculus
Q8VCA5	mus musculus
P00747	homo sapien

ALIGNMENTS

RESULT 1
TRB2_HUMAN
ID TRB2_HUMAN STANDARD; PRT: 275 AA.
AC P20231: Q95827; Q15664; Q9UQI6; Q9UQI7;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tryptase beta-2 precursor (EC 3.4.21.59) (Tryptase II).
GN TPSB2 OR TPS2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (VARIANT BETA-2).
RC TISSUE=Lung;
RX MEDLINE=90369005; PubMed=2203827;
RA Miller J.S., Moxley G., Schwartz L.B.;
RT "Cloning and characterization of a second complementary DNA for human
RT tryptase.";
RL J. Clin. Invest. 86:864-870(1990).
RN [2]
RP SEQUENCE FROM N.A. (VARIANT BETA-2).
RX MEDLINE=93166209; PubMed=8434231;
RA Blom T., Hellman L.;
RT "Characterization of a tryptase mRNA expressed in the human basophil
RT cell line KU812.";
RL Scand. J. Immunol. 37:203-208(1993).
RN [3]
RP SEQUENCE FROM N.A. (VARIANTS BETA-2 AND BETA-3).
RX MEDLINE=90251647; PubMed=2187193;
RA Vanderslice P., Ballinger S.M., Tam E.K., Goldstein S.M., Craik C.S.,
RA Caughey G.H.;
RT "Human mast cell tryptase: multiple cDNAs and genes reveal a
RT multigene serine protease family.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:3811-3815(1990).
RN [4]
RP SEQUENCE FROM N.A. (VARIANTS BETA-2 AND BETA-3).
RX MEDLINE=99121069; PubMed=9920877;
RA Pallaro M., Fejzo M.S., Shayeesteh L., Blount J.L., Caughey G.H.;
RT "Characterization of genes encoding known and novel human mast cell
RT tryptases on chromosome 16p13.3.";
RL J. Biol. Chem. 274:3355-3362(1999).
RN [5]
RP REVISIONS.
RA Pallaro M., Fejzo M.S., Shayeesteh L., Blount J.L., Caughey G.H.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RX MEDLINE=98180625; PubMed=9521329;
 RA Pereira P.J.B., Bergner A., Macedo-Ribeiro S., Huber R.,
 RA Matschner G., Fritz H., Sommerhoff C.P., Bode W.;
 RA "Human beta-tryptase is a ring-like tetramer with active sites facing
 RT a central pore";
 RL Nature 392:306-311 (1998).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (3.4 ANGSTROMS).
 RX MEDLINE=99432168; PubMed=10500112;
 RA Sommerhoff C.P., Bode W., Pereira P.J.B., Stubbs M.T.,
 RA Suerzebecher J., Piechottka G.P., Matschner G., Bergner A.;
 RT "The structure of the human detail-tryptase tetramer: fo(u)r better or
 RT worse";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10984-10991 (1999).
 CC -1- FUNCTION: Tryptase is the major neutral protease present in mast
 CC cells and is secreted upon the coupled activation-degranulation
 CC response of this cell type.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
 CC with more restricted specificity than trypsin.
 CC -1- SUBUNIT: Homotetramer.
 CC -1- SUBCELLULAR LOCATION: Released from the secretory granules upon
 CC mast cell activation.
 CC -1- POLYMORPHISM: There are two alleles, beta-II and beta-III which
 CC differ by 3 residues.
 CC -1- SIMILARITY: Belongs to peptidase family S1. Tryptase subfamily.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; M37488; AAA51843.1; -;
 DR EMBL; M33492; AAA36779.1; -;
 DR EMBL; M33493; AAA36780.1; -;
 DR EMBL; S55551; AAD13876.1; -;
 DR EMBL; AF099143; AAD17859.2; -;
 DR EMBL; AF099145; AAD17857.1; -;
 DR EMBL; AF099146; AAD17858.1; -;
 DR EMBL; BC029356; AAH29356.1; -;
 DR PIR; B35863; B35863;
 DR PDB; 1A0L; 31-JAN-94.
 DR MEROPS; S01.027; -;
 DR MEROPS; S01.242; -;
 DR Genew; HGNC:14120; TPST2.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PROSITE; PS0240; TRYPSIN DOM; 1.
 DR PROSITE; PS00134; TRYPSIN HIS; 1.
 DR PROSITE; PS00135; TRYPSIN SER; 1.
 KW Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
 KW Polymorphism; 3D-structure.
 FT SIGNAL 1 18 POTENTIAL.
 FT PROPEP 19 30 ACTIVATION PEPTIDE.
 FT CHAIN 31 275 TRYPTASE BETA-2.
 FT ACT_SITE 74 74 CHARGE RELAY SYSTEM.
 FT ACT_SITE 121 121 CHARGE RELAY SYSTEM.
 FT ACT_SITE 224 224 CHARGE RELAY SYSTEM.
 FT DISULFID 59 75
 FT DISULFID 155 230
 FT DISULFID 188 211
 FT DISULFID 220 248
 FT CARBOHYD 233 233
 FT VARIANT 51 53
 FT CONFLICT 132 132
 FT CONFLICT K -> N (IN REF. 3).
 SQ SEQUENCE 275 AA; 30529 MW; 2B27396C51F5C7A0 CRC64;
 Query Match 98.2%; Score 1368; DB 1; Length 275;
 Best Local Similarity 99.6%; Pred. No. 2.6e-118;
 Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 IVGGQAPRSKWPQVSLRVHGPYVWHFVCGSLHPQWLTAAACVGPDKDLAARVQL 64
 DB 31 IVGGQAPRSKWPQVSLRVHGPYVWHFVCGSLHPQWLTAAACVGPDKDLAARVQL 90
 QY 65 REQLHYQDQLLYSLIIVHPQYTAQIGADIALLEELPEPKVSSHHVHTVTLPPASETP 124
 DB 91 REQLHYQDQLLYSLIIVHPQYTAQIGADIALLEELPEPKVSSHHVHTVTLPPASETP 150
 QY 125 PGMPCWVTGWDVNDERLPPFPPLKQVKVPIENHICDAKYLHGLGAYTGDVIRVDDML 184
 DB 151 PGMPCWVTGWDVNDERLPPFPPLKQVKVPIENHICDAKYLHGLGAYTGDVIRVDDML 210
 QY 185 CAGNTRRDSQGGSGGGLVCKVNGTWTQAGVSWGEGCAQPNRPGIYTRVYLDWIHY 244
 DB 211 CAGNTRRDSQGGSGGGLVCKVNGTWTQAGVSWGEGCAQPNRPGIYTRVYLDWIHY 270
 QY 245 VPKKP 249
 DB 271 VPKKP 275
 RESULT 2
 TRBL_HUMAN STANDARD; PRT; 275 AA.
 AC Q15661; Q15663; Q9H2Y4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2003 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tryptase beta-1 precursor (EC 3.4.21.59) (Tryptase 1) (Tryptase I).
 GN TPST1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90251647; PubMed=2187193;
 RA Vanderslice P., Ballinger S.M., Tam E.K., Goldstein S.M., Craik C.S.,
 RA Caughey G.H.;
 RT "Human mast cell tryptase: multiple cDNAs and genes reveal a multigene
 RT serine protease family";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3811-3815 (1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99121069; PubMed=9920877;
 RA Pallaro M., Fejzo M.S., Shavesteh L., Blount J.L., Caughey G.H.;
 RT "Characterization of genes encoding known and novel human mast cell
 RT tryptases on chromosome 16p13.3";

```

RL J. Biol. Chem. 274:3355-3362(1999).
RN [3]
RP SEQUENCE OF 54-275 FROM N.A. (ISOFORM 2).
RA Wang H.W., McNeil H.P., Thomas P.S., Murphy B.N., Webster M.J.,
RA Hettiaratchi A., King G., Heywood G.J., Huang C., Stevens R.L.,
RA Hunt J.E.;
RT "Molecular cloning and characterization of novel human tryptase cDNAs
RL and splicing variants.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Tryptase is the major neutral protease present in mast
CC cells and is secreted upon the coupled activation-degranulation
CC response of this cell type.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC with more restricted specificity than trypsin.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Released from the secretory granules upon
CC mast cell activation.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q15661-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q15661-2; Sequence=VSP_005375;
CC -!- SIMILARITY: Belongs to peptidase family S1. Tryptase subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; M33494; AAC83172.1; -.
CC EMBL; M33491; AAA36778.1; -.
CC EMBL; AF099144; AAD17860.1; -.
CC EMBL; AF206667; AAG35697.1; -.
CC PIR; A35863; A35863.
CC HSSP; P20231; LAOL.
CC MEROPS; S01.242; -.
CC Genew; HGNC:12019; TPSSL1.
CC MIN; 191081; -.
CC InterPro; IPR009003; Cys Ser trypsin.
CC InterPro; IPR001254; Peptidase S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00089; trypsin, 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PROSITE; PS50240; TRYPsin_DOM; 1.
CC PROSITE; PS00134; TRYPsin_HIS; 1.
CC PROSITE; PS00135; TRYPsin_SER; 1.
CC Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
KW Alternative splicing; Polymorphism.
FT SIGNAL 1 18
FT PROPEP 19 30 ACTIVATION PEPTIDE (BY SIMILARITY).
FT CHAIN 31 275 TRYPTASE BETA-1.
FT ACT_SITE 74 74 CHARGE RELAY SYSTEM.
FT ACT_SITE 121 121 CHARGE RELAY SYSTEM.
FT ACT_SITE 224 224 CHARGE RELAY SYSTEM.
FT DISULFID 59 75 BY SIMILARITY.
FT DISULFID 155 230 BY SIMILARITY.
FT DISULFID 188 211 BY SIMILARITY.
FT DISULFID 220 248 BY SIMILARITY.
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPIC 79 87 Missing (in isoform 2).
FT VARIANT 18 18 A -> V (in dbSNP:1800984).
FT VARIANT 23 23 G -> V (in dbSNP:1800986).
FT VARIANT 85 85 A -> T (in dbSNP:2234902).
FT VARIANT 132 132 N -> K (in dbSNP:1800991).

```

```

FT VARIANT 141 141 /FTid=VAR_016102.
FT T -> A (in dbSNP:1800992).
FT /FTid=VAR_014560.
FT D -> N (in dbSNP:2234641).
FT /FTid=VAR_014561.
FT P -> S (in dbSNP:2234904).
FT /FTid=VAR_014562.
FT T -> S (in dbSNP:2234905).
FT /FTid=VAR_014563.
FT R -> Q (in dbSNP:2234906).
FT /FTid=VAR_014564.
SQ SEQUENCE 275 AA; 30515 MW; ADC48FDC51F37112 CRC64;
Query Match 97.8%; Score 1363; DB 1; Length 275;
Best Local Similarity 99.2%; Pred. No. 7.4e-118;
Matches 243; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 IVGGQAPRSKWPQVSLRVHGPYMMHFCGSLIHPQVLTAAACVGPDPVXDLAALRVQL 64
DB 31 IVGGQAPRSKWPQVSLRVHGPYMMHFCGSLIHPQVLTAAHCVGPDVXDLAALRVQL 90
QY 65 REQLHYQDQLLPVSRRIIVHPQFYTAIGADIALLELEPEPVKVVSHVTVTLPPASETFP 124
DB 91 REQLHYQDQLLPVSRRIIVHPQFYTAIGADIALLELEPEPVVSVSHVTVTLPPASETFP 150
QY 125 PGMPCWVTGWGDVNDERLPPPEPLKQVKVPIMENHICDAKYHLGAYTGGDDVIRVDOML 184
DB 151 PGMPCWVTGWGDVNDERLPPPEPLKQVKVPIMENHICDAKYHLGAYTGGDDVIRVDOML 210
QY 185 CAGNTRRDSQCGSGGPLVCKVNGTWTQAGVYVSVGEGCAQPNRFGIYTRVYVYLDWIHY 244
DB 211 CAGNTRRDSQCGSGGPLVCKVNGTWTQAGVYVSVGEGCAQPNRFGIYTRVYVYLDWIHY 270
QY 245 VPKKP 249
DB 271 VPKKP 275
RESULT 3
TRYNA HUMAN
ID TRYNA_HUMAN STANDARD; PRT; 275 AA.
AC P15157; Q9H2Y5; Q9UQ11;
DT 01-APR-1990 (Rel. 14, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-tryptase precursor (EC 3.4.21.59) (trypsin 1).
GN TPS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Lung;
RX MEDLINE=90009311; PubMed=2677049;
RA Miller J.S., Westin E.H., Schwartz L.B.;
RT "Cloning and characterization of complementary DNA for human
RT tryptase.";
RL J. Clin. Invest. 84:1188-1195(1989).
RN [2]
RP REVISIONS TO 89-93 AND 108.
RA Schwartz L.B.;
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99121069; PubMed=9920877;
RA Pallaro M., Fejzo M.S., Shavesteh L., Blount J.L., Caughey G.H.;
RT "Characterization of genes encoding known and novel human mast cell
RL tryptases on chromosome 16p13.3.";
RN J. Biol. Chem. 274:3355-3362(1999).
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Lung;

```

RA Wang H.W., McNeil H.P., Thomas P.S., Murphy B.N., Webster M.J.,
RA Hettiaratchi A., King G., Heywood G.J., Huang C., Stevens R.L.,
RA Hunt J.E.;
RT "Molecular cloning and characterization of novel human trypsin cDNAs
and splicing variants.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 31-50, AND PITUITARY, SEQUENCE OF 31-38.
RC TISSUE=Lung;
RX MEDLINE=97109258; PubMed=3543004;
RA Cromlish J.A., Seidah N.G., Marcinkiewicz M., Hamelin J., Johnson D.A.,
RA Chretien M.;
RT "Human pituitary trypsin: molecular forms, NH2-terminal sequence,
RT immunocytochemical localization, and specificity with prohormone and
RT fluorogenic substrates";
RL J. Biol. Chem. 262:1363-1373 (1987).
CC -1- FUNCTION: Trypsin is the major neutral protease present in mast
CC cells and is secreted upon the coupled activation-degranulation
CC response of this cell type.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC with more restricted specificity than trypsin.
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Released from the secretory granules upon
CC mast cell activation.
CC -1- ALTERNATIVE PRODUCTS.
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P15157-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P15157-2; Sequence=VSP_005374;
CC -1- SIMILARITY: Belongs to peptidase family S1. Trypsin subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M30038; AAA86934.1; -;
DR EMBL; AF098328; AAD17846.1; -;
DR EMBL; AF206665; AAG35695.1; -;
DR EMBL; AF206666; AAG35696.1; -;
DR HSSP; P20231; 1A0L.
DR MEROPS; S01.015; -;
DR MEROPS; S01.143; -;
DR Genew; HGNC:12018; TPS1.
DR MIM; 191080; -;
DR GO; GO:0008236; F:serine-type peptidase activity; TAS.
DR GO; GO:0006952; P:defense response; TAS.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS0240; TRYPsin DOM; 1.
DR PROSITE; PS00134; TRYPsin HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
KW Polymorphism; Alternative splicing.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 30 ACTIVATION PEPTIDE.
FT CHAIN 31 275 ALPHA-TRYPTASE.
FT ACT_SITE 74 74 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 121 121 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 224 224 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 59 75 BY SIMILARITY.
FT DISULFID 155 230 BY SIMILARITY.
FT DISULFID 188 211 BY SIMILARITY.
FT DISULFID 220 248 BY SIMILARITY.
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 233 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT

FT VARSPLIC 79 87 Missing (in isoform 2).
FT FTID=VSP_005374.
FT VARIANT 15 15 R -> P (IN ALPHA-II).
FT FTID=VAR_012102.
FT VARIANT 221 221 K -> Q (IN ALPHA-II; dbSNP:1137382).
FT CONFLICT 215 216 FTID=VAR_012103.
FT SQ SEQUENCE 275 AA; 30772 MW; B9BAC4BBCB9ICE75 CRC64;
Query Match 92.0%; Score 1282; DB 1; Length 275;
Best local Similarity 93.1%; Pred. No. 2e-110;
Matches 228; Conservative 4; Mismatches 13; Indels 0; Gaps 0;
QY 5 IVGGQAPRSPKWPQVSLRVHGVVWHFVCGSLHPOWLTAAACVGPDKDLAALRVQL 64
DB 31 IVGGQAPRSPKWPQVSLRVHGVVWHFVCGSLHPOWLTAAACVGPDKDLAALRVQL 90
QY 65 REGHLYYQDQLPVSRIIVHVPFYTAIGADIALLELEPEVKVSSHVHTVLPASTFP 124
DB 91 REGHLYYQDQLPVSRIIVHVPFYTAIGADIALLELEPEVKVSSHVHTVLPASTFP 150
QY 125 PGMPCVWTGWDVNDERLPPPLKQVKVPIVNHICDAKYHLGAYTGDVRIVRDML 184
DB 151 PGMPCVWTGWDVNDERLPPPLKQVKVPIVNHICDAKYHLGAYTGDVRIVRDML 210
QY 185 CAGNTRRDSQGDGGGGLVCKVNGTWLQAGVSWGEGCAQPNRPPIYTRYIYLDWIHY 244
DB 211 CAGNTRRDSQGDGGGGLVCKVNGTWLQAGVSWGEGCAQPNRPPIYTRYIYLDWIHY 270
QY 245 VPKKP 249
DB 271 VPKKP 275
RESULT 4
ID MCT6_MOUSE STANDARD; PRT; 276 AA.
AC P21845; Q61962;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mast cell protease 6 precursor (EC 3.4.21.59) (MMP-6) (Trypsase).
GN MCTP6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139682; PubMed=1995638;
RA Reynolds D.S., Gurley D.S., Austen K.F., Serafin W.E.;
RT "Cloning of the cDNA and gene of mouse mast cell protease-6.
RT Transcription by progenitor mast cells and mast cells of the
RT connective tissue subclass.";
RL J. Biol. Chem. 266:3847-3853 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Leaden X A1;
RC MEDLINE=94023807; PubMed=8210998;
RA Huang R., Abrik M., Gobl A.E., Nilsson G., Aveskog M., Larsson L.G.,
RA Nilsson K., Hellman L.;
RT "Expression of a mast cell tryptase in the human monocytic cell lines
RT U-937 and Mono Mac 6.";
RL Scand. J. Immunol. 38:359-367 (1993).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC STRAIN=Leaden X A1;
RX MEDLINE=95048582; PubMed=7959952;
RA Huang R., Hellman L.T.;
RT "Genes for mast-cell serine protease and their molecular evolution.";
RL Immunogenetics 40:397-414 (1994).
RN [4]
RP SEQUENCE OF 32-54.

```

RX MEDLINE=90222202; PubMed=2326280;
RA Reynolds D.S., Stevens R.L., Lane W.S., Carr M.H., Austen K.F.,
RA Serafin W.E.;
RT "Different mouse mast cell populations express various combinations
RT of at least six distinct mast cell serine proteases.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:3230-3234(1990).
CC -!- FUNCTION: Trypsin is the major neutral protease present in mast
CC cells and is secreted upon the coupled activation-degranulation
CC response of this cell type.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC with more restricted specificity than trypsin.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=P21845-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=P21845-2; Sequence=VSP_005376, VSP_005377;
CC Note=Probably non functional;
CC -!- SIMILARITY: Belongs to peptidase family S1. Trypsin subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M57626; AAA39988.1; -;
DR EMBL; M57625; AAA39987.1; -;
DR EMBL; L31853; AAA39725.1; -;
DR EMBL; X78542; CAA55288.1; -;
DR PIR; A38654; A38654;
DR PIR; I48685; I48685;
DR HSSP; P20231; IAAO.
DR MEROPS; S01.025; -.
DR MGD; MGI:96942; Mcpt6.
DR GO; GO:0008201; F:heparin binding; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0005515; F:trypsin binding; IPI.
DR GO; GO:0030019; F:trypsin activity; IDA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS02040; TRYP_SIN_DOM; 1.
DR PROSITE; PS00134; TRYP_SIN_HIS; 1.
DR PROSITE; PS00135; TRYP_SIN_SER; 1.
DR Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
KW Alternative splicing.
FT SIGNAL 1 21
FT PROPEP 22 31
FT CHAIN 32 276
FT ACT_SITE 75 75
FT ACT_SITE 122 122
FT ACT_SITE 225 225
FT ACT_SITE 225 225
FT DISULFID 60 76
FT DISULFID 156 231
FT DISULFID 189 212
FT DISULFID 221 249
FT CARBOHYD 133 133
FT VARSPPLIC 223 230
FT VARSPPLIC 231 276
FT Missing (in isoform Short).
FT /FTid=VSP_005377.
FT /FTid=VSP_005377.
SQ SEQUENCE 276 AA; 30927 MW; 525B2C9A0472200 CRC64;
Query Match 78.3%; Score 1091; DB 1; Length 276;
Best Local Similarity 78.2%; Pred. No. 7e-93;
Matches 190; Conservative 19; Mismatches 34; Indels 0; Gaps 0;

```

```

Db 32 IVGHEASESKWPMQVSLRFLKNTWIHFQCGSLHPQWLTAACVGHPIKSPQLFRVOL 91
Qy 65 REQHLXYQDQLLPVSRIRIIVHPQFYTAQIGADIALLELEPVPKVSHTVTLPPASSETFP 124
Db 92 REQLYLYGQDQLLSLNRIVVHPHYTATGGADVALLEVPVNVSTHPIHPIPLPASETFP 151
Qy 125 PGMECWWTGWDVNDRLPPPLKQVKVPIPMENHICDAKYHLGAYTGDVRIVRDDML 184
Db 152 PGTSCWWTGWDIDNDRLPPPLKQVKVPIPMENHICDAKYHLGAYTGDVRIVRDDML 211
Qy 185 CAGNTRRDSQCGSDGGLPVCKVNGTWTQAGVVSWGEGCAQENRPGIYTRVYYLDWIHY 244
Db 212 CAGNTRRDSQCGSDGGLPVCKVNGTWTQAGVVSWGEGCAQENRPGIYTRVYYLDWIHY 271
Qy 245 VPK 247
Db 272 VPE 274

RESULT 5
TRYPT CANFA
ID TRYPT CANFA STANDARD; PRT; 275 AA.
AC P15944;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Trypsin precursor (EC 3.4.21.59).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89352460; PubMed=2504277;
RA Vanderslice P., Craik C.S., Nadel J.A., Caughey G.H.;
RT "Molecular cloning of dog mast cell trypsin and a related protease:
RT structural evidence of a unique mode of serine protease activation.";
RL Biochemistry 28:4148-4155(1989).
CC -!- FUNCTION: Trypsin is the major neutral protease present in mast
CC cells and is secreted upon the coupled activation-degranulation
CC response of this cell type.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC with more restricted specificity than trypsin.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Released from the secretory granules upon
CC mast cell activation.
CC -!- SIMILARITY: Belongs to peptidase family S1. Trypsin subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M24664; AAA30854.1; -;
DR PIR; A32410; A32410.
DR HSSP; P20231; IAAO.
DR MEROPS; S01.143; -.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS02040; TRYP_SIN_DOM; 1.
DR PROSITE; PS00134; TRYP_SIN_HIS; 1.
DR PROSITE; PS00135; TRYP_SIN_SER; 1.
DR Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen.
FT SIGNAL 1 20
FT PROPEP 21 30
FT ACTIVATION PEPTIDE (BY SIMILARITY).

```



```

FT CHAIN 31 275 TRYPTASE.
FT ACT_SITE 74 74 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 121 121 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 224 224 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 59 75 BY SIMILARITY.
FT DISULFID 155 230 BY SIMILARITY.
FT DISULFID 188 211 BY SIMILARITY.
FT DISULFID 220 248 BY SIMILARITY.
FT CARBOHYD 132 132 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 275 AA; 30088 MW; C3B869251P248D5B CRC64;

Query Match 77.3%; Score 1077; DB 1; Length 275;
Best Local Similarity 77.1%; Pred. No. 1.3e-91;
Matches 189; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

QY 5 IVGGQAPRKPQVSLRVHVPYMHFCGSLHPQWLTAACVGPVYKDLAALRVQL 64
DB 31 IVGGQAPRKPQVSLRVHVPYMHFCGSLHPQWLTAACVGPVYKDLAALRVQL 90
QY 65 REQHLYQDQLLPVSRIVHPQYTAQIGADIALLELEPKVSSHVHTVTLPPASSTFP 124
DB 91 REQHLYQDQLLPVSRIVHPQYTAQIGADIALLELEPKVSSHVHTVTLPPASSTFP 150
QY 125 PGMPCWVTGMDVNDRLPPPLKQVKVPIENHICDAKYHLGAYTGDVIRVDDML 184
DB 151 TGTPTCWTGMDVNDRLPPPLKQVKVPIENHICDAKYHLGAYTGDVIRVDDML 210
QY 185 CAGNTRDSCQSGGGLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVYLDWIHY 244
DB 211 CAGNTRDSCQSGGGLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVYLDWIHY 270
QY 245 VPKEP 249
DB 271 VPKEP 275

RESULT 6
TRYPTASE
ID TRYPTASE STANDARD; PRT; 270 AA.
AC P50342;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Mast cell tryptase precursor (EC 3.4.21.59)
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGS/SEA; TISSUE=Intestine;
RX MEDLINE=95366971; PubMed=7639711;
RA Murakumo Y., Ide H., Itoh H., Tomita M., Kobayashi T.,
RA Maruyama H., Horii Y., Nawa Y.;
RT "Cloning of the cDNA encoding mast cell tryptase of Mongolian gerbil,
RT Meriones unguiculatus, and its preferential expression in the
RT intestinal mucosa.";
RL Biochem. J. 309:921-926(1995).
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC with more restricted specificity than trypsin.
CC -1- SIMILARITY: Belongs to peptidase family S1. Trypsin subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D31789; BAA06598.1; -
DR PIR; S56160; S56160.

```

```

DR HSSP; P20231; IAAO.
DR MEROPS; S01.143; -.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS02040; TRYPsin DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Hydrolase; Serine protease; Signal; Glycoprotein.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 270 MAST CELL TRYPTASE.
FT ACT_SITE 69 69 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 116 116 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 219 219 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 54 70 BY SIMILARITY.
FT DISULFID 150 225 BY SIMILARITY.
FT DISULFID 183 206 BY SIMILARITY.
FT DISULFID 215 243 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 127 127 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 270 AA; 30166 MW; 1BE102DB86943401 CRC64;

Query Match 77.2%; Score 1075; DB 1; Length 270;
Best Local Similarity 77.4%; Pred. No. 2e-91;
Matches 188; Conservative 18; Mismatches 37; Indels 0; Gaps 0;

QY 5 IVGGQAPRKPQVSLRVHVPYMHFCGSLHPQWLTAACVGPVYKDLAALRVQL 64
DB 26 IVGGQAPRKPQVSLRVHVPYMHFCGSLHPQWLTAACVGPVYKDLAALRVQL 85
QY 65 REQHLYQDQLLPVSRIVHPQYTAQIGADIALLELEPKVSSHVHTVTLPPASSTFP 124
DB 86 REQHLYQDQLLPVSRIVHPQYTAQIGADIALLELEPKVSSHVHTVTLPPASSTFP 145
QY 125 PGMPCWVTGMDVNDRLPPPLKQVKVPIENHICDAKYHLGAYTGDVIRVDDML 184
DB 146 SGTLCWVTGMDVNDRLPPPLKQVKVPIENHICDAKYHLGAYTGDVIRVDDML 205
QY 185 CAGNTRDSCQSGGGLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVYLDWIHY 244
DB 206 CAGNTRDSCQSGGGLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVYLDWIHY 265
QY 245 VPK 247
DB 266 VPK 268

RESULT 7
MCT7 MOUSE
ID MCT7_MOUSE STANDARD; PRT; 273 AA.
AC Q02844;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mast cell protease 7 precursor (EC 3.4.21.59) (WMP-7) (Trypsin).
GN MCT7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DEA/2;
RX MEDLINE=93087489; PubMed=1454796;
RA McNeil H.P., Reynolds D.S., Schiller V., Gildyal N., Gurley D.S.,
RA Austen K.F., Stevens R.L.;
RT "Isolation, characterization, and transcription of the gene encoding
RT mouse mast cell protease 7.";
RT Proc. Natl. Acad. Sci. U.S.A. 89:11174-11178(1992).

```



```

[2]
SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=C57BL/6J;
RX MEDLINE=96162033; PubMed=8576265;
RA Hunt J.E., Stevens R.L., Austen K.F., Zhang J., Xia Z.,
RA Gildyal N.;
RT "Natural disruption of the mouse mast cell protease 7 gene in the
RT C57BL/6 mouse."
RL J. Biol. Chem. 271:2851-2855(1996).
CC -!- FUNCTION: Trypsin is the major neutral protease present in mast
CC cells and is secreted upon the coupled activation-degranulation
CC response of this cell type.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC with more restricted specificity than trypsin.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Comment=The alternative splicing event is due to a G to A point
CC mutation at the exon 2/intron 2 splice site and causes loss of
CC protein expression. The alternatively spliced transcript is only
CC found in C57BL/6 mouse;
CC Name=1;
CC IsoId=Q02844-1; Sequence=Displayed;
CC Name=2; Synonyms=truncated;
CC IsoId=Q02844-2; Sequence=VSP_005378, VSP_005379;
CC -!- DEVELOPMENTAL STAGE: Is not expressed in mature serosal or mucosal
CC mast cells and is expressed only transiently at an early stage of
CC in vitro mast cell differentiation.
CC -!- SIMILARITY: Belongs to peptidase family S1. Trypsin subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L00654; AAA39993.1; -
CC EMBL; L00653; AAA39992.1; -
CC EMBL; U42405; AAA97874.1; -
CC EMBL; U42406; AAA97875.1; -
CC PIR; A47246; A47246.
CC HSP; P20231; IAAO.
CC MEROPS; S01.026; -.
CC MGD; MGI:96943; Mcpt7.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Glycolase; Serine protease; Signal; Zymogen; Alternative splicing;
KW Glycoprotein.
FT SIGNAL 1 18
FT PROPEP 19 28
FT CHAIN 29 273
FT ACT_SITE 72 72
FT ACT_SITE 119 119
FT ACT_SITE 222 222
FT ACT_SITE 222 222
FT DISULFID 57 73
FT DISULFID 153 228
FT DISULFID 186 209
FT DISULFID 218 246
FT CARBOHYD 49 49
FT CARBOHYD 130 130
FT VARSPIC 44 46
FT VARSPIC 47 273
FT SEQUENCE 273 AA; 30337 MW; 50BCB4765294205E CRC64;
SQ

```

```

Query Match 75.7%; Score 1054; DB 1; Length 273;
Best Local Similarity 76.5%; Pred. No. 1.7e-89;
Matches 186; Conservative 17; Mismatches 40; Indels 0; Gaps 0;
Oy 5 IVGGQEPKRPKWPQVSRVHGPVYMHFCGSLHHPQWVLTAAACVGPDPVKDLAALRVQL 64
Db 29 IVGGQEPKRPKWPQVSRVHGPVYMHFCGSLHHPQWVLTAAACVGPDPVKDLAALRVQL 88
Oy 65 REQLHYQDQLLPVSRIVHPOFTTAQIGADIALLELEPVPKVVSHVHTVLPASSTFP 124
Db 89 RKQYLYHDLMTVSQITTHPDFIVQDGDIALKLTNPVNI SDYVHPVPLPASETFP 148
Oy 125 PGMPQWTVGMDVNDRLPPLPKVQVPMENHICDAKYHLGAYTGDDVIRVDDML 184
Db 149 SGTLCWTVGMDVNDRLPPLPKVQVPMENHICDAKYHLGAYTGDDVIRVDDML 208
Oy 185 CAGNTRDSCQDGGPLVCKVNGTWTQAGVSVWGEGCAQNRFGIYTRVYYLDWIHY 244
Db 209 CAGNEGHDSQDGGPLVCKVNGTWTQAGVSVWGEGCAQNRFGIYTRVYYLDWIHY 268
Oy 245 VPK 247
Db 269 VPK 271
RESULT 8
MCT6_RAT MCT6_RAT STANDARD; PRT; 274 AA.
ID P50343; P97593; AC P50343;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mast cell protease 6 precursor (EC 3.4.21.59) (RMCP-6) (Trypsin).
GN MCPT6 OR MCP6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peritoneal mast cells;
RX MEDLINE=96015171; PubMed=8537314;
RA Ide H., Itoh H., Tomita M., Murakumo Y., Kobayashi T.,
RA Maruyama H., Osada Y., Nawa Y.;
RT "cDNA sequencing and expression of rat mast cell trypsinase.";
RL J. Biochem. 118:210-215(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Peritoneal mast cells;
RX MEDLINE=97149430; PubMed=8996238;
RA Lutzelshwab C., Pejler G., Aveskogh M., Hellman L.;
RT "Secretory granule proteases in rat mast cells. Cloning of 10
RT different serine proteases and a carboxypeptidase A from various rat
RT mast cell populations.";
RL J. Exp. Med. 185:13-29(1997).
CC -!- FUNCTION: Trypsin is the major neutral protease present in mast
CC cells and is secreted upon the coupled activation-degranulation
CC response of this cell type.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC with more restricted specificity than trypsin.
CC -!- SIMILARITY: Belongs to peptidase family S1. Trypsin subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D38455; BAA07486.1; -
CC EMBL; U67909; AAB48262.1; -
DR

```

```

DR PIR; JC4171; JC4171.
DR HSP; P20231; 1AAO.
DR MEROPS; S01.025; -.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00240; TRYPsin DOM; 1.
DR PROSITE; PS00134; TRYPsin HIS; 1.
DR PROSITE; PS00135; TRYPsin SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Multigene family;
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 29 ACTIVATION PEPTIDE.
FT CHAIN 30 274 MAST CELL PROTEASE 6.
FT ACT_SITE 73 73 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 120 120 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 223 223 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 223 223 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 58 74 BY SIMILARITY.
FT DISULFID 154 229 BY SIMILARITY.
FT DISULFID 187 210 BY SIMILARITY.
FT DISULFID 219 247 BY SIMILARITY.
FT CARBOHYD 104 104 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CONFLICT 128 128 I -> N (IN REF. 2).
FT CONFLICT 139 139 I -> T (IN REF. 2).
SQ SEQUENCE 274 AA; 30508 MW; DF84D55668CA1A25 CRC64;

Query Match 75.4%; Score 1051; DB 1; Length 274;
Best Local Similarity 75.8%; Pred. No. 3.3e-89;
Matches 185; Conservative 21; Mismatches 38; Indels 0; Gaps 0;

QY 5 IVGGQAPRSGKWPQVSLRVHGPVMMHFCGSLHPQWLTAACVGDVKKDLAALRVQL 64
DB 30 IVGGRASESKNPQVSLRVHGPVMMHFCGSLHPQWLTAACVGDVKKDLAALRVQL 89
QY 65 REQLYYQDQLPVSRILVHPQYTAQIGADIALLEELPEPKVSSHVHTVTLPPASTFP 124
DB 90 REQLYYQDQLPVSRILVHPQYTAQIGADIALLEELPEPKVSSHVHTVTLPPASTFP 149
QY 125 PGVPCVWTCGVNDVNDRLPPPLKQVYPIMENHICDAKYLHGLGATGDDVIRVDDML 184
DB 150 SGTSCWVTGMDIDSDPEPLPPVLPKQVYPIMENHICDAKYLHGLGATGDDVIRVDDML 209
QY 185 CAGNTRSDSCQGSGLGGLVCKVGTWLVQAGVSWGEGCAENRPGIYTRYVYLDWTHY 244
DB 210 CAGNTRSDSCQGSGLGGLVCKVGTWLVQAGVSWGEGCAENRPGIYTRYVYLDWTHY 269
QY 245 VPKK 248
DB 270 VPQR 273

RESULT 9
MCIT7_RAT STANDARD; PRT; 273 AA.
AC P27435; P27436;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE MAST cell protease 7 precursor (EC 3.4.21.59) (RMCP-7) (Trypsin,
DE skin).
GN MCP7 OR MCP7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97149430; PubMed=8996238;
RA Lutzelschwab C., Pejler G., Aveskog M., Hellman L.;

```

```

RT "Secretory granule proteases in rat mast cells. Cloning of 10
RT different serine proteases and a carboxypeptidase A from various rat
RT mast cell populations."
RL J. Exp. Med. 185:13-29(1997).
RN [2]
RP SEQUENCE OF 29-53.
RC STRAIN=Sprague-Dawley; TISSUE=Skin;
RX MEDLINE=91242400; PubMed=2036367;
RA Braganza V.J., Simmons W.H.;
RT "Trypsin from rat skin: purification and properties.";
RL Biochemistry 30:4997-5007(1991).
RN [3]
RP SEQUENCE OF 29-51.
RC TISSUE=Breast carcinoma;
RX MEDLINE=92231826; PubMed=1314562;
RA Eto I., Grubbs C.J.;
RT "Separation, purification and N-terminal sequence analysis of a novel
RT leupeptin-sensitive serine endopeptidase present in chemically
RT induced rat mammary tumour.";
RL Biochem. J. 283:209-216(1992).
CC -!- FUNCTION: Trypsin is the major neutral protease present in mast
CC cells and is secreted upon the coupled activation-degranulation
CC response of this cell type.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC with more restricted specificity than trypsin.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Released from the secretory granules upon
CC mast cell activation.
CC -!- TISSUE SPECIFICITY: Mast cells.
CC -!- FMW: Glycosylated (Probable).
CC -!- SIMILARITY: Belongs to peptidase family S1. Trypsin subfamily.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
DR EMBL; U67910; AAB48263.1; -.
DR PIR; A23698; A23698.
DR PIR; S21275; S21275.
DR HSP; P20231; 1AAO.
DR MEROPS; S01.026; -.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp SPC; 1.
DR PROSITE; PS00240; TRYPsin DOM; 1.
DR PROSITE; PS00134; TRYPsin HIS; 1.
DR PROSITE; PS00135; TRYPsin SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
KW Multigene family.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 28 ACTIVATION PEPTIDE.
FT CHAIN 29 273 MAST CELL PROTEASE 7.
FT ACT_SITE 72 72 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 119 119 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 222 222 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 57 73 BY SIMILARITY.
FT DISULFID 153 228 BY SIMILARITY.
FT DISULFID 186 209 BY SIMILARITY.
FT DISULFID 218 246 BY SIMILARITY.
FT CARBOHYD 49 49 N-LINKED (GLCNAC... ) (PROBABLE).
FT CONFLICT 42 42 W -> V (IN REF. 3).
FT CONFLICT 49 51 NDT -> WLP (IN REF. 3).
SQ SEQUENCE 273 AA; 30400 MW; 65A5ED4D279FB284 CRC64;

Query Match 74.4%; Score 1037; DB 1; Length 273;

```

Query Match 73.9%; Score 1030; DB 1; Length 273;
Best Local Similarity 73.1%; Pred. No. 2.8e-87;
Matches 179; Conservative 27; Mismatches 39; Indels 0; Gaps 0;

Dd	29	IIGGKEAPSGRMPQVSLVRVDQYWRHQCGGSLIHPQWLTAAHCTIGPELQBPSPDFRVCE
Qy	65	RQQLHYIQDQLLPYSRIIVHPOFYTAOIGADIALLELRPVKVSSSHVTWTLPPASETH
Dd	89	RQQLHYIQDRLLPSRVLPHPHYTWENGADIALQLLEPVSISRHVQPVTLPPLASETH
Qy	125	PQPCQWTVTGWGDVNDERLPPFPFLKQVKVIPMENHICDAKYHLGAYTGDDVRIVRDDMD
Dd	149	PSSCQWTVTGWGDVNGRELPPPYELKQVKPIVENSCDKYHSGLSTDYSVPVIQEDN
Qy	185	CAGNTRRDSOCGSDGGPLVCVKNGTWLQAQVSWGSGCAQPNRPGIYTRVYYLDWIHH
Dd	209	CAGDGRRDSCQSDGGPLVCVKNGTWLQAQVSWGSGCAQPNRPGIYTRITSYLDWIHQ
Qy	245	VPKKP 249 ::
Dd	269	VQEP 273 ::
RESULT 11		
TRYPT_PIG STANDARD; PRT; 275 AA.		
AC	Q9N2DI;	
ID	TRYPT_PIG	
DT	16-OCT-2001 (Rel. 40, Created)	
DE	16-OCT-2001 (Rel. 40, Last sequence update)	
DE	28-FEB-2003 (Rel. 41, Last annotation update)	
DE	Tryptase precursor [EC 3.4.21.59].	
GN	MCT7.	
OS	Sus scrofa (Pig).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OX	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	
NCBI_TaxID=9823;	[1]	
RN	SEQUENCE FROM N.A.	
RP	TISSUE=Lung;	
RC	MEDLINE=20285343; PubMed=10824103;	
RX	Chen Y., Shiota M., Ohuchi M., Towatari T., Tashiro J., Murakami M.,	
RA	Yano M., Yang B., Kido H.:	
RA	"Mast cell tryptase from pig lungs triggers infection by pneumotropic	
RT	Sendai and influenza A viruses. Purification and characterization."	
RL	Eur. J. Biochem. 267:3189-3197(2000).	
CC	-!- FUNCTION: Tryptase is the major neutral protease present in mast	
CC	cells and is secreted upon the coupled activation-degranulation	
CC	response of this cell type.	
CC	-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg - - , Lys - - , but	
CC	with more restricted specificity than trypsin.	
CC	-!- SUBUNIT: Homotetramer (By similarity).	
CC	-!- SUBCELLULAR LOCATION: Released from the secretory granules upon	
CC	mast cell activation	

```
CC --!- SIMILARITY: Belongs to peptidase family S1. Trypsin subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB038652; BAA93614.1; -.
DR HSP; P20231; IAAO.
DR MEROPS; S01.143; -.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen.
FT SIGNAL 1 30
FT PROPEP 21 30 ACTIVATION PEPTIDE (BY SIMILARITY).
FT CHAIN 31 275
FT ACT_SITE 74 74 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 121 121 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 224 224 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 59 75 BY SIMILARITY.
FT DISULFID 155 230 BY SIMILARITY.
FT DISULFID 188 211 BY SIMILARITY.
FT DISULFID 220 248 BY SIMILARITY.
FT CARBOHYD 132 132 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 275 AA; 30439 MW; ACC582647FCCB973 CRC64;
Query Match 72.2%; Score 1006; DB 1; Length 275;
Best Local Similarity 74.2%; Pred. No. 4.5e-85;
Matches 181; Conservative 20; Mismatches 43; Indels 0; Gaps 0;
QY 5 IVGGQAPRSKWPQVSLRVHGYVWHFCCGSLHPQWLTAACVGPVDKDAALRVQL 64
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
31 IVGGKAPGKWPQVSLRVHGYVWHFCCGSLHPQWLTAACVGPVDKDAALRVQL 90
QY 65 RECHLYYQDQLLVSRILVHPQVTAQIGADIALLELEPEVKVSSHVHTVTLPPASETFP 124
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
91 GECHLYYQDQLLVSRILVHPQVTAQIGADIALLELEPEVKVSSHVHTVTLPPASETFP 150
QY 125 PGMPWCWVGVDYNDRLPPPLKQVKVPIPMENHICDAKYHLGAYTGDDVIRVDDML 184
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
151 KGRFCWVTGWGVHSGWPLPPYPLKQVRVPIVENSECDMQYHLGLSTGDNIPVIRDDML 210
QY 185 CAGNTRRDCSGSGGLVCKVNGTWLQAGVSWGEGCAQNPBGIVTRYVYLDWTHY 244
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
211 CAGSEGHDCSGSGGLVCKVNGTWLQAGVSWGEGCALNRPBGIVTRYVYLDWTHY 270
QY 245 VPKK 248
Db ::::
271 IPRE 274
RESULT 12
TRYD_HUMAN STANDARD; PRT; 235 AA.
AC Q9BZJ3; Q9BZJ3; Q9BZJ3; Q9BZJ3; Q9BZJ3; Q9BZJ3; Q9BZJ3; Q9BZJ3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Trypsin delta precursor (EC 3.4.21.59) (Delta trypsinase) (Mast cell
DE mMCP-7-like) (hMCP-3-like trypsinase III).
GN TP5D1.
OS Homo sapiens (Human).
```

```
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
CC [1]
CC NCBI_TaxID=9606;
CC -----
CC SEQUENCE FROM N.A., AND VARIANTS ARG-15 AND MET-76.
CC MEDLINE=99121069; PubMed=9920877;
CC RA Pallaro M., Pejzo M.S., Shayesteh L., Blount J.L., Caughey G.H.;
CC "Characterization of genes encoding known and novel human mast cell
CC tryptases on chromosome 16p13.3";
CC J. Biol. Chem. 274:3355-3362(1999).
CC [2]
CC SEQUENCE FROM N.A.
CC MEDLINE=21101554; PubMed=11174199;
CC RA Min H.-K., Kambe N., Schwartz L.B.;
CC "Human mouse mast cell protease 7-like trypsin genes are
CC pseudogenes";
CC J. Allergy Clin. Immunol. 107:315-321(2001).
CC [3]
CC SEQUENCE FROM N.A.
CC MEDLINE=21096910; PubMed=11157797;
CC RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
CC Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
CC Higgs D.R.;
CC "Sequence, structure and pathology of the fully annotated terminal 2
CC Mb of the short arm of human chromosome 16.";
CC Hum. Mol. Genet. 10:339-352(2001).
CC [4]
CC SEQUENCE OF 33-235 FROM N.A. (ISOFORMS 1 AND 2), ENZYMATIC ACTIVITY,
CC TISSUE SPECIFICITY, AND VARIANT MET-76.
CC MEDLINE=22278650; PubMed=12391231;
CC RA Wang H.-W., McNeil H.P., Husein A., Liu K., Tedla N., Thomas P.S.,
CC Raftery M., King G.C., Cai Z.-Y., Hunt J.E.;
CC "Delta trypsinase is expressed in multiple human tissues, and a
CC recombinant form has proteolytic activity.";
CC J. Immunol. 169:5145-5152(2002).
CC --!- FUNCTION: trypsinase is the major neutral protease present in mast
CC cells and is secreted upon the coupled activation-degranulation
CC response of this cell type (By similarity).
CC --!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
CC with more restricted specificity than trypsin.
CC --!- SUBUNIT: Homotrimer (By similarity).
CC --!- SUBCELLULAR LOCATION: Released from the secretory granules upon
CC mast cell activation (By similarity).
CC --!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9BZJ3-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9BZJ3-2; Sequence=VSP_008319;
CC --!- TISSUE SPECIFICITY: Expressed in colon, lung, heart and synovial
CC tissue. May be specific to mast cells.
CC --!- SIMILARITY: Belongs to peptidase family S1. Trypsin subfamily.
CC --!- CAUTION: Although Ref.2 reported this as a pseudogene, Ref.4
CC showed it is expressed and has proteolytic activity when expressed
CC in bacterial cells.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF098327; AAD17845.1; ALT_INIT.
CC EMBL; AF099147; AAD17861.1; -.
CC EMBL; AF318074; AAK12909.1; -.
CC EMBL; AE006466; AAK61272.1; ALT_INIT.
CC EMBL; AF206664; AAG35694.1; -.
CC EMBL; AF421357; AAL86695.1; -.
CC EMBL; AY055427; AAL17874.1; -.
CC HSP; P20231; IAAO.
CC MEROPS; S01.054; -.
```

```

DR Genew; HGNC:14118; TPSP1.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Signal; Zymogen; Glycoprotein;
KW Alternative splicing; Polymorphism.
FT SIGNAL 1 18
FT PROPEP 19 30
FT CHAIN 31 235
FT ACT_SITE 74 74
FT ACT_SITE 121 121
FT ACT_SITE 224 224
FT DISULFID 59 75
FT DISULFID 155 230
FT DISULFID 188 211
FT CARBOHYD 132 132
FT VARSPLIC 79 87
FT VARIANT 15 15
FT VARIANT 18 18
FT VARIANT 76 76
FT CONFLICT 18 18
FT CONFLICT 171 171
SQ SEQUENCE 235 AA; 25816 MW; B1FF6C2A8006B22 CRC64;

Query Match 70.9%; Score 988; DB 1; Length 235;
Best local Similarity 84.4%; Pred. No. 1.7e-83;
Matches 173; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 5 IVGQEAAPRSKWPQVSLRVHGPYMHFCGSLIHPOWLVLTAAACVGPDKDLAALRVQL 64
DB 31 IVGQEAAPRSKWPQVSLRVHGPYMHFCGSLIHPOWLVLTAAACVGPDKDLAALRVQL 90
QY 65 REQLHYQDQLLPVSRIVVHPQFYTAQIGADIALLELEPEPVKVS SHVHTVLPASETFP 124
DB 91 REQLHYQDQLLPVSRIVVHPQFYIIQTGADIALLELEPEPVKVS SHVHTVLPASETFP 150
QY 125 PGMPCWVTGWGDVNDERLPPFPPLKQVKVPIPMENHICDAKYHGLGAYTGDDVRIVRDML 184
DB 151 PGMPCWVTGWGDVNDVNNVHLPFPPLKQVKVPIPMENHICDAKYHGLGAYTGDDVRIVRDML 210
QY 185 CAGNTRDSCQDGGGGLVCKVNGT 209
DB 211 CAGNTRDSCQDGGGGLVCKVNGT 235

RESULT 13
TRYM CANFA
ID TRYM CANFA STANDARD; PRT; 269 AA.
AC P19236;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mastocytoma protease precursor (EC 3.4.21.-).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RX MEDLINE=89352460; PubMed=2504277;
RA Vanderslice P., Craik C.S., Nadel J.A., Caughey G.H.;
RT "Molecular cloning of dog mast cell tryptase and a related protease;
RT structural evidence of a unique mode of serine protease activation.";
```

```

RL Biochemistry 28:4148-4155(1989).
CC -!- FUNCTION: Mast cell protease.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M24665; AAA30855.1; -.
CC PIR; B32410; B32410.
CC HSP; P00763; LDPO.
CC MEROPS; S01.145; -.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; FALSE NEG.
KW Hydrolase; Serine protease; Signal; Glycoprotein.
FT SIGNAL 1 19
FT CHAIN 20 269
FT ACT_SITE 66 66
FT ACT_SITE 116 116
FT ACT_SITE 217 217
FT DISULFID 51 67
FT DISULFID 150 223
FT DISULFID 183 204
FT DISULFID 213 241
FT CARBOHYD 95 95
FT CARBOHYD 106 106
SQ SEQUENCE 269 AA; 29824 MW; B4A4AF7B4E2FD4E5 CRC64;

Query Match 49.1%; Score 684.5; DB 1; Length 269;
Best local Similarity 52.6%; Pred. No. 1.4e-55;
Matches 132; Conservative 32; Mismatches 78; Indels 9; Gaps 4;

QY 5 IVGQEAAPRSKWPQVSLRVHGPYMHFCGSLIHPOWLVLTAAACVGPDKDLAALRVQL 61
DB 20 IVGCKVPARYPWQVSLRVHGPYMHFCGSLIHPOWLVLTAAACVGPDKDLAALRVQL 79
QY 62 VOLREQLHYQDQLLPVSRIVVHPQFYTAQIGADIALLELEPEPVKVS SHVHTVLP 118
DB 80 VQVQLRLYDHDQLCNVTEIIRHFNPNMWSWGWTDADIALLELEPEPVKVS SHVHTVLP 139
QY 119 ASETFPMPGMPCWVTGWGDVNDERLPPFPPLKQVKVPIPMENHICDAKYHGLGAYTGDDVRI 178
DB 140 PSLIVPEGMCLCWVTGWGDVNDERLPPFPPLKQVKVPIPMENHICDAKYHGLGAYTGDDVRI 197
QY 179 VRDMLCAGNTRDSCQDGGGGLVCKVNGT 209
DB 198 IKQDMLCAGSEGHDSQDGGGGLVCKVNGT 267
QY 239 DWIHHYVPEKPK 249
DB 257 SWIHOHPLSP 267

RESULT 14
TRYM MOUSE
ID TRYM MOUSE STANDARD; PRT; 311 AA.
AC Q30UL7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tryptase gamma precursor (EC 3.4.21.-) (Transmembrane tryptase).
GN TFSG1 OR TMT.
```

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv, and BALB/c;
 RX MEDLINE=99452974; PubMed=10521469;
 RA Wong G.W., Tang Y., Feyfant E., Sali A., Li L., Li Y., Huang C.,
 RA Friend D.S., Krilis S.A., Stevens R.L.;
 RT "Identification of a new member of the tryptase family of mouse and
 RT human mast cell proteases which possesses a novel COOH-terminal
 RT hydrophobic extension.";
 RL J. Biol. Chem. 274:30784-30793(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=2388257; PubMed=12477932;
 RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klauser R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeb B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Murny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnarch A., Schein J.E., Jones S.J.M., Warra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Membrane-anchored (Potential).
 CC -!- TISSUE SPECIFICITY: Expressed in many tissues.
 CC -!- SIMILARITY: Belongs to peptidase family S1. Tryptase subfamily.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AF175760; AAF03698.1; -.
 DR EMBL; AF175523; AAF03696.1; -.
 DR EMBL; BC052325; AAH52325.1; -.
 DR HSSP; P20231; 1AAO.
 DR MEROPS; S01.028; -.
 DR MGD; MGI:1349391; Tpsgl.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPsin.
 DR PROSITE; PS02440; TRYPsin DOM; 1.
 DR PROSITE; PS00134; TRYPsin HIS; 1.
 DR PROSITE; PS00135; TRYPsin SSR; FALSE NEG.
 KW Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
 KW Transmembrane.
 FT SIGNAL 1 16 POTENTIAL.
 FT CHAIN 17 28 TRYPTASE GAMMA LIGHT CHAIN.
 FT CHAIN 30 311 TRYPTASE GAMMA HEAVY CHAIN.
 FT TRANSMEM 277 297 POTENTIAL.
 FT ACT_SITE 70 70 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 117 117 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 214 214 CHARGE RELAY SYSTEM (BY SIMILARITY).

FT DISULFID 18 137 INTERCHAIN (POTENTIAL).
 FT DISULFID 55 71 BY SIMILARITY.
 FT DISULFID 151 220 BY SIMILARITY.
 FT DISULFID 184 202 BY SIMILARITY.
 FT DISULFID 210 238 BY SIMILARITY.
 FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 311 AA; 32656 MW; 7FC9D6FF6A2A8808 CRC64;
 Query Match 43.5%; Score 605.5; DB 1; Length 311;
 Best Local Similarity 48.6%; Pred. No. 3.1e-48;
 Matches 121; Conservative 31; Mismatches 78; Indels 19; Gaps 6;
 QY 4 RIVGGQEAAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWLTAACVGPDKDLAALRVQ 63
 DB 29 RIVGGHAAAGTWPQASLRHK---VHVGCSLLSPFWLTAACHFCGSVNS-SDYQVH 84
 QY 64 LREQHLYYQDQLLPVSRIRIVHPOFYTAQTG-----ADIALLELEEPKVSSHVHTLPP 118
 DB 85 LGELATVTLSPHFSTVKRIIM---YTGSPGPPGSGDIALVQLSSPVALSSQVPVCLPE 140
 QY 119 ASGTPPFGMPCWVTGWDVNDRLPPPLPKQVKPIMENHICDAKYHLGAYTGDDVRI 178
 DB 141 ASADFVPGMQCWVTGWTGTYGEGEPLAPPNLOEAKVSVVDVKTCSQ-----AIVNSPNSL 195
 QY 179 VRDDMLCAGNRDRSDCGSGGLVCKVNGTQWLAGVSWGEGCAQPNRPGIYTRYTYL 238
 DB 196 IQPDMLCARGP-GDACQDSDGGPLVCQVAGTWQAGVSWGEGCGRPRPGVYRTAYV 254
 QY 239 DWIHHVVPK 247
 DB 255 NWIHHIPE 263
 RESULT 15
 TRYGL HUMAN STANDARD; PRT; 321 AA.
 ID TRYGL HUMAN Q9NR02; Q9NR08; Q9UBB2;
 AC Q9NR02; Q9NR08; Q9UBB2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tryptase gamma precursor (EC 3.4.21.-) (Transmembrane tryptase).
 GN TPSG1 OR TMT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (VARIANTS GAMMA-1 AND GAMMA-2).
 RX MEDLINE=20302813; PubMed=10843716;
 RA Caughey G.H., Raymond W.W., Blount J.L., Hau L.W., Pallaro M.,
 RA Wolters P.J., Verghese G.M.;
 RT "Characterization of human gamma-tryptases, novel members of the
 RT chromosome 16p mast cell tryptase and prostatic gene families.";
 RL J. Immunol. 164:6566-6575(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99452974; PubMed=10521469;
 RA Wong G.W., Tang Y., Feyfant E., Sali A., Li L., Li Y., Huang C.,
 RA Friend D.S., Krilis S.A., Stevens R.L.;
 RT "Identification of a new member of the tryptase family of mouse and
 RT human mast cell proteases which possesses a novel COOH-terminal
 RT hydrophobic extension.";
 RL J. Biol. Chem. 274:30784-30793(1999).
 RN [3]
 RP SEQUENCE OF 220-321 FROM N.A.
 RA Mittman S., Agnew W.S.;
 RT "Organization and alternative splicing of CACNAH.";
 RL Submitted [JAN-2001] to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Membrane-anchored (Potential).
 CC -!- TISSUE SPECIFICITY: Expressed in many tissues.
 CC -!- POLYMORPHISM: There are two alleles; gamma-I and gamma-II which
 CC differ by 5 residues.

CC --!- SIMILARITY: Belongs to peptidase family S1. Trypsin subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; AF191031; AAF76457.1; -
DR EMBL; AF195508; AAF76458.1; -
DR EMBL; AF175759; AAF03697.1; -
DR EMBL; AF175522; AAF03695.1; -
DR EMBL; AF223563; AAG48852.2; -
DR HSP; P00763; LDPO.
DR MEROPS; S01.028; -
DR Genew; HGNC:14134; TPST1.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS00240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; FALSE NEG.
DR Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
KW Transmembrane; Polymorphism.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 36 TRYPTASE GAMMA LIGHT CHAIN.
FT CHAIN 38 321 TRYPTASE GAMMA HEAVY CHAIN.
FT TRANSMEM 284 304 POTENTIAL.
FT ACT_SITE 78 78 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 125 125 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 222 222 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 26 145 INTERCHAIN (POTENTIAL).
FT DISULFID 63 79 BY SIMILARITY.
FT DISULFID 159 228 BY SIMILARITY.
FT DISULFID 192 210 BY SIMILARITY.
FT DISULFID 218 246 BY SIMILARITY.
FT CARBOHYD 85 85 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARIANT 60 60 M -> V (IN GAMMA-II).
FT VARIANT 126 126 /FTID=VAR_012097.
FT VARIANT 132 132 I -> M (IN GAMMA-II).
FT VARIANT 204 204 S -> T (IN GAMMA-II).
FT VARIANT 288 288 /FTID=VAR_012099.
FT VARIANT 288 288 L -> I (IN GAMMA-II).
FT VARIANT 288 288 L -> F (IN GAMMA-II).
FT CONFLICT 160 160 /FTID=VAR_012101.
FT CONFLICT 321 AA; 33827 MW; PFF7B06E3C4A962D CRC64;
SQ SEQUENCE 321 AA; 33827 MW; PFF7B06E3C4A962D CRC64;

Query Match 42.6%; Score 593.5; DB 1; Length 321;
Best Local Similarity 48.8%; Pred. No. 4e-47;
Matches 119; Conservative 32; Mismatches 80; Indels 13; Gaps 6;
QY 4 RIVGGQAPRSKWPQVSLRVHGVYWHFCCGSLIHPQWVLTAAACVGPDKDLALRVQ 63
Db 37 RIVGGHAAPAGAPWQASLRLLR---MHVCGSLSPQWVLTAAHCFSGSLNS-SDYQVH 92
QY 64 LREQHLYYQQLLPVSRIVHPQFYTAQIG-ADIALLEELPEPVKSSHVHTVLTPEASE 121
Db 93 LGELEITLSPHFSIVRQIILHSS-PSGQPGTSGDIALVELSVPTLSRLPVCLEPSAD 151
QY 122 TFPFGMPCWVTGWGDVNDRELPPFPPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRD 181
Db 152 DFCFGIRCWVTGWYTRGEGPLPPYSLREVKSVVDTECRD-----YFGPGSILQP 206
QY 182 DMLCAGNTRDSCGDSGGPLVCKNGTWLQAGVSWGEGCAQPNRPGIYTRYLDWI 241
Db 207 DMLCARGP-GDACQDDSGGLVQVNGAWVQAGIVSWGEGCGRNPGRPGVTRVPAYVNI 265

QY 242 HHV 245
Db 266 RRHI 269

Search completed: July 22, 2004, 15:23:30
Job time : 54 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 22, 2004, 13:24:46 ; Search time 98 seconds
(without alignments)
717.901 Million cell updates/sec

Title: US-09-598-982-21
Perfect score: 1393
Sequence: 1 LEKIVGGQAPRSKWPQV.....IYTRVTYLDWIHHVVKP 249

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1393	100.0	249	5	AAU12009 Human bet
2	1388	99.6	249	5	AAU12017 Human bet
3	1387	99.6	249	3	AAU55011 Human bet
4	1387	99.6	249	5	AAU12007 Human bet
5	1384	99.4	249	5	AAU12011 Human bet
6	1384	99.4	249	5	AAU12012 Human bet
7	1382	99.2	249	5	AAU12006 Human bet
8	1379	99.0	249	5	AAU12020 Human bet
9	1379	99.0	249	5	AAU12010 Human bet
10	1379	99.0	249	5	AAU12019 Human bet
11	1374	98.6	245	5	AAU12013 Human bet
12	1374	98.6	245	5	AAU12018 Human bet
13	1369	98.3	245	5	AAU12021 Human bet
14	1368	98.2	245	5	AAU12008 Human bet
15	1368	98.2	274	2	AAW64240 Human mas
16	1368	98.2	274	2	AAW63175 Human mas
17	1365	98.0	245	5	AAU12016 Human bet
18	1365	98.0	245	5	AAU12015 Human bet
19	1363	97.8	245	3	AAU55010 Human bet
20	1363	97.8	245	5	AAU12005 Human bet
21	1363	97.8	273	2	AAW64238 Human mas
22	1363	97.8	273	2	AAW63174 Human mas
23	1361	97.7	244	2	AAU25925 Human lun
24	1360	97.6	245	5	AAU12014 Human bet
25	1360	97.6	245	5	AAU12023 Human bet

ALIGNMENTS

RESULT 1

AAU12009
ID AAU12009 standard; protein; 249 AA.

XX AC AAU12009;

XX DT 09-APR-2002 (first entry)

XX DE Human beta-II tryptase active site mutant H44A #1.

XX KW Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
XX OS enzyme; mutant; mutein.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200198470-A2.

XX PD 27-DEC-2001.

XX PF 20-JUN-2001; 2001WO-US019681.

XX PR 21-JUN-2000; 2000US-00598982.

XX PA (PROM-) PROMEGA CORP.

XX PI Maffit M, Niles AL, Haak-Frendscho M;

XX XX WPI; 2002-114578/15.

XX DR N-PSDB; AAS20775.

XX PT DNA construct for producing enzymatically-inactive proteolytic tryptase,
XX PT comprises DNA sequence encoding proteolytic tryptase having an active
XX PT site mutation.

XX PS Claim 8; Page 84-85; 126pp; English.

XX CC The present invention relates to recombinant human proteolytic tryptases,
XX CC active site mutants of these tryptases and the methods for producing
XX CC these. The method involves the production of a DNA expression construct
XX CC comprising a promoter operably linked to a secretion signal sequence
XX CC which is operably linked to a DNA sequence encoding a proteolytic
XX CC tryptase with an active site mutation (the construct drives expression of
XX CC a mature proteolytic tryptase that lacks enzymatic activity due to the
XX CC active site mutation, in hosts transformed to contain the construct). The
XX CC method is useful for producing enzymatically-active beta-II tryptase. The
XX CC active site mutants of proteolytic tryptase provide a tool to investigate
XX CC the structural and functional properties of the protease and its

enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic trypsin produced are useful as an antigen to generate anti-human trypsin antibodies and in drug screening for compounds which act as trypsin inhibitors, antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant human beta-II trypsin active site mutants

Sequence 249 AA;

Query Match 100.0%; Score 1393; DB 5; Length 249;
 Best Local Similarity 100.0%; Pred. No. 1e-122;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LEKRIVGQAPRSKWPQVSLRVHGPYWMHFGGSLIHPQWVLTAAACVGPDKDLAAL 60
 1 LEKRIVGQAPRSKWPQVSLRVHGPYWMHFGGSLIHPQWVLTAAACVGPDKDLAAL 60

61 RVQLRQHLVYQDQLLPVSRILVHGPYTAQIGADIALLELEPVPKVSHTVTLPPAS 120
 61 RVQLRQHLVYQDQLLPVSRILVHGPYTAQIGADIALLELEPVPKVSHTVTLPPAS 120

121 ETFFPGMPCWVTGWGDVNDRLPPPLKQVKVPIMENHICDAKYLHGYTGDDVIRV 180
 121 ETFFPGMPCWVTGWGDVNDRLPPPLKQVKVPIMENHICDAKYLHGYTGDDVIRV 180

181 DMCLCAGNTRDSCQDGGSLVCKNGTQLQAGVSWGEGCAQPNRPGLYTRVYYLDW 240
 181 DMCLCAGNTRDSCQDGGSLVCKNGTQLQAGVSWGEGCAQPNRPGLYTRVYYLDW 240

241 IHYVPPKKP 249
 241 IHYVPPKKP 249

RESULT 2
 AAU12017
 ID AAU12017 standard; protein; 249 AA.
 AC AAU12017;
 DT 09-APR-2002 (first entry)
 XX Human beta-II trypsin active site mutant H44A #3.
 XX Human; proteolytic trypsin; protease; recombinant beta-II trypsin;
 KW enzyme; mutant; mutin.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200198470-A2.
 XX 27-DEC-2001.
 XX 20-JUN-2001; 2001WO-US019681.
 XX 21-JUN-2000; 2000US-00598982.
 XX (PROM-) PROMEGA CORP.
 XX Maffitt M, Niles AL, Haak-Frendscho M;
 XX WPI; 2002-114578/15.
 XX N-PSDB; AAS20783.
 XX DNA construct for producing enzymatically-inactive proteolytic trypsin,
 PT comprises DNA sequence encoding proteolytic trypsin having an active
 PT site mutation.
 XX Claim 8; Page 105-106; 126pp; English.
 XX The present invention relates to recombinant human proteolytic trypsin,
 CC active site mutants of these trypsinases and the methods for producing

these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic trypsin with an active site mutation (the construct drives expression of a mature proteolytic trypsin that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II trypsin. The active site mutants of proteolytic trypsin provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic trypsin produced are useful as an antigen to generate anti-human trypsin antibodies and in drug screening for compounds which act as trypsin inhibitors, antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant human beta-II trypsin active site mutants

Sequence 249 AA;

Query Match 99.6%; Score 1388; DB 5; Length 249;
 Best Local Similarity 99.6%; Pred. No. 3e-122;
 Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 LEKRIVGQAPRSKWPQVSLRVHGPYWMHFGGSLIHPQWVLTAAACVGPDKDLAAL 60
 1 LEKRIVGQAPRSKWPQVSLRVHGPYWMHFGGSLIHPQWVLTAAACVGPDKDLAAL 60

61 RVQLRQHLVYQDQLLPVSRILVHGPYTAQIGADIALLELEPVPKVSHTVTLPPAS 120
 61 RVQLRQHLVYQDQLLPVSRILVHGPYTAQIGADIALLELEPVPKVSHTVTLPPAS 120

121 ETFFPGMPCWVTGWGDVNDRLPPPLKQVKVPIMENHICDAKYLHGYTGDDVIRV 180
 121 ETFFPGMPCWVTGWGDVNDRLPPPLKQVKVPIMENHICDAKYLHGYTGDDVIRV 180

181 DMCLCAGNTRDSCQDGGSLVCKNGTQLQAGVSWGEGCAQPNRPGLYTRVYYLDW 240
 181 DMCLCAGNTRDSCQDGGSLVCKNGTQLQAGVSWGEGCAQPNRPGLYTRVYYLDW 240

241 IHYVPPKKP 249
 241 IHYVPPKKP 249

RESULT 3
 AAY55011
 ID AAY55011 standard; protein; 249 AA.
 AC AAY55011;
 DT 18-FEB-2000 (first entry)
 XX Human beta-trypsin protein sequence.
 XX Beta-trypsin; human; DNA expression construct; protein production;
 KW combinatorial library screening; X ray crystallography; antigen;
 XX antibody generation.
 XX Homo sapiens.
 XX WO9960139-A1.
 XX 25-NOV-1999.
 XX 29-OCT-1998; 98WO-US022994.
 XX 15-MAY-1998; 98US-00079970.
 XX (PROM-) PROMEGA CORP.
 XX Maffitt MA, Niles AL, Haak-Frendscho M;
 XX WPI; 2000-053300/04.
 XX N-PSDB; AAZ40175.

XX New DNA expression construct for production of enzymatically active
PT recombinant human beta-tryptase.
XX
XX
PS Disclosure; Page 43-44; 50pp; English.
XX
CC This sequence is the human beta-tryptase. The invention relates to a DNA
CC expression construct comprising (5' to 3') a promoter linked to a signal
CC sequence which is linked to a sequence encoding human beta-tryptase. The
CC DNA construct is useful for transforming host cells to express, post
CC translationally process and secrete enzymatically active human tryptase.
CC The method is useful for the production of large amounts of tryptase with
CC defined specifications. The transformant is useful for pharmacological
CC studies, combinatorial library screens and X ray crystallographic
CC studies. The tryptase produced allows for the development of tryptase
CC agonists and/or antagonists, is useful as an antigen to generate
CC anti-human tryptase antibodies in various animals, can be used in
CC screening for compounds which act as tryptase inhibitors, antagonists,
CC agonists etc. and to assay for the presence of tryptase in biological
CC or other solutions. Tryptase inhibitors, antagonists, agonists etc. may be
CC useful as therapeutics. The tryptase does not require any post-expression
CC or post-purification modifications or manipulations to initiate tryptase
CC activity and it has enzymatic activity which compares favourably with
CC cadaveric tryptase. The availability of enzymatically active tryptase
CC facilitates the large scale screening of combinatorial libraries for
CC specific tryptase inhibitors as potential therapeutics and advances the
CC understanding of the biological significance of tryptase in mast cell
CC mediated diseases. The tryptase can be used to detect low levels of
CC tryptase
XX
XX Sequence 249 AA;
SQ
Query Match 99.6%; Score 1387; DB 3; Length 249;
Best Local Similarity 99.6%; Pred. No. 3.7e-122;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LEKRVGGQAPRSKWPQVSLRVHGPYMHFCGSLIHPQWVLTAAACVGPDKDLAAL 60
Db 1 LEKRVGGQAPRSKWPQVSLRVHGPYMHFCGSLIHPQWVLTAAACVGPDKDLAAL 60
Qy 61 RVQLREQHLYYQDQLLPVSRILVHPQFYTAQIGADIALLELEPVPKSSHVHTVTLPPAS 120
Db 61 RVQLREQHLYYQDQLLPVSRILVHPQFYTAQIGADIALLELEPVPKSSHVHTVTLPPAS 120
Qy 121 ETFFPGMPCWVTGWDVNDERLPPFPFLKQVKVPIIMENHICDAKYHLGAYTGDDVRI 180
Db 121 ETFFPGMPCWVTGWDVNDERLPPFPFLKQVKVPIIMENHICDAKYHLGAYTGDDVRI 180
Qy 181 DDMLCAGNTRRDSQGDGGPLVCKVNGTWLQAGVWSWEGCAQPNRPGIYTRYTYLDW 240
Db 181 DDMLCAGNTRRDSQGDGGPLVCKVNGTWLQAGVWSWEGCAQPNRPGIYTRYTYLDW 240
Qy 241 IHVYVPKKP 249
Db 241 IHVYVPKKP 249
RESULT 4
AAU12007
ID AAU12007 standard; protein; 249 AA.
XX AAU12007;
AC AAU12007;
XX
XX 09-APR-2002 (first entry)
DE Recombinant human beta-II tryptase.
XX Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW enzyme; mutein; mutant.
XX
XX Homo sapiens.
OS Synthetic.
XX

PN WO200198470-A2.
XX
PD 27-DEC-2001.
XX
PF 20-JUN-2001; 2001WO-US019681.
XX
PR 21-JUN-2000; 2000US-00598982.
XX
PA (PROM-) PROMEGA CORP.
XX
PI Maffit M, Niles AL, Haak-Frendscho M;
XX WPI; 2002-114578/15.
XX N-PSDB; AAS20765.
XX
PT DNA construct for producing enzymatically-inactive proteolytic tryptase,
PT comprises DNA sequence encoding proteolytic tryptase having an active
PT site mutation.
XX
PS Claim 60; Page 77-78; 126pp; English.
XX
CC The present invention relates to recombinant human proteolytic tryptases,
CC active site mutants of these tryptases and the methods for producing
CC these. The method involves the production of a DNA expression construct
CC comprising a promoter operably linked to a secretion signal sequence
CC which is operably linked to a DNA sequence encoding a proteolytic
CC tryptase with an active site mutation (the construct drives expression of
CC a mature proteolytic tryptase that lacks enzymatic activity due to the
CC active site mutation, in hosts transformed to contain the construct). The
CC method is useful for producing enzymatically-active beta-II tryptase. The
CC active site mutants of proteolytic tryptase provide a tool to investigate
CC the structural and functional properties of the protease and its
CC enzymatic activity, and for modelling studies. The enzymatically-active,
CC recombinant proteolytic tryptase produced are useful as an antigen to
CC generate anti-human tryptase antibodies and in drug screening for
CC compounds which act as tryptase inhibitors, antagonists, agonists, etc.
CC The present sequence represents recombinant human beta-II tryptase
XX
XX Sequence 249 AA;
SQ

Query Match 99.6%; Score 1387; DB 5; Length 249;
Best Local Similarity 99.6%; Pred. No. 3.7e-122;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LEKRVGGQAPRSKWPQVSLRVHGPYMHFCGSLIHPQWVLTAAACVGPDKDLAAL 60
Db 1 LEKRVGGQAPRSKWPQVSLRVHGPYMHFCGSLIHPQWVLTAAACVGPDKDLAAL 60
Qy 61 RVQLREQHLYYQDQLLPVSRILVHPQFYTAQIGADIALLELEPVPKSSHVHTVTLPPAS 120
Db 61 RVQLREQHLYYQDQLLPVSRILVHPQFYTAQIGADIALLELEPVPKSSHVHTVTLPPAS 120
Qy 121 ETFFPGMPCWVTGWDVNDERLPPFPFLKQVKVPIIMENHICDAKYHLGAYTGDDVRI 180
Db 121 ETFFPGMPCWVTGWDVNDERLPPFPFLKQVKVPIIMENHICDAKYHLGAYTGDDVRI 180
Qy 181 DDMLCAGNTRRDSQGDGGPLVCKVNGTWLQAGVWSWEGCAQPNRPGIYTRYTYLDW 240
Db 181 DDMLCAGNTRRDSQGDGGPLVCKVNGTWLQAGVWSWEGCAQPNRPGIYTRYTYLDW 240
Qy 241 IHVYVPKKP 249
Db 241 IHVYVPKKP 249
RESULT 5
AAU12011
ID AAU12011 standard; protein; 249 AA.
XX AAU12011;
AC AAU12011;
XX
XX 09-APR-2002 (first entry)
DT
XX

```
DE Human beta-II tryptase active site mutant S194A #1.
XX
XX
KW Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW enzyme; mutant; mutein.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200198470-A2.
XX
XX 27-DEC-2001.
XX
XX 20-JUN-2001; 2001WO-US019681.
XX
XX 21-JUN-2000; 2000US-00598982.
XX
XX (PROM-) PROMEGA CORP.
XX
XX Maffit M, Niles AL, Haak-Frendscho M;
XX
XX WPI; 2002-114578/15.
XX N-PSDB; AAS20777.
XX
XX DNA construct for producing enzymatically-inactive proteolytic tryptase,
XX comprises DNA sequence encoding proteolytic tryptase having an active
XX site mutation.
XX
XX Claim 8; Page 90-91; 126pp; English.
XX
XX The present invention relates to recombinant human proteolytic tryptases,
XX active site mutants of these tryptases and the methods for producing
XX these. The method involves the production of a DNA expression construct
XX comprising a promoter operably linked to a secretion signal sequence
XX which is operably linked to a DNA sequence encoding a proteolytic
XX tryptase with an active site mutation (the construct drives expression of
XX a mature proteolytic tryptase that lacks enzymatic activity due to the
XX active site mutation, in hosts transformed to contain the construct). The
XX method is useful for producing enzymatically-active beta-II tryptase. The
XX active site mutants of proteolytic tryptase provide a tool to investigate
XX the structural and functional properties of the protease and its
XX enzymatic activity, and for modelling studies. The enzymatically-active,
XX recombinant proteolytic tryptase produced are useful as an antigen to
XX generate anti-human tryptase antibodies and in drug screening for
XX compounds which act as tryptase inhibitors, antagonists, agonists, etc.
XX AAU12009-AAU12024 represent recombinant human beta-II tryptase active
XX site mutants
XX
XX Sequence 249 AA;
XX
XX Query Match 99.4%; Score 1384; DB 5; Length 249;
XX Best Local Similarity 99.2%; Pred. No. 7.1e-122;
XX Matches 247; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 LEKRVGQAEAPRSKWPQVSLRVHGPYMHFCGSLIHPQWVLTAAACVGPDKDLAAL 60
XX Db 1 LEKRVGQAEAPRSKWPQVSLRVHGPYMHFCGSLIHPQWVLTAAACVGPDKDLAAL 60
XX
XX QY 61 RVQLREQLHYQDQLLPVSRILVHPQFYTAQIGADIALLEELPEEPVKVSSHVHTVTLPPAS 120
XX Db 61 RVQLREQLHYQDQLLPVSRILVHPQFYTAQIGADIALLEELPEEPVKVSSHVHTVTLPPAS 120
XX
XX QY 121 ETFFPGMPCWVTGWGVDNDRLLPPFPFLKQVKVPIIMENHICDAKYHLGAYTGDDVRIVR 180
XX Db 121 ETFFPGMPCWVTGWGVDNDRLLPPFPFLKQVKVPIIMENHICDAKYHLGAYTGDDVRIVR 180
XX
XX QY 181 DMLCAGNTRDSCQDAGGLVCKVNGTWTQAGVSWGEGCAQPNRPGIYTRVYILDW 240
XX Db 181 DMLCAGNTRDSCQDAGGLVCKVNGTWTQAGVSWGEGCAQPNRPGIYTRVYILDW 240
XX
XX QY 241 IHVVVKKP 249
XX Db 241 IHVVVKKP 249
```

```
RESULT 6
AAU12012
ID AAU12012 standard; protein; 249 AA.
XX
XX AAU12012;
XX
XX 09-APR-2002 (first entry)
XX
XX Human beta-II tryptase active site mutant S194A #2.
XX
XX Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
XX enzyme; mutant; mutein.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200198470-A2.
XX
XX 27-DEC-2001.
XX
XX 20-JUN-2001; 2001WO-US019681.
XX
XX 21-JUN-2000; 2000US-00598982.
XX
XX (PROM-) PROMEGA CORP.
XX
XX Maffit M, Niles AL, Haak-Frendscho M;
XX
XX WPI; 2002-114578/15.
XX N-PSDB; AAS20778.
XX
XX DNA construct for producing enzymatically-inactive proteolytic tryptase,
XX comprises DNA sequence encoding proteolytic tryptase having an active
XX site mutation.
XX
XX Claim 8; Page 93; 126pp; English.
XX
XX The present invention relates to recombinant human proteolytic tryptases,
XX active site mutants of these tryptases and the methods for producing
XX these. The method involves the production of a DNA expression construct
XX comprising a promoter operably linked to a secretion signal sequence
XX which is operably linked to a DNA sequence encoding a proteolytic
XX tryptase with an active site mutation (the construct drives expression of
XX a mature proteolytic tryptase that lacks enzymatic activity due to the
XX active site mutation, in hosts transformed to contain the construct). The
XX method is useful for producing enzymatically-active beta-II tryptase. The
XX active site mutants of proteolytic tryptase provide a tool to investigate
XX the structural and functional properties of the protease and its
XX enzymatic activity, and for modelling studies. The enzymatically-active,
XX recombinant proteolytic tryptase produced are useful as an antigen to
XX generate anti-human tryptase antibodies and in drug screening for
XX compounds which act as tryptase inhibitors, antagonists, agonists, etc.
XX AAU12009-AAU12024 represent recombinant human beta-II tryptase active
XX site mutants
XX
XX Sequence 249 AA;
XX
XX Query Match 99.4%; Score 1384; DB 5; Length 249;
XX Best Local Similarity 99.2%; Pred. No. 7.1e-122;
XX Matches 247; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 LEKRVGQAEAPRSKWPQVSLRVHGPYMHFCGSLIHPQWVLTAAACVGPDKDLAAL 60
XX Db 1 LEKRVGQAEAPRSKWPQVSLRVHGPYMHFCGSLIHPQWVLTAAACVGPDKDLAAL 60
XX
XX QY 61 RVQLREQLHYQDQLLPVSRILVHPQFYTAQIGADIALLEELPEEPVKVSSHVHTVTLPPAS 120
XX Db 61 RVQLREQLHYQDQLLPVSRILVHPQFYTAQIGADIALLEELPEEPVKVSSHVHTVTLPPAS 120
XX
XX QY 121 ETFFPGMPCWVTGWGVDNDRLLPPFPFLKQVKVPIIMENHICDAKYHLGAYTGDDVRIVR 180
XX Db 121 ETFFPGMPCWVTGWGVDNDRLLPPFPFLKQVKVPIIMENHICDAKYHLGAYTGDDVRIVR 180
```

QY 181 DMLCAGNTRRDS CQDGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYYLDW 240
 |||||
 Db 181 DMLCAGNTRRDS CQDAGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYYLDW 240
 |||||
 QY 241 IHYYVPKXP 249
 |||||
 Db 241 IHYYVPKXP 249
 |||||

RESULT 7
 AAUI2006
 ID AAUI2006 standard; protein; 249 AA.
 XX AC AAUI2006;
 XX DT 09-APR-2002 (first entry)
 XX DE Human beta-I tryptase.
 XX DE Human; proteolytic tryptase; protease; beta-I tryptase; enzyme.
 XX KW Homo sapiens.
 XX OS
 XX FN WO200198470-A2.
 XX PD 27-DEC-2001.
 XX PF 20-JUN-2001; 2001WO-US019681.
 XX PF 21-JUN-2000; 2000US-00598982.
 XX PR (PROM-) PROMEGA CORP.
 XX PA Maffit M, Niles AL, Haak-Frendscho M;
 XX PI WPI; 2002-114578/15.
 XX DR N-PSDB; AAS20763.
 XX PT DNA construct for producing enzymatically-inactive proteolytic tryptase,
 PT comprises DNA sequence encoding proteolytic tryptase having an active
 PT site mutation.
 XX PS Disclosure; Page 74-75; 126pp; English.
 XX CC The present invention relates to recombinant human proteolytic tryptases,
 CC active site mutants of these tryptases and the methods for producing
 CC these. The method involves the production of a DNA expression construct
 CC comprising a promoter operably linked to a secretion signal sequence
 CC which is operably linked to a DNA sequence encoding a proteolytic
 CC tryptase with an active site mutation (the construct drives expression of
 CC a mature proteolytic tryptase that lacks enzymatic activity due to the
 CC active site mutation, in hosts transformed to contain the construct). The
 CC method is useful for producing enzymatically-active beta-II tryptase. The
 CC active site mutants of proteolytic tryptase provide a tool to investigate
 CC the structural and functional properties of the protease and its
 CC enzymatic activity, and for modelling studies. The enzymatically-active,
 CC recombinant proteolytic tryptase produced are useful as an antigen to
 CC generate anti-human tryptase antibodies and in drug screening for
 CC compounds which act as tryptase inhibitors, antagonists, agonists, etc.
 CC The present sequence represents human beta-I tryptase
 XX Sequence 249 AA;
 SQ

Query Match 99.2%; Score 1382; DB 5; Length 249;
 Best Local Similarity 99.2%; Pred. No. 1.1e-121;
 Matches 247; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LEKIVGGQAPRSKWPQVSLRVGHPVWVHFCGSLIHPQWLTAACVGPVVDKLAAL 60
 |||||
 Db 1 LEKIVGGQAPRSKWPQVSLRVGHPVWVHFCGSLIHPQWLTAACVGPVVDKLAAL 60
 |||||

QY 61 RVQLREQHLYYQDQLPVSRIIVHFQFYTAQIGADIALLELEPKNVSSHVHTVTLPPAS 120
 |||||

Db 61 RVQLREQHLYYQDQLPVSRIIVHFQFYTAQIGADIALLELEPKNVSSHVHTVTLPPAS 120
 |||||
 QY 121 ETFFPGMFCWVTGWDVNDERLPPFPFLKQVKVPIEMENHICDAKVLHGAYTGDDVRIVR 180
 |||||
 Db 121 ETFFPGMFCWVTGWDVNDERLPPFPFLKQVKVPIEMENHICDAKVLHGAYTGDDVRIVR 180
 |||||
 QY 181 DMLCAGNTRRDS CQDGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYYLDW 240
 |||||
 Db 181 DMLCAGNTRRDS CQDGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYYLDW 240
 |||||
 QY 241 IHYYVPKXP 249
 |||||
 Db 241 IHYYVPKXP 249
 |||||

RESULT 8
 AAUI2020
 ID AAUI2020 standard; protein; 249 AA.
 XX AC AAUI2020;
 XX DT 09-APR-2002 (first entry)
 XX DE Human beta-II tryptase active site mutant SI94A #6.
 XX DE Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
 XX KW enzyme; mutant; mutein.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX XX WO200198470-A2.
 XX PD 27-DEC-2001.
 XX PF 20-JUN-2001; 2001WO-US019681.
 XX PF 21-JUN-2000; 2000US-00598982.
 XX PR (PROM-) PROMEGA CORP.
 XX PA Maffit M, Niles AL, Haak-Frendscho M;
 XX PI WPI; 2002-114578/15.
 XX DR N-PSDB; AAS20786.
 XX PT DNA construct for producing enzymatically-inactive proteolytic tryptase,
 PT comprises DNA sequence encoding proteolytic tryptase having an active
 PT site mutation.
 XX PS Claim 8; Page 114-115; 126pp; English.
 XX CC The present invention relates to recombinant human proteolytic tryptases,
 CC active site mutants of these tryptases and the methods for producing
 CC these. The method involves the production of a DNA expression construct
 CC comprising a promoter operably linked to a secretion signal sequence
 CC which is operably linked to a DNA sequence encoding a proteolytic
 CC tryptase with an active site mutation (the construct drives expression of
 CC a mature proteolytic tryptase that lacks enzymatic activity due to the
 CC active site mutation, in hosts transformed to contain the construct). The
 CC method is useful for producing enzymatically-active beta-II tryptase. The
 CC active site mutants of proteolytic tryptase provide a tool to investigate
 CC the structural and functional properties of the protease and its
 CC enzymatic activity, and for modelling studies. The enzymatically-active,
 CC recombinant proteolytic tryptase produced are useful as an antigen to
 CC generate anti-human tryptase antibodies and in drug screening for
 CC compounds which act as tryptase inhibitors, antagonists, agonists, etc.
 CC AAUI2009-AAUI2024 represent recombinant human beta-II tryptase active
 CC site mutants
 SQ Sequence 249 AA;

```
Query Match          99.0%; Score 1379; DB 5; Length 249;
Best Local Similarity 98.8%; Pred. No. 2.1e-121;
Matches 246; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LEKRIVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWVLTAAACVGPDPVKDLAAL 60
   |||||
Db 1 LEKRIVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWVLTAAHCVGPDPVKDLAAL 60
   |||||

QY 61 RVQLRQHLHYQDQLLPVSRILVHPOFYTAQIGADTALLEBEPVSVSHVHTVTLPPAS 120
   |||||
Db 61 RVQLRQHLHYQDQLLPVSRILVHPOFYTAQIGADTALLEBEPVSVSHVHTVTLPPAS 120
   |||||

QY 121 ETPPPGMPCWVTGWDVNDERLPPPPPLKQVKVPIMENHICDAKXHLGAYTGDVRIVR 180
   |||||
Db 121 ETPPPGMPCWVTGWDVNDERLPPPPPLKQVKVPIMENHICDAKXHLGAYTGDVRIVR 180
   |||||

QY 181 DDMLCAGNTRRDSQQGDSGGPLVCKVNGTWLQAGVSWGEGCAQPNRPPIYTRVYYLDW 240
   |||||
Db 181 DDMLCAGNTRRDSQQGDSGGPLVCKVNGTWLQAGVSWGEGCAQPNRPPIYTRVYYLDW 240
   |||||

QY 241 IHHYVPKKP 249
   |||||
Db 241 IHHYVPKKP 249
   |||||

RESULT 9
AAU12010
AC AAU12010;
XX
XX
DT 09-APR-2002 (first entry)
DE Human beta-II tryptase active site mutant D91A #1.
XX
XX Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW enzyme; mutant; mutein.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX WO200198470-A2.
XX
XX 27-DEC-2001.
XX
XX 20-JUN-2001; 2001WO-US019681.
XX
XX 21-JUN-2000; 2000US-00598982.
XX
XX (PROM-) PROMEGA CORP.
XX
XX Maffit M, Niles AL, Haak-Frendscho M;
XX
XX WPI; 2002-114578/15.
XX
XX N-PSDB; AAS20776.
XX
XX DNA construct for producing enzymatically-inactive proteolytic tryptase,
PT comprises DNA sequence encoding proteolytic tryptase having an active
PI site mutation.
XX
XX Claim 8; Page 87-88; 126pp; English.
XX
XX The present invention relates to recombinant human proteolytic tryptases,
CC active site mutants of these tryptases and the methods for producing
CC these. The method involves the production of a DNA expression construct
CC comprising a promoter operably linked to a secretion signal sequence
CC which is operably linked to a DNA sequence encoding a proteolytic
CC tryptase with an active site mutation (the construct drives expression of
CC a mature proteolytic tryptase that lacks enzymatic activity due to the
CC active site mutation, in hosts transformed to contain the construct). The
CC method is useful for producing enzymatically-active beta-II tryptase. The
CC active site mutants of proteolytic tryptase provide a tool to investigate
CC the structural and functional properties of the protease and its
```

```
enzymatic activity, and for modelling studies. The enzymatically-active,
recombinant proteolytic tryptase produced are useful as an antigen to
generate anti-human tryptase antibodies and in drug screening for
compounds which act as tryptase inhibitors, antagonists, agonists, etc.
AAU12009-AAU12024 represent recombinant human beta-II tryptase active
site mutants
XX
XX Sequence 249 AA;

Query Match          99.0%; Score 1379; DB 5; Length 249;
Best Local Similarity 99.2%; Pred. No. 2.1e-121;
Matches 247; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LEKRIVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWVLTAAACVGPDPVKDLAAL 60
   |||||
Db 1 LEKRIVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWVLTAAHCVGPDPVKDLAAL 60
   |||||

QY 61 RVQLRQHLHYQDQLLPVSRILVHPOFYTAQIGADTALLEBEPVSVSHVHTVTLPPAS 120
   |||||
Db 61 RVQLRQHLHYQDQLLPVSRILVHPOFYTAQIGADTALLEBEPVSVSHVHTVTLPPAS 120
   |||||

QY 121 ETPPPGMPCWVTGWDVNDERLPPPPPLKQVKVPIMENHICDAKXHLGAYTGDVRIVR 180
   |||||
Db 121 ETPPPGMPCWVTGWDVNDERLPPPPPLKQVKVPIMENHICDAKXHLGAYTGDVRIVR 180
   |||||

QY 181 DDMLCAGNTRRDSQQGDSGGPLVCKVNGTWLQAGVSWGEGCAQPNRPPIYTRVYYLDW 240
   |||||
Db 181 DDMLCAGNTRRDSQQGDSGGPLVCKVNGTWLQAGVSWGEGCAQPNRPPIYTRVYYLDW 240
   |||||

QY 241 IHHYVPKKP 249
   |||||
Db 241 IHHYVPKKP 249
   |||||

RESULT 10
AAU12019
ID AAU12019 standard; protein; 249 AA.
XX
XX AAU12019;
XX
XX 09-APR-2002 (first entry)
XX
XX Human beta-II tryptase active site mutant S194A #5.
XX
XX Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW enzyme; mutant; mutein.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX WO200198470-A2.
XX
XX 27-DEC-2001.
XX
XX 20-JUN-2001; 2001WO-US019681.
XX
XX 21-JUN-2000; 2000US-00598982.
XX
XX (PROM-) PROMEGA CORP.
XX
XX Maffit M, Niles AL, Haak-Frendscho M;
XX
XX WPI; 2002-114578/15.
XX
XX N-PSDB; AAS20785.
XX
XX DNA construct for producing enzymatically-inactive proteolytic tryptase,
PT comprises DNA sequence encoding proteolytic tryptase having an active
PI site mutation.
XX
XX Claim 8; Page 111-112; 126pp; English.
XX
XX The present invention relates to recombinant human proteolytic tryptases,
CC active site mutants of these tryptases and the methods for producing
```

these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic trypsin with an active site mutation (the construct drives expression of a mature proteolytic trypsin that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II trypsin. The active site mutants of proteolytic trypsin provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic trypsin produced are useful as an antigen to generate anti-human trypsin antibodies and in drug screening for compounds which act as trypsin inhibitors, antagonists, agonists, etc. AAU12009-AAU12024 represent recombinant human beta-II trypsin active site mutants

XX Sequence 249 AA;

Query Match 99.0%; Score 1379; DB 5; Length 249;
Best Local Similarity 98.8%; Pred. No. 2.1e-121;
Matches 246; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LEKIVGQEAAPRSKMPQVSLRVHGPYMHFPCGSLIHPQWVLTAAACVGPDKDLAAL 60
DB 1 LEKIVGQEAAPRSKMPQVSLRVHGPYMHFPCGSLIHPQWVLTAAACVGPDKDLAAL 60

QY 61 RVQLREQLHYQDQLLPVSRILVHPQFYTAQIGADIALLELEPEPKVSSHVHTVLPAS 120

DB 61 RVQLREQLHYQDQLLPVSRILVHPQFYTAQIGADIALLELEPEPKVSSHVHTVLPAS 120

QY 121 ETFFPGMPCWVTGWDVNDRLPPFPPLKQVKPIMENHICDAKYHLGAYTGDDVIRV 180

DB 121 ETFFPGMPCWVTGWDVNDRLPPFPPLKQVKPIMENHICDAKYHLGAYTGDDVIRV 180

QY 181 DDMLCAGNTRDSCQDGGGLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVYILDW 240

DB 181 DDMLCAGNTRDSCQDGGGLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVYILDW 240

QY 241 IHHVVPKPK 249

DB 241 IHHVVPKPK 249

RESULT 11

AAU12013

ID AAU12013 standard; protein; 245 AA.

XX AAU12013;

XX 09-APR-2002 (first entry)

XX Human beta-II trypsin active site mutant H44A #2.

XX Human; proteolytic trypsin; protease; recombinant beta-II trypsin;
XX enzyme; mutant; mutein.

OS Homo sapiens.

OS Synthetic.

XX WO200198470-A2.

XX 27-DEC-2001.

XX 20-JUN-2001; 2001WO-US019681.

XX 21-JUN-2000; 2000US-00598982.

XX (PROM-) PROMEGA CORP.

XX Maffit M, Niles AL, Haak-Frendscho M;

XX WPI; 2002-114578/15.

DR N-PSDB; AAS20779.

XX DNA construct for producing enzymatically-inactive proteolytic trypsin,
PT comprises DNA sequence encoding proteolytic trypsin having an active
PT site mutation.

XX Claim 40; Page 95-96; 126pp; English.

XX The present invention relates to recombinant human proteolytic trypsin,
CC active site mutants of these trypsin and the methods for producing
CC these. The method involves the production of a DNA expression construct
CC comprising a promoter operably linked to a secretion signal sequence
CC which is operably linked to a DNA sequence encoding a proteolytic
CC trypsin with an active site mutation (the construct drives expression of
CC a mature proteolytic trypsin that lacks enzymatic activity due to the
CC active site mutation, in hosts transformed to contain the construct). The
CC method is useful for producing enzymatically-active beta-II trypsin. The
CC active site mutants of proteolytic trypsin provide a tool to investigate
CC the structural and functional properties of the protease and its
CC enzymatic activity, and for modelling studies. The enzymatically-active,
CC recombinant proteolytic trypsin produced are useful as an antigen to
CC generate anti-human trypsin antibodies and in drug screening for
CC compounds which act as trypsin inhibitors, antagonists, agonists, etc.
CC AAU12009-AAU12024 represent recombinant human beta-II trypsin active
CC site mutants

SQ Sequence 245 AA;

Query Match 98.6%; Score 1374; DB 5; Length 245;

Best Local Similarity 100.0%; Pred. No. 6.1e-121;

Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IVGQEAAPRSKMPQVSLRVHGPYMHFPCGSLIHPQWVLTAAACVGPDKDLAALRVOL 64

DB 1 IVGQEAAPRSKMPQVSLRVHGPYMHFPCGSLIHPQWVLTAAACVGPDKDLAALRVOL 60

QY 65 REQLHYQDQLLPVSRILVHPQFYTAQIGADIALLELEPEPKVSSHVHTVLPASSETFP 124

DB 61 REQLHYQDQLLPVSRILVHPQFYTAQIGADIALLELEPEPKVSSHVHTVLPASSETFP 120

QY 125 PGMPCWVTGWDVNDRLPPFPPLKQVKPIMENHICDAKYHLGAYTGDDVIRVDDML 184

DB 121 PGMPCWVTGWDVNDRLPPFPPLKQVKPIMENHICDAKYHLGAYTGDDVIRVDDML 180

QY 185 CAGNTRDSCQDGGGLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVYILDWIIHY 244

DB 181 CAGNTRDSCQDGGGLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVYILDWIIHY 240

QY 245 VPKPK 249

DB 241 VPKPK 245

RESULT 12

AAU12018

ID AAU12018 standard; protein; 249 AA.

XX AAU12018;

XX 09-APR-2002 (first entry)

XX Human beta-II trypsin active site mutant D91A #3.

XX Human; proteolytic trypsin; protease; recombinant beta-II trypsin;
XX enzyme; mutant; mutein.

OS Homo sapiens.

OS Synthetic.

XX WO200198470-A2.

XX 27-DEC-2001.

XX 20-JUN-2001; 2001WO-US019681.

XX 21-JUN-2000; 2000US-00598982.
 XX (PROM-) PROMEGA CORP.
 XX Maffit M, Niles AL, Haak-Frendscho M;
 XX WPI; 2002-114578/15.
 XX N-PSDB; AAS20784.
 XX DNA construct for producing enzymatically-inactive proteolytic trypsinase,
 XX comprises DNA sequence encoding proteolytic trypsinase having an active
 XX site mutation.
 XX Claim 8; Page 109-110; 126pp; English.
 XX The present invention relates to recombinant human proteolytic trypsinases,
 XX active site mutants of these trypsinases and the methods for producing
 XX these. The method involves the production of a DNA expression construct
 XX comprising a promoter operably linked to a secretion signal sequence
 XX which is operably linked to a DNA sequence encoding a proteolytic
 XX trypsinase with an active site mutation (the construct drives expression of
 XX a mature proteolytic trypsinase that lacks enzymatic activity due to the
 XX active site mutation, in hosts transformed to contain the construct). The
 XX method is useful for producing enzymatically-active beta-II trypsinase. The
 XX active site mutants of proteolytic trypsinase provide a tool to investigate
 XX the structural and functional properties of the protease and its
 XX enzymatic activity, and for modelling studies. The enzymatically-active,
 XX recombinant human trypsinase produced are useful as an antigen to
 XX generate anti-human trypsinase antibodies and in drug screening for
 XX compounds which act as trypsinase inhibitors, antagonists, agonists, etc.
 XX AAU12009-AAU12024 represent recombinant human beta-II trypsinase active
 XX site mutants
 XX Sequence 249 AA;
 XX
 Query Match 98.6%; Score 1374; DB 5; Length 249;
 Best Local Similarity 98.8%; Pred. No. 6.2e-121;
 Matches 246; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LEKRIIVGGQAPRSKWPQVSLRVHGPYVMMHFCGSLIHPQWVLTAAACVGPDKDLAAL 60
 DB 1 LEKRIIVGGQAPRSKWPQVSLRVHGPYVMMHFCGSLIHPQWVLTAAACVGPDKDLAAL 60
 QY 61 RVQLREQLHYQDQLLPVSRIVHVPQYTAQIGADIALLELEPVSSSHVHTVTLPPAS 120
 DB 61 RVQLREQLHYQDQLLPVSRIVHVPQYTAQIGADIALLELEPVSSSHVHTVTLPPAS 120
 QY 121 ETTPPGMPCWVTGWDVNDERLPPPPPLKQVKVPIIMENHICDAKYHLGAYTGDDVIRV 180
 DB 121 ETTPPGMPCWVTGWDVNDERLPPPPPLKQVKVPIIMENHICDAKYHLGAYTGDDVIRV 180
 QY 181 DDMLCAGNTRDSCQSGGGLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRYTYLDW 240
 DB 181 DDMLCAGNTRDSCQSGGGLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRYTYLDW 240
 QY 241 IHVYVKKP 249
 DB 241 IHVYVKKP 249
 RESULT 13
 AAU12021
 ID AAU12021 standard; protein; 245 AA.
 AC AAU12021;
 XX
 DT 09-APR-2002 (first entry)
 XX Human beta-II trypsinase active site mutant H44A #4.
 XX Human; proteolytic trypsinase; protease; recombinant beta-II trypsinase;
 XX enzyme; mutant; mutain.

XX Homo sapiens.
 OS Synthetic.
 XX WO200198470-A2.
 XX 27-DEC-2001.
 XX 20-JUN-2001; 2001WO-US019681.
 XX 21-JUN-2000; 2000US-00598982.
 XX (PROM-) PROMEGA CORP.
 XX Maffit M, Niles AL, Haak-Frendscho M;
 XX WPI; 2002-114578/15.
 XX N-PSDB; AAS20787.
 XX DNA construct for producing enzymatically-inactive proteolytic trypsinase,
 XX comprises DNA sequence encoding proteolytic trypsinase having an active
 XX site mutation.
 XX Claim 40; Page 117-118; 126pp; English.
 XX The present invention relates to recombinant human proteolytic trypsinases,
 XX active site mutants of these trypsinases and the methods for producing
 XX these. The method involves the production of a DNA expression construct
 XX comprising a promoter operably linked to a secretion signal sequence
 XX which is operably linked to a DNA sequence encoding a proteolytic
 XX trypsinase with an active site mutation (the construct drives expression of
 XX a mature proteolytic trypsinase that lacks enzymatic activity due to the
 XX active site mutation, in hosts transformed to contain the construct). The
 XX method is useful for producing enzymatically-active beta-II trypsinase. The
 XX active site mutants of proteolytic trypsinase provide a tool to investigate
 XX the structural and functional properties of the protease and its
 XX enzymatic activity, and for modelling studies. The enzymatically-active,
 XX recombinant human trypsinase produced are useful as an antigen to
 XX generate anti-human trypsinase antibodies and in drug screening for
 XX compounds which act as trypsinase inhibitors, antagonists, agonists, etc.
 XX AAU12009-AAU12024 represent recombinant human beta-II trypsinase active
 XX site mutants
 XX Sequence 245 AA;
 XX
 Query Match 98.3%; Score 1369; DB 5; Length 245;
 Best Local Similarity 99.6%; Pred. No. 1.8e-120;
 Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 IVGGQAPRSKWPQVSLRVHGPYVMMHFCGSLIHPQWVLTAAACVGPDKDLAALRVQL 64
 DB 1 IVGGQAPRSKWPQVSLRVHGPYVMMHFCGSLIHPQWVLTAAACVGPDKDLAALRVQL 60
 QY 65 REQLHYQDQLLPVSRIVHVPQYTAQIGADIALLELEPVSSSHVHTVTLPPASSTFP 124
 DB 61 REQLHYQDQLLPVSRIVHVPQYTAQIGADIALLELEPVSSSHVHTVTLPPASSTFP 120
 QY 125 PGMPCWVTGWDVNDERLPPPPPLKQVKVPIIMENHICDAKYHLGAYTGDDVIRVDDML 184
 DB 121 PGMPCWVTGWDVNDERLPPPPPLKQVKVPIIMENHICDAKYHLGAYTGDDVIRVDDML 180
 QY 185 CAGNTRDSCQSGGGLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRYTYLDWIHHY 244
 DB 181 CAGNTRDSCQSGGGLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRYTYLDWIHHY 240
 QY 245 VPKKP 249
 DB 241 VPKKP 245
 RESULT 14
 AAU12008
 ID AAU12008 standard; protein; 245 AA.

XX AC AAU12008;
 XX DT 09-APR-2002 (first entry)
 XX DE Recombinant human mature beta-II tryptase.
 XX KW Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
 KW enzyme; mutein; mutant.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO2001198470-A2.
 XX PD 27-DEC-2001.
 XX PF 20-JUN-2001; 2001WO-US019681.
 XX PR 21-JUN-2000; 2000US-00598982.
 XX PA (PROM-) PROMEGA CORP.
 XX PI Maffit M, Niles AL, Haak-Frendscho M;
 XX DR WPI; 2002-114578/15.
 XX DR N-PSDB; AAS20766.
 XX PT DNA construct for producing enzymatically-inactive proteolytic tryptase,
 PT comprises DNA sequence encoding proteolytic tryptase having an active
 PT site mutation.
 XX PS Claim 61; Page 80; 126pp; English.
 XX CC The present invention relates to recombinant human proteolytic tryptases,
 CC active site mutants of these tryptases and the methods for producing
 CC these. The method involves the production of a DNA expression construct
 CC comprising a promoter operably linked to a secretion signal sequence
 CC which is operably linked to a DNA sequence encoding a proteolytic
 CC tryptase with an active site mutation (the construct drives expression of
 CC a mature proteolytic tryptase that lacks enzymatic activity due to the
 CC active site mutation, in hosts transformed to contain the construct). The
 CC method is useful for producing enzymatically-active beta-II tryptase. The
 CC active site mutants of proteolytic tryptase provide a tool to investigate
 CC the structural and functional properties of the protease and its
 CC enzymatic activity, and for modelling studies. The enzymatically-active,
 CC recombinant proteolytic tryptase produced are useful as an antigen to
 CC generate anti-human tryptase antibodies and in drug screening for
 CC compounds which act as tryptase inhibitors and antagonists, etc.
 CC The present sequence represents recombinant human mature beta-II tryptase
 XX SQ Sequence 245 AA;
 Query Match 98.2%; Score 1368; DB 5; Length 245;
 Best Local Similarity 99.6%; Pred. No. 2.2e-120;
 Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 IVGQEAAPRSKWPQVSLRVHGPYWMHFCGSLHPQWLTAACVGPVDVLDLALRVQL 64
 DB 1 IVGQEAAPRSKWPQVSLRVHGPYWMHFCGSLHPQWLTAACVGPVDVLDLALRVQL 60
 QY 65 REQHLHYQDQLLPVSRITVHPQFYTAQIGADIALLEPEPVKVSHTVTLPPASETFP 124
 DB 61 REQHLHYQDQLLPVSRITVHPQFYTAQIGADIALLEPEPVKVSHTVTLPPASETFP 120
 QY 125 PGMPCWVTGWGDVNDERLPFPPLKQVKVPIEMENHICDAKHILGAYTGDDVIRVDDML 184
 DB 121 PGMPCWVTGWGDVNDERLPFPPLKQVKVPIEMENHICDAKHILGAYTGDDVIRVDDML 180
 QY 185 CAGNTRRDSGCGSGPLVCKVNGTWLQAGVYVSWGEGCAQPNRPGIYTRVYYLDWIHY 244
 DB 181 CAGNTRRDSGCGSGPLVCKVNGTWLQAGVYVSWGEGCAQPNRPGIYTRVYYLDWIHY 240

QY 245 VPKKP 249
 DB 241 VPKKP 245
 RESULT 15
 AAW64240
 ID AAW64240 standard; protein; 274 AA.
 XX AC AAW64240;
 XX DT 24-NOV-1998 (first entry)
 XX DE Human mast cell tryptase II/beta.
 XX KW Mast cell tryptase II/beta; human; MCP-7; mast cell protease 7;
 KW blood clot; anticoagulant; myocardial infarction; reocclusion;
 KW thromboembolism; cerebral embolism; thrombosis; therapy.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Peptide 1..18
 FT Peptide /label= Sig_peptide
 FT Peptide 19..28
 FT Protein /label= Pro_peptide
 FT Protein 29..274
 FT Protein /label= Mat_protein
 XX PN WO9824886-A1.
 XX PD 11-JUN-1998.
 XX PF 25-NOV-1997; 97WO-US021620.
 XX PR 04-DEC-1996; 96US-0032354P.
 XX PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 XX PI Stevens RL;
 XX WPI; 1998-333308/29.
 XX N-PSDB; AAW44330.
 XX New compositions containing tryptase-7, e.g. mouse mast cell protease-7 -
 XX are used to treat clot formation in e.g. myocardial infarction,
 XX reocclusion following angioplasty or pulmonary thrombo-embolism.
 XX PS Disclosure; Page 66-67; 92pp; English.
 XX CC This is the deduced amino acid sequence of human mast cell tryptase
 CC II/beta (see also AAW44330). The invention provides: compositions
 CC comprising an isolated tryptase-7 that may include chimeric proteins that
 CC contain (a) a human tryptase for all but the active site region and (b)
 CC the substrate-binding pocket of mouse tryptase-7 or its homologues (see
 CC AAW64233-39); a method for treating a blood clot by administering a
 CC nucleic acid molecule that codes for a tryptase-7, or an expression
 CC product, to decrease fibrinogen activity; a nucleic acid encoding a
 CC serine protease (SP); and a method of producing a mature SP by expressing
 CC the inactive zymogen in a host cell, and cleaving the enterokinase
 CC susceptibility domain. The tryptase-7 polypeptides can be used to treat
 CC disorders mediated by undesirable thrombus clot formation such as
 CC myocardial infarction and reocclusion following angioplasty of blood
 CC clots associated with pulmonary thromboembolism, deep vein thrombosis,
 CC cerebral embolism, renal vein and peripheral arterial thrombosis. They
 CC are also useful for all surgical procedures that require decreased blood
 CC clots
 XX SQ Sequence 274 AA;
 Query Match 98.2%; Score 1368; DB 2; Length 274;
 Best Local Similarity 99.6%; Pred. No. 2.6e-120;
 Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	5	IVCGQAPRSKWPNOVSLRVHGPYMMHFCGSLIHPQWVLTAAACVGPDKDLAALRVQL	64
Db	30	IVGGQAPRSKWPNOVSLRVHGPYMMHFCGSLIHPQWVLTAAHCVGPDVKDLAALRVQL	89
QY	65	REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPKVSSSHVHTVTLPPASETFP	124
Db	90	REQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPKVSSSHVHTVTLPPASETFP	149
QY	125	PGMPCWVTGWDVNDNDRLPPLKQVKVPIMENHI CD AKYHLGAYTGDVRIVRDDML	184
Db	150	PGMPCWVTGWDVNDNDRLPPLKQVKVPIMENHI CD AKYHLGAYTGDVRIVRDDML	209
QY	185	CAGNTRDSCGSDSGGFLVCKVNGTWLQAGVWSWEGCAQPNRPGIYTRVTYILDWIIHY	244
Db	210	CAGNTRDSCGSDSGGFLVCKVNGTWLQAGVWSWEGCAQPNRPGIYTRVTYILDWIIHY	269
QY	245	VPKKP	249
Db	270	VPKKP	274

Search completed: July 22, 2004, 15:22:25
Job time : 100 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 22, 2004, 15:20:41 ; Search time 58 seconds
(without alignments)
221.636 Million cell updates/sec

Title: US-09-598-982-21

Perfect score: 1393

Sequence: 1 LEKRIVGQAEAPRSKWPQV.....IYTRVYYLDWIHHVVKKP 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1387	99.6	249	3	US-09-079-970A-5
2	1368	98.2	245	3	US-09-079-970A-6
3	1368	98.2	245	4	US-09-601-318-1
4	1368	98.2	274	2	US-09-016-366A-21
5	1368	98.2	274	2	US-08-978-404B-16
6	1363	97.8	273	2	US-09-016-366A-19
7	1363	97.8	273	2	US-08-978-404B-14
8	1361	97.7	244	4	US-09-601-318-4
9	1361	97.7	244	4	US-09-601-318-5
10	1361	97.7	244	4	US-09-601-318-6
11	1361	97.7	244	4	US-09-601-318-7
12	1344	96.5	267	2	US-09-016-366A-23
13	1344	96.5	267	2	US-08-978-404B-18
14	1274	91.5	245	3	US-08-944-483-69
15	1274	91.5	275	2	US-09-016-366A-17
16	1274	91.5	275	2	US-08-978-404B-12
17	1091	78.3	276	2	US-09-016-366A-15
18	1091	78.3	276	2	US-08-978-404B-21
19	1075	77.2	270	2	US-08-978-404B-8
20	1054	75.7	273	2	US-08-978-404B-3
21	1051	75.4	274	2	US-08-978-404B-5
22	1037	74.4	273	2	US-08-978-404B-6
23	702	50.4	190	2	US-08-845-998-4
24	702	50.4	190	3	US-09-206-537-4
25	702	50.4	190	3	US-09-430-854-4
26	698	50.1	190	2	US-08-845-998-6
27	698	50.1	190	3	US-09-206-537-6

28	698	50.1	190	3	US-09-430-854-6	Sequence 6, Appli
29	684.5	49.1	269	2	US-08-978-404B-10	Sequence 10, Appl
30	563.5	40.5	290	4	US-09-386-653A-7	Sequence 7, Appli
31	554.5	39.8	315	4	US-09-386-653A-9	Sequence 9, Appli
32	536.5	38.5	284	4	US-09-387-375-7	Sequence 7, Appli
33	527.5	37.9	316	4	US-09-387-375-9	Sequence 9, Appli
34	507	36.4	319	4	US-09-386-642-12	Sequence 12, Appl
35	507	36.4	328	4	US-09-386-642-11	Sequence 11, Appl
36	506	36.3	299	3	US-08-944-483-66	Sequence 66, Appl
37	501.5	36.0	317	4	US-09-386-629-7	Sequence 7, Appli
38	501.5	36.0	317	4	US-09-907-794A-263	Sequence 263, App
39	501.5	36.0	317	4	US-09-905-125A-263	Sequence 263, App
40	501.5	36.0	317	4	US-09-902-775A-263	Sequence 263, App
41	499.5	35.9	312	4	US-09-023-942A-4	Sequence 4, Appli
42	493.5	35.4	314	3	US-09-008-271A-3	Sequence 3, Appli
43	493.5	35.4	314	4	US-09-907-794A-257	Sequence 257, App
44	493.5	35.4	314	4	US-09-905-125A-257	Sequence 257, App
45	493.5	35.4	314	4	US-09-902-775A-257	Sequence 257, App

ALIGNMENTS

RESULT 1

US-09-079-970A-5

; Sequence 5, Application US/09079970A

; Patent No. 6274366

; GENERAL INFORMATION:

; APPLICANT: Maffitt, Mark A.

; APPLICANT: Niles, Andrew L.

; APPLICANT: Haak-Frendscho, Mary

; TITLE OF INVENTION: Enzymatically-Active Recombinant Human

; TITLE OF INVENTION: Beta-Tryptase and Method of Making Same

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Intellectual Property Department

; STREET: 8000 Excelsior Drive, Suite 401

; CITY: Madison

; STATE: WISCONSIN

; COUNTRY: U.S.A.

; ZIP: 53717-1914

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/079,970A

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Leone, Joseph T.

; REGISTRATION NUMBER: 37,170

; REFERENCE/DOCKET NUMBER: 34506.073

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (608) 831-2100

; TELEFAX: (608) 831-2106

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 249 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-079-970A-5

Query Match 99.6%; Score 1387; DB 3; Length 249;

Best Local Similarity 99.6%; Pred. No. 5, 5e-141;

Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEKRIVGQAEAPRSKWPQVSLRVHGVYMHFCGSLIHPQVLTAAACVGVGVKDLAAL 60

DB 1 LEKRIVGQAEAPRSKWPQVSLRVHGVYMHFCGSLIHPQVLTAAACVGVGVKDLAAL 60

QY 61 RVQLREQLHYQQDQLLPVSRILVHPQFYTAQIGADIALLELEBPVKVSSHVHTVTLPPAS 120
Db 61 RVQLREQLHYQQDQLLPVSRILVHPQFYTAQIGADIALLELEBPVKVSSHVHTVTLPPAS 120
QY 121 ETTPPGMPCWVTGMDVNDRLPPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIVR 180
Db 121 ETTPPGMPCWVTGMDVNDRLPPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIVR 180
QY 181 DDMCAGNTRDSCQDGGPLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVYYLDW 240
Db 181 DDMCAGNTRDSCQDGGPLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVYYLDW 240
QY 241 IHVYVKKP 249
Db 241 IHVYVKKP 249

RESULT 2
US-09-079-970A-6
; Sequence 6, Application US/09079970A
; Patent No. 6274366
; GENERAL INFORMATION:
; APPLICANT: Maffitt, Mark A.
; APPLICANT: Niles, Andrew L.
; APPLICANT: Haak-Frendscho, Mary
; TITLE OF INVENTION: Enzymatically-Active Recombinant Human
; TITLE OF INVENTION: Beta-Tryptase and Method of Making Same
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Intellectual Property Department
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WISCONSIN
; COUNTRY: U.S.A.
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/079, 970A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Leone, Joseph T.
; REGISTRATION NUMBER: 37,170
; REFERENCE/DOCKET NUMBER: 34506.073
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-079-970A-6

Query Match 98.2%; Score 1368; DB 3; Length 245;
Best Local Similarity 99.6%; Pred. No. 5.9e-139;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 IVGGQAPRSKWPQVSLRVHGPYMHFPCGSLIHPQWVLTAAACVGPDKDLAALRVOL 64
Db 1 IVGGQAPRSKWPQVSLRVHGPYMHFPCGSLIHPQWVLTAAACVGPDKDLAALRVOL 60
QY 65 REQHLHYQDQLLPVSRILVHPQFYTAQIGADIALLELEBPVKVSSHVHTVTLPPASETFP 124
Db 61 REQHLHYQDQLLPVSRILVHPQFYTAQIGADIALLELEBPVKVSSHVHTVTLPPASETFP 120
QY 125 PMPCWVTGMDVNDRLPPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIVRDDML 184
Db 125 PMPCWVTGMDVNDRLPPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIVRDDML 184

Db 121 PMPCWVTGMDVNDRLPPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIVRDDML 180
QY 185 CAGNTRDSCQDGGPLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVYYLDWIHHY 244
Db 181 CAGNTRDSCQDGGPLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVYYLDWIHHY 240
QY 245 VPKKP 249
Db 241 VPKKP 245

RESULT 3
US-09-601-318-1
; Sequence 1, Application US/09601318
; Patent No. 6613769
; GENERAL INFORMATION:
; APPLICANT: Max-Planck-Gesellschaft z. Frd. d. Wissenschaft. e.V
; APPLICANT: Byk Gulden Lomberg Chemische Fabrik GmbH
; APPLICANT: Bode, Wolfram
; APPLICANT: Moroder, Luis
; APPLICANT: Pereira, Pedro Jose Barbosa
; APPLICANT: Bergner, Andreas
; APPLICANT: Huber, Robert
; APPLICANT: Sommerhoff, Christian
; APPLICANT: Schaschke, No. 6613769bert
; APPLICANT: Br. Thomas
; APPLICANT: Martin, Thomas
; APPLICANT: Stadlwieser, Josef
; APPLICANT: Ulrich, Wolf-Rdiger
; APPLICANT: Dominik, Andreas
; APPLICANT: Thibaut, Ulrich
; APPLICANT: Bundschuh, Daniela
; APPLICANT: Beume, Rolf
; APPLICANT: Goebel, Karl-Josef
; TITLE OF INVENTION: Trypsin-Inhibitoren
; FILE REFERENCE: 17674p WO-1
; CURRENT APPLICATION NUMBER: US/09/601.318
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: DE19804761.4
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: DE19851300.3
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-601-318-1

Query Match 98.2%; Score 1368; DB 4; Length 245;
Best Local Similarity 99.6%; Pred. No. 5.9e-139;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 IVGGQAPRSKWPQVSLRVHGPYMHFPCGSLIHPQWVLTAAACVGPDKDLAALRVOL 64
Db 1 IVGGQAPRSKWPQVSLRVHGPYMHFPCGSLIHPQWVLTAAACVGPDKDLAALRVOL 60
QY 65 REQHLHYQDQLLPVSRILVHPQFYTAQIGADIALLELEBPVKVSSHVHTVTLPPASETFP 124
Db 61 REQHLHYQDQLLPVSRILVHPQFYTAQIGADIALLELEBPVKVSSHVHTVTLPPASETFP 120
QY 125 PMPCWVTGMDVNDRLPPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIVRDDML 184
Db 121 PMPCWVTGMDVNDRLPPPLKQVKVPIIMENHICDAKYHLGAYTGDDVRIVRDDML 180
QY 185 CAGNTRDSCQDGGPLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVYYLDWIHHY 244
Db 181 CAGNTRDSCQDGGPLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVYYLDWIHHY 240
QY 245 VPKKP 249
Db 241 VPKKP 245

RESULT 4

US-09-016-366A-21
; Sequence 21, Application US/09016366A
; Patent No. 5955431
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; APPLICANT: Huang, Chifu
; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016.366A
; FILING DATE: January 30, 1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,090
; FILING DATE: 05-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7093
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-016-366A-21

Query Match 98.2%; Score 1368; DB 2; Length 274;
Best Local Similarity 99.6%; Pred. No. 6.9e-139;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	5	IVGQEA	PRSKWPQVSLRVHG	PYWMHFCGSLIH	PQWVLTAAACVGP	VDKDLAALRVQL	64
Db	30	IVGQEA	PRSKWPQVSLRVHG	PYWMHFCGSLIH	PQWVLTAAACVGP	VDKDLAALRVQL	89
Qy	65	REQLHY	QDQLLPVSR	IIVHPQFYTA	QIGADIALLE	EEPVKVSSHVHTV	124
Db	90	REQLHY	QDQLLPVSR	IIVHPQFYTA	QIGADIALLE	EEPVKVSSHVHTV	149
Qy	125	PGMPCW	TGWDVND	DERLPPFP	LKQVKVP	IMENHICDAKYH	184
Db	150	PGMPCW	TGWDVND	DERLPPFP	LKQVKVP	IMENHICDAKYH	209
Qy	185	CAGNTR	RDSCOGDS	GGPLVCK	VNGTWLQ	AGVVS	244
Db	210	CAGNTR	RDSCOGDS	GGPLVCK	VNGTWLQ	AGVVS	269
Qy	245	VPKKP	249				
Db	270	VPKKP	274				

RESULT 5

US-09-016-366A-19

; Sequence 19, Application US/09016366A

; Patent No. 5955431

US-08-978-404B-16

; Sequence 16, Application US/08978404B
; Patent No. 5968782
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
; TITLE OF INVENTION: FIBRINOGEN
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978.404B
; FILING DATE: 25-NOV-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/032,354
; FILING DATE: 04-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5968782e
US-08-978-404B-16

Query Match 98.2%; Score 1368; DB 2; Length 274;
Best Local Similarity 99.6%; Pred. No. 6.9e-139;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	5	IVGQEA	PRSKWPQVSLRVHG	PYWMHFCGSLIH	PQWVLTAAACVGP	VDKDLAALRVQL	64
Db	30	IVGQEA	PRSKWPQVSLRVHG	PYWMHFCGSLIH	PQWVLTAAACVGP	VDKDLAALRVQL	89
Qy	65	REQLHY	QDQLLPVSR	IIVHPQFYTA	QIGADIALLE	EEPVKVSSHVHTV	124
Db	90	REQLHY	QDQLLPVSR	IIVHPQFYTA	QIGADIALLE	EEPVKVSSHVHTV	149
Qy	125	PGMPCW	TGWDVND	DERLPPFP	LKQVKVP	IMENHICDAKYH	184
Db	150	PGMPCW	TGWDVND	DERLPPFP	LKQVKVP	IMENHICDAKYH	209
Qy	185	CAGNTR	RDSCOGDS	GGPLVCK	VNGTWLQ	AGVVS	244
Db	210	CAGNTR	RDSCOGDS	GGPLVCK	VNGTWLQ	AGVVS	269
Qy	245	VPKKP	249				
Db	270	VPKKP	274				

RESULT 6

US-09-016-366A-19

; Sequence 19, Application US/09016366A

; Patent No. 5955431

; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; APPLICANT: Huang, Chifu
 ; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
 ; TITLE OF INVENTION: INHIBITORS
 ; NUMBER OF SEQUENCES: 65
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: U.S.A.
 ; ZIP: 02210-2211
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,366A
 ; FILING DATE: January 30, 1998
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/037,090
 ; FILING DATE: 05-FEB-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Plumer, Elizabeth R.
 ; REGISTRATION NUMBER: 36,637
 ; REFERENCE/DOCKET NUMBER: B0801/7093
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-720-3500
 ; TELEFAX: 617-720-2441
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 273 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-016-366A-19

Query Match 97.8%; Score 1363; DB 2; Length 273;
 Best Local Similarity 99.2%; Pred. No. 2.4e-138;
 Matches 243; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 IVGQEARPSKWPQVSLRVHGPYWMHFCGSLIHPQWLTAAACVGPDKDLAALRVQL 64
 DB 29 IVGQEARPSKWPQVSLRVHGPYWMHFCGSLIHPQWLTAAACVGPDKDLAALRVQL 88
 QY 65 REQLHYQDQLLPVSRRIIVHPQFYTAQIGADIALLELEPVSSSHVHTVTLPPASETFP 124
 DB 89 REQLHYQDQLLPVSRRIIVHPQFYTAQIGADIALLELEPVSSSHVHTVTLPPASETFP 148
 QY 125 PGMPCWVTGWGDVNDNDRLEPPPLKQVKVPIIMENHICDAKYHLGAYTGGDVRIVRDDML 184
 DB 149 PGMPCWVTGWGDVNDNDRLEPPPLKQVKVPIIMENHICDAKYHLGAYTGGDVRIVRDDML 208
 QY 185 CAGNTRDSCQSGSGGLPVCKVNGTWTQAGVSWGEGCAQPNRPGIYTRVYILDWIHHY 244
 DB 209 CAGNTRDSCQSGSGGLPVCKVNGTWTQAGVSWGEGCAQPNRPGIYTRVYILDWIHHY 268
 QY 245 VPKKP 249
 DB 269 VPKKP 273

RESULT 7
 US-09-978-404B-14
 ; Sequence 14, Application US/08978404B
 ; Patent No. 5968782
 ; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES

; TITLE OF INVENTION: FIBRINOGEN
 ; NUMBER OF SEQUENCES: 74
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: U.S.A.
 ; ZIP: 02210-2211
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/978,404B
 ; FILING DATE: 25-NOV-97
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/032,354
 ; FILING DATE: 04-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Plumer, Elizabeth R.
 ; REGISTRATION NUMBER: 36,637
 ; REFERENCE/DOCKET NUMBER: B0801/7090
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-720-3500
 ; TELEFAX: 617-720-2441
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 273 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: No. 5968782e
 ; US-08-978-404B-14

Query Match 97.8%; Score 1363; DB 2; Length 273;
 Best Local Similarity 99.2%; Pred. No. 2.4e-138;
 Matches 243; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 IVGQEARPSKWPQVSLRVHGPYWMHFCGSLIHPQWLTAAACVGPDKDLAALRVQL 64
 DB 29 IVGQEARPSKWPQVSLRVHGPYWMHFCGSLIHPQWLTAAACVGPDKDLAALRVQL 88
 QY 65 REQLHYQDQLLPVSRRIIVHPQFYTAQIGADIALLELEPVSSSHVHTVTLPPASETFP 124
 DB 89 REQLHYQDQLLPVSRRIIVHPQFYTAQIGADIALLELEPVSSSHVHTVTLPPASETFP 148
 QY 125 PGMPCWVTGWGDVNDNDRLEPPPLKQVKVPIIMENHICDAKYHLGAYTGGDVRIVRDDML 184
 DB 149 PGMPCWVTGWGDVNDNDRLEPPPLKQVKVPIIMENHICDAKYHLGAYTGGDVRIVRDDML 208
 QY 185 CAGNTRDSCQSGSGGLPVCKVNGTWTQAGVSWGEGCAQPNRPGIYTRVYILDWIHHY 244
 DB 209 CAGNTRDSCQSGSGGLPVCKVNGTWTQAGVSWGEGCAQPNRPGIYTRVYILDWIHHY 268
 QY 245 VPKKP 249
 DB 269 VPKKP 273

RESULT 8
 US-09-601-318-4
 ; Sequence 4, Application US/09601318
 ; Patent No. 6613769
 ; GENERAL INFORMATION:
 ; APPLICANT: Byk-Planck-Gesellschaft z. Frd. d. Wissensch. e.v
 ; APPLICANT: Byk Gulden Lomberg Chemische Fabrik GmbH
 ; APPLICANT: Bode, Wolfram
 ; APPLICANT: Moroder, Luis
 ; APPLICANT: Pereira, Pedro Jose Barbosa

```

/ APPLICANT: Bergner, Andreas
/ APPLICANT: Huber, Robert
/ APPLICANT: Sommerhoff, Christian
/ APPLICANT: Schaschke, No. 6613769bert
/ APPLICANT: Br. Thomas
/ APPLICANT: Martin, Thomas
/ APPLICANT: Stadlwieser, Josef
/ APPLICANT: Ulrich, Wolf-Rüdiger
/ APPLICANT: Dominik, Andreas
/ APPLICANT: Thibaut, Ulrich
/ APPLICANT: Bundschuh, Daniela
/ APPLICANT: Beume, Rolf
/ APPLICANT: Goebel, Karl-Josof
/ TITLE OF INVENTION: Typtase-Inhibitoren
/ FILE REFERENCE: 17674P WO-1
/ CURRENT APPLICATION NUMBER: US/09/601,318
/ CURRENT FILING DATE: 2001-01-22
/ PRIOR APPLICATION NUMBER: DE19804761.4
/ PRIOR FILING DATE: 1998-02-06
/ PRIOR APPLICATION NUMBER: DE19851300.3
/ PRIOR FILING DATE: 1998-11-06
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 244
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-601-318-4

```

Query Match	97.7%	Score 1361;	DB 4;	Length 244;
Best Local Similarity	99.6%;	Pred. No. 3.3e-138;		
Matches 243;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	5	IVGGQAPRSKWPQVSLRVHGPVYMHFPCGSLIHPQWLTAACACVGPDKDLAALRVQL	64	
Db	1	IVGGQAPRSKWPQVSLRVHGPVYMHFPCGSLIHPQWLTAACVGPDKDLAALRVQL	60	
QY	65	REQHLYYQDOLLIVSRILIVHPQYTAIGADIALLELEPVPKVSSHVHTVTLPPASFTFP	124	
Db	61	REQHLYYQDOLLIVSRILIVHPQYTAIGADIALLELEPVPKVSSHVHTVTLPPASFTFP	120	
QY	125	PGMPCWVTGWDVNDERLPPPLPKQVKVPIIMENHICDAKYHLGAYTGDDVRIVRDMML	184	
Db	121	PGMPCWVTGWDVNDERLPPPLPKQVKVPIIMENHICDAKYHLGAYTGDDVRIVRDMML	180	
QY	185	CAGNTRRDSQQSGSGPLVCKNGTWTIQAQVSWGEGCAQPNRPGIIVRTVYILDWTHHY	244	
Db	181	CAGNTRRDSQQSGSGPLVCKNGTWTIQAQVSWGEGCAQPNRPGIIVRTVYILDWTHHY	240	
QY	245	VPKK 248		
Db	241	VPKK 244		

```

RESULT 9
US-09-601-318-5
; Sequence 5, Application US/09601318
; Patent No. 6613769
; GENERAL INFORMATION:
; APPLICANT: Max-planck-Gesellschaft z. Frd. d. Wissenssch. e.v.
; APPLICANT: Byk Gulden Lomborg Chemische Fabrik GmbH
; APPLICANT: Bocde, Wolfram
; APPLICANT: Moroder, Luis
; APPLICANT: Pereira, Pedro Jose Barbosa
; APPLICANT: Bergner, Andreas
; APPLICANT: Huber, Robert
; APPLICANT: Sommerhoff, Christian
; APPLICANT: Schaschke, No. 6613769bert
; APPLICANT: Br, Thomas
; APPLICANT: Martin, Thomas
; APPLICANT: Stadlwieser, Josef
; APPLICANT: Ulrich, Wolf-Rdiger
; APPLICANT: Dominik, Andreas

```

```

/ APPLICANT: Thibaut, Ulrich
/ APPLICANT: Bundschuh, Daniela
/ APPLICANT: Beume, Rolf
/ APPLICANT: Goebel, Karl-Josef
/ TITLE OF INVENTION: Typcast-Inhibitoren
/ FILE REFERENCE: 17674P WO-1
/ CURRENT APPLICATION NUMBER: US/09/601,318
/ CURRENT FILING DATE: 2001-01-22
/ PRIOR APPLICATION NUMBER: DE19804761.4
/ PRIOR FILING DATE: 1998-02-06
/ PRIOR APPLICATION NUMBER: DE19851300.3
/ PRIOR FILING DATE: 1998-11-06
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 244
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-601-318-5

```

Query Match	97.7%	Score 1361;	DB 4;	Length 244;
Best Local Similarity	99.6%;	Pred. No. 3.3e-138;		
Matches 243;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	5	IVGQEA PRSKWPQVNSLRVHGYPYWMHFCGSLIHPQWVLTAAACVGPDKDLAALRVQL	64	
Db	1	IVGQEA PRSKWPQVNSLRVHGYPYWMHFCGSLIHPQWVLTAAHCVGPDKDLAALRVQL	60	
Qy	65	REGHLYYQDQLLPVSRITIVHPQFVTAQIGADIALLELEEPVKVSSHVHTVTLPPASFTFP	124	
Db	61	REGHLYYQDQLLPVSRITIVHPQFVTAQIGADIALLELEEPVKVSSHVHTVTLPPASFTFP	120	
Qy	125	PGMPCWVTGWDVNDERLPPPLPKQVKVPIIMENHICDAKYHLGATVGGDVRIVRDDML	184	
Db	121	PGMPCWVTGWDVNDERLPPPLPKQVKVPIIMENHICDAKYHLGATVGGDVRIVRDDML	180	
Qy	185	CAGNTRRDS CQGDGGPLVCKVNGTWLQAGVWSGEGCAQPNRPGIYTRVTYYLDWIHHY	244	
Db	181	CAGNTRRDS CQGDGGPLVCKVNGTWLQAGVWSGEGCAQPNRPGIYTRVTYYLDWIHHY	240	
Qy	245	VPKK 248		
Db	241	VPKK 244		

```

RESULT 10
US-09-601-318-6
; Sequence 6, Application US/09601318
; Patent No. 6613769
; GENERAL INFORMATION:
; APPLICANT: Max-Planck-Gesellschaft z. Fkd. d. Wissensch. e. V.
; APPLICANT: Byk Gulden Lomberg Chemische Fabrik GmbH
; APPLICANT: Bode, Wolfram
; APPLICANT: Moroder, Luis
; APPLICANT: Pereira, Pedro Jose Barbosa
; APPLICANT: Bergner, Andreas
; APPLICANT: Huber, Robert
; APPLICANT: Sommerhoff, Christian
; APPLICANT: Schaschke, No. 6613769bert
; APPLICANT: Br. Thomas
; APPLICANT: Martin, Thomas
; APPLICANT: Stadlwieser, Josef
; APPLICANT: Ulrich, Wolf-Rdiger
; APPLICANT: Dominik, Andreas
; APPLICANT: Thibaut, Ulrich
; APPLICANT: Bundschuh, Daniela
; APPLICANT: Beume, Rolf
; APPLICANT: Goebel, Karl-Josef
; TITLE OF INVENTION: Tryptase-Inhibitoren
; FILE REFERENCE: 17674P WO-1
; CURRENT APPLICATION NUMBER: US/09/601,318
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: DE19804761.4

```

```
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: DE19851300.3
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-601-318-6

Query Match          97.7%; Score 1361; DB 4; Length 244;
Best Local Similarity 99.6%; Pred. No. 3.3e-138;
Matches 243; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWLTAAACVGPDKDLAALRVQL 64
   |||||
Db 1 IVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWLTAAACVGPDKDLAALRVQL 60

QY 65 REQLHYQDQLLPVSRILVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
   |||||
Db 61 REQLHYQDQLLPVSRILVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 120

QY 125 PGMPCWWTGWDVNDRLPPPLKQVKVPIPMENHICDAKYHLGAYTGGDVRIVRDDML 184
   |||||
Db 121 PGMPCWWTGWDVNDRLPPPLKQVKVPIPMENHICDAKYHLGAYTGGDVRIVRDDML 180

QY 185 CAGNTRRDSQSGSGGGLVCKVNGTWMQAGVWSWGEGCAQPNRPGIYTRVYYLDWIHHY 244
   |||||
Db 181 CAGNTRRDSQSGSGGGLVCKVNGTWMQAGVWSWGEGCAQPNRPGIYTRVYYLDWIHHY 240

QY 245 VPXK 248
   |||||
Db 241 VPXK 244

RESULT 11
US-09-601-318-7
; Sequence 7, Application US/09601318
; Patent No. 6613769
; GENERAL INFORMATION:
; APPLICANT: Max-Planck-Gesellschaft z. Fnd. d. Wissensch. e.V
; APPLICANT: Byk Gulden Lomberg Chemische Fabrik GmbH
; APPLICANT: Bode, Wolfram
; APPLICANT: Moroder, Luis
; APPLICANT: Pereira, Pedro Jose Barbosa
; APPLICANT: Bergner, Andreas
; APPLICANT: Huber, Robert
; APPLICANT: Sommerhoff, Christian
; APPLICANT: Schaschke, No. 6613769bert
; APPLICANT: Br, Thomas
; APPLICANT: Martin, Thomas
; APPLICANT: Stadlwieser, Josef
; APPLICANT: Ulrich, Wolf-Rdiger
; APPLICANT: Dominik, Andreas
; APPLICANT: Thibaut, Ulrich
; APPLICANT: Bundschuh, Daniela
; APPLICANT: Beume, Rolf
; APPLICANT: Goebel, Karl-Josef
; TITLE OF INVENTION: Tryptase-Inhibitoren
; FILE REFERENCE: 17674P WO-1
; CURRENT APPLICATION NUMBER: US/09/601,318
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: DE19804761.4
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: DE19851300.3
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-601-318-7
Query Match          97.7%; Score 1361; DB 4; Length 244;
Best Local Similarity 99.6%; Pred. No. 3.3e-138;
Matches 243; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWLTAAACVGPDKDLAALRVQL 64
   |||||
Db 1 IVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWLTAAACVGPDKDLAALRVQL 60

QY 65 REQLHYQDQLLPVSRILVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
   |||||
Db 61 REQLHYQDQLLPVSRILVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 120

QY 125 PGMPCWWTGWDVNDRLPPPLKQVKVPIPMENHICDAKYHLGAYTGGDVRIVRDDML 184
   |||||
Db 121 PGMPCWWTGWDVNDRLPPPLKQVKVPIPMENHICDAKYHLGAYTGGDVRIVRDDML 180

QY 185 CAGNTRRDSQSGSGGGLVCKVNGTWMQAGVWSWGEGCAQPNRPGIYTRVYYLDWIHHY 244
   |||||
Db 181 CAGNTRRDSQSGSGGGLVCKVNGTWMQAGVWSWGEGCAQPNRPGIYTRVYYLDWIHHY 240

QY 245 VPXK 248
   |||||
Db 241 VPXK 244

RESULT 12
US-09-016-366A-23
; Sequence 23, Application US/09016366A
; Patent No. 5955431
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; APPLICANT: Huang, Chifu
; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,366A
; FILING DATE: January 30, 1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,090
; FILING DATE: 05-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-016-366A-23
Query Match          96.5%; Score 1344; DB 2; Length 267;
```


Best Local Similarity 98.4%; Pred. No. 2.5e-136;
Matches 241; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 IVGQEAAPRKPQVSLRVHGPVMMHFCGSLIHPQWVLTAAACVGPDKDLAALRVQL 64
DB 23 IVGQEAAPRKPQVSLRVHGPVMMHFCGSLIHPQWVLTAAACVGPDKDLAALRVQL 82

QY 65 REQLHYQDQLLPVSRILVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
DB 83 REQLHYQDQLLPVSRILVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 142

QY 125 PGMPCWWTGWDVNDRLPPFPFLKQVKVPIIMENHICDAKYHLGAYTGDDVRIVRDML 184
DB 143 PGMPCWWTGWDVNDRLPPFPFLKQVKVPIIMENHICDAKYHLGAYTGDDVRIVRDML 202

QY 185 CAGNTRDSCQDGGGGLVCKVNGTWTQAGVWSWEGCAQPNRPGIYTRVYYLDWIHHY 244
DB 203 CAGNTRDSCQDGGGGLVCKVNGTWTQAGVWSWEGCAQPNRPGIYTRVYYLDWIHHY 262

QY 245 VPKKP 249
DB 263 VPKKP 267

RESULT 13
US-08-978-404B-18
; Sequence 18, Application US/08978404B
; Patent No. 5968782
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
; TITLE OF INVENTION: FBRINOGEN
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA: US/08/978,404B
; FILING DATE: 25-NOV-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/032,354
; FILING DATE: 04-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5968782e
US-08-978-404B-18

Query Match 96.5%; Score 1344; DB 2; Length 267;
Best Local Similarity 98.4%; Pred. No. 2.5e-136;
Matches 241; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 IVGQEAAPRKPQVSLRVHGPVMMHFCGSLIHPQWVLTAAACVGPDKDLAALRVQL 64
DB 23 IVGQEAAPRKPQVSLRVHGPVMMHFCGSLIHPQWVLTAAACVGPDKDLAALRVQL 82

QY 65 REQLHYQDQLLPVSRILVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
DB 83 REQLHYQDQLLPVSRILVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 142

QY 125 PGMPCWWTGWDVNDRLPPFPFLKQVKVPIIMENHICDAKYHLGAYTGDDVRIVRDML 184
DB 143 PGMPCWWTGWDVNDRLPPFPFLKQVKVPIIMENHICDAKYHLGAYTGDDVRIVRDML 202

QY 185 CAGNTRDSCQDGGGGLVCKVNGTWTQAGVWSWEGCAQPNRPGIYTRVYYLDWIHHY 244
DB 203 CAGNTRDSCQDGGGGLVCKVNGTWTQAGVWSWEGCAQPNRPGIYTRVYYLDWIHHY 262

QY 245 VPKKP 249
DB 263 VPKKP 267

RESULT 14
US-08-944-483-69
; Sequence 69, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6183. US. 01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6232456e
US-08-944-483-69

Query Match 91.5%; Score 1274; DB 3; Length 245;
 Best Local Similarity 92.2%; Pred. No. 7.5e-129;
 Matches 226; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 5 IVGGQAPRSKWPQVSLRVHGYWVHFCGSLIHPQWVLTAAACVGPDPVKDLAALRVQL 64
 DB 1 IVGGQAPRSKWPQVSLRVHGYWVHFCGSLIHPQWVLTAAACVGPDPVKDLAALRVQL 60
 QY 65 REQHLXYQDQLLPVSRILVHPQFYTAIGADIALLELEBPVKVSSHVHTVTLPPASETFP 124
 DB 61 REQHLXYQDQLLPVSRILVHPQFYIIQTGADIALLELEBPVNISSRVHTVMLPPASETFP 120
 QY 125 PGMPCWVTGWDVNDNERLPPPPPLKQVKVPIIMENHICDAKYHLGAYTGGDDVRIVRDDML 184
 DB 121 PGMPCWVTGWDVNDNERLPPPPPLKQVKVPIIMENHICDAKYHLGAYTGGDDVRIVRDDML 180
 QY 185 CAGNTRDSCQSGGGLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVYYLDWIHHY 244
 DB 181 CAGNSQDSCGSGGLVCKVNGTWLQAGVSWDEGCAQPNRPGIYTRVYYLDWIHHY 240
 QY 245 VPKKP 249
 DB 241 VPKKP 245

RESULT 15
 US-09-016-366A-17
 ; Sequence 17, Application US/09016366A
 ; Patent No. 5953431
 ; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; APPLICANT: Huang, Chifu
 ; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
 ; TITLE OF INVENTION: INHIBITORS
 ; NUMBER OF SEQUENCES: 65
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: U.S.A.
 ; ZIP: 02210-2211
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,366A
 ; FILING DATE: January 30, 1998
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/037,090
 ; FILING DATE: 05-FEB-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Plumer, Elizabeth R.
 ; REGISTRATION NUMBER: 36,637
 ; REFERENCE/DOCKET NUMBER: B0801/7093
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-720-3500
 ; TELEFAX: 617-720-2441
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 275 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-016-366A-17

Query Match 91.5%; Score 1274; DB 2; Length 275;

Best Local Similarity 92.2%; Pred. No. 8.8e-129;
 Matches 226; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 5 IVGGQAPRSKWPQVSLRVHGYWVHFCGSLIHPQWVLTAAACVGPDPVKDLAALRVQL 64
 DB 31 IVGGQAPRSKWPQVSLRVHGYWVHFCGSLIHPQWVLTAAACVGPDPVKDLAALRVQL 90
 QY 65 REQHLXYQDQLLPVSRILVHPQFYTAIGADIALLELEBPVKVSSHVHTVTLPPASETFP 124
 DB 91 REQHLXYQDQLLPVSRILVHPQFYIIQTGADIALLELEBPVNISSRVHTVMLPPASETFP 150
 QY 125 PGMPCWVTGWDVNDNERLPPPPPLKQVKVPIIMENHICDAKYHLGAYTGGDDVRIVRDDML 184
 DB 151 PGMPCWVTGWDVNDNERLPPPPPLKQVKVPIIMENHICDAKYHLGAYTGGDDVRIVRDDML 210
 QY 185 CAGNTRDSCQSGGGLVCKVNGTWLQAGVSWGEGCAQPNRPGIYTRVYYLDWIHHY 244
 DB 211 CAGNSQDSCGSGGGLVCKVNGTWLQAGVSWDEGCAQPNRPGIYTRVYYLDWIHHY 270
 QY 245 VPKKP 249
 DB 271 VPKKP 275

Search completed: July 22, 2004, 15:27:27
 Job time : 59 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 22, 2004, 15:25:12 ; Search time 940 Seconds
(without alignments)
82.953 Million cell updates/sec

Title: US-09-598-982-21

Perfect score: 1393

Sequence: 1 LKRIVGGQAPRSKWFQV.....IYTRVTVYLDWIHVVPKPK 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1288442 seqs, 313154207 residues

Total number of hits satisfying chosen parameters: 1288442

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1368	98.2	254	12	US-10-150-813-74
2	1368	98.2	254	12	US-10-139-854-74
3	1368	98.2	254	14	US-10-131-409-74
4	1368	98.2	254	15	US-10-150-811-74
5	1368	98.2	256	12	US-10-150-813-92
6	1368	98.2	256	12	US-10-139-854-92
7	1368	98.2	256	14	US-10-131-409-92
8	1368	98.2	256	15	US-10-150-811-92
9	1368	98.2	264	12	US-10-150-813-104
10	1368	98.2	264	12	US-10-139-854-104
11	1368	98.2	264	14	US-10-131-409-104
12	1368	98.2	264	15	US-10-150-811-104
13	1368	98.2	275	10	US-09-813-432-44
14	1368	98.2	275	12	US-10-246-583-44
15	1368	98.2	275	15	US-10-352-684A-48

16	1368	98.2	275	15	US-10-174-364-44
17	1368	98.2	275	16	US-10-287-226-94
18	1368	98.2	275	16	US-10-689-832-44
19	1363	97.8	272	14	US-10-287-226-92
20	1347.5	96.7	272	14	US-10-117-323-40
21	1329	95.4	691	16	US-10-275-505-13
22	1323	95.0	275	16	US-10-287-226-90
23	1317	94.5	266	12	US-10-150-813-84
24	1317	94.5	266	12	US-10-139-854-84
25	1317	94.5	266	14	US-10-131-409-84
26	1317	94.5	266	15	US-10-150-811-84
27	1312	94.2	279	16	US-10-287-226-88
28	1274	91.5	275	14	US-10-117-323-36
29	1274	91.5	275	15	US-10-352-684A-46
30	1270	91.2	231	10	US-09-898-837A-52
31	1104	79.3	199	12	US-10-150-813-98
32	1104	79.3	199	12	US-10-139-854-98
33	1104	79.3	199	14	US-10-131-409-98
34	1104	79.3	199	15	US-10-150-811-98
35	1091	78.3	252	10	US-09-813-432-42
36	1091	78.3	252	12	US-10-246-583-42
37	1091	78.3	252	15	US-10-174-364-42
38	1091	78.3	252	16	US-10-689-832-42
39	1091	78.3	276	14	US-10-117-323-35
40	1077	77.3	276	14	US-10-311-955-3
41	1064	76.4	247	12	US-10-150-813-86
42	1064	76.4	247	12	US-10-139-854-86
43	1064	76.4	247	14	US-10-131-409-86
44	1064	76.4	247	15	US-10-150-811-86
45	1054	75.7	310	16	US-10-275-505-8

ALIGNMENTS

RESULT 1
US-10-150-813-74
; Sequence 74, Application US/10150813
; Publication No. US20030224367A1
; GENERAL INFORMATION:
; APPLICANT: Majumder
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-675CIP1CON2
; CURRENT APPLICATION NUMBER: US/10/150,813
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: 09/898,954
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/182,733
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/182,724
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/183,896
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/184,497
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/224,157
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,744
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/197,083
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/233,405
; PRIOR FILING DATE: 2000-09-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-150-813-74

Db 190 CAGNTRRDS CGDGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYYLDWIHY 249
 QY 245 VPKKP 249
 Db 250 VPKKP 254

RESULT 4
 US-10-150-811-74
 ; Sequence 74, Application US/10150811
 ; Publication No. US20040010120A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Malyankar et al.
 ; TITLE OF INVENTION: No. US20040010120A1el Polypeptides and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 15966-675CIP2CON1
 ; CURRENT APPLICATION NUMBER: US/10/150,811
 ; CURRENT FILING DATE: 2002-05-17
 ; PRIOR APPLICATION NUMBER: 09/970,607
 ; PRIOR FILING DATE: 2001-10-03
 ; PRIOR APPLICATION NUMBER: 60/182,733
 ; PRIOR FILING DATE: 2000-02-15
 ; PRIOR APPLICATION NUMBER: 60/182,724
 ; PRIOR FILING DATE: 2000-02-15
 ; PRIOR APPLICATION NUMBER: 60/183,896
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: 60/184,497
 ; PRIOR FILING DATE: 2000-02-23
 ; PRIOR APPLICATION NUMBER: 60/224,157
 ; PRIOR FILING DATE: 2000-08-10
 ; PRIOR APPLICATION NUMBER: 60/184,482
 ; PRIOR FILING DATE: 2000-02-23
 ; PRIOR APPLICATION NUMBER: 60/184,744
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: 60/197,083
 ; PRIOR FILING DATE: 2000-04-13
 ; PRIOR APPLICATION NUMBER: 60/233,405
 ; PRIOR FILING DATE: 2000-09-18
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 138
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 74
 ; LENGTH: 254
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-150-811-74

Query Match 98.2%; Score 1368; DB 15; Length 254;
 Best Local Similarity 99.6%; Pred. No. 1.5e-124;
 Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 IVGGQAPRSKWPQVSLRVHGPYMMHFCGSLTHPQVLTAAACVGPDKDLAALRVOL 64
 Db 10 IVGGQAPRSKWPQVSLRVHGPYMMHFCGSLTHPQVLTAAACVGPDKDLAALRVOL 69
 QY 65 REQHLYYQDQLLPVSRILVHPQFYTAQIGADIALLELEPEPVKSSHVHTVTLPPASETFP 124
 Db 70 REQHLYYQDQLLPVSRILVHPQFYTAQIGADIALLELEPEPVKSSHVHTVTLPPASETFP 129
 QY 125 PGMPCWVTGWDVNDRLPPFPFLKQVKVPIMENHICDAKYHLGAYTGDDVIRVRDML 184
 Db 130 PGMPCWVTGWDVNDRLPPFPFLKQVKVPIMENHICDAKYHLGAYTGDDVIRVRDML 189
 QY 185 CAGNTRRDS CGDGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYYLDWIHY 244
 Db 190 CAGNTRRDS CGDGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYYLDWIHY 249
 QY 245 VPKKP 249
 Db 250 VPKKP 254

RESULT 5

US-10-150-813-92
 ; Sequence 92, Application US/10150813
 ; Publication No. US20030224367A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Majumder
 ; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 15966-675CIP1CON2
 ; CURRENT APPLICATION NUMBER: US/10/150,813
 ; CURRENT FILING DATE: 2002-12-03
 ; PRIOR APPLICATION NUMBER: 09/898,954
 ; PRIOR FILING DATE: 2001-07-03
 ; PRIOR APPLICATION NUMBER: 60/182,733
 ; PRIOR FILING DATE: 2000-02-15
 ; PRIOR APPLICATION NUMBER: 60/182,724
 ; PRIOR FILING DATE: 2000-02-15
 ; PRIOR APPLICATION NUMBER: 60/183,896
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: 60/184,497
 ; PRIOR FILING DATE: 2000-02-23
 ; PRIOR APPLICATION NUMBER: 60/224,157
 ; PRIOR FILING DATE: 2000-08-10
 ; PRIOR APPLICATION NUMBER: 60/184,482
 ; PRIOR FILING DATE: 2000-02-23
 ; PRIOR APPLICATION NUMBER: 60/184,744
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: 60/197,083
 ; PRIOR FILING DATE: 2000-04-13
 ; PRIOR APPLICATION NUMBER: 60/233,405
 ; PRIOR FILING DATE: 2000-09-18
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 135
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 92
 ; LENGTH: 256
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-150-813-92

Query Match 98.2%; Score 1368; DB 12; Length 256;
 Best Local Similarity 99.6%; Pred. No. 1.6e-124;
 Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 IVGGQAPRSKWPQVSLRVHGPYMMHFCGSLTHPQVLTAAACVGPDKDLAALRVOL 64
 Db 12 IVGGQAPRSKWPQVSLRVHGPYMMHFCGSLTHPQVLTAAACVGPDKDLAALRVOL 71
 QY 65 REQHLYYQDQLLPVSRILVHPQFYTAQIGADIALLELEPEPVKSSHVHTVTLPPASETFP 124
 Db 72 REQHLYYQDQLLPVSRILVHPQFYTAQIGADIALLELEPEPVKSSHVHTVTLPPASETFP 131
 QY 125 PGMPCWVTGWDVNDRLPPFPFLKQVKVPIMENHICDAKYHLGAYTGDDVIRVRDML 184
 Db 132 PGMPCWVTGWDVNDRLPPFPFLKQVKVPIMENHICDAKYHLGAYTGDDVIRVRDML 191
 QY 185 CAGNTRRDS CGDGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYYLDWIHY 244
 Db 192 CAGNTRRDS CGDGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYYLDWIHY 251
 QY 245 VPKKP 249
 Db 252 VPKKP 256

RESULT 6
 US-10-139-854-92
 ; Sequence 92, Application US/10139854
 ; Publication No. US20030202971A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Majumder, Kumud
 ; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 15966-675CON2
 ; CURRENT APPLICATION NUMBER: US/10/139,854
 ; CURRENT FILING DATE: 2002-12-02

```
; PRIOR APPLICATION NUMBER: 09/783,429
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,733
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/182,724
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/183,896
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/184,497
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/224,157
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,744
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,497
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/182,733
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/182,724
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/183,896
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/184,497
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/233,405
; PRIOR FILING DATE: 2000-09-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-409-92

Query Match          98.2%; Score 1368; DB 12; Length 256;
Best Local Similarity 99.6%; Pred. No. 1.6e-124;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  5  IVGQEARSKWPQVSLRVHGPVYMHFCGSLIHPQWLTAAACVGPDKDLAALRVQL 64
Db  12  IVGQEARSKWPQVSLRVHGPVYMHFCGSLIHPQWLTAAACVGPDKDLAALRVQL 71

Qy  65  REQLHYQDQLLPVSRILVHPQFYTAQIGADIALLELEPVPKVSSSHVHTVTLPPASETFP 124
Db  72  REQLHYQDQLLPVSRILVHPQFYTAQIGADIALLELEPVPKVSSSHVHTVTLPPASETFP 131

Qy  125  PGMPCWWTGWDVNDRLPPFPPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDML 184
Db  132  PGMPCWWTGWDVNDRLPPFPPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDML 191

Qy  185  CAGNTRDSCQSGGGLVCKVNGTWTQAGVWSWGEGCAQPNRPGIYTRVYILDWIIHY 244
Db  192  CAGNTRDSCQSGGGLVCKVNGTWTQAGVWSWGEGCAQPNRPGIYTRVYILDWIIHY 251

Qy  245  VPKKP 249
Db  252  VPKKP 256

RESULT 7
US-10-131-409-92
; Sequence 92, Application US/10131409
; Publication No. US20030199465A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar et al.
; TITLE OF INVENTION: No. US20030199465A1el Polypeptides and Nucleic Acids Encoding Sam
; FILE REFERENCE: 15966-675CIP1CON1
; CURRENT APPLICATION NUMBER: US/10/131,409
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/898,954
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/182,733
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/182,724
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/183,896
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/184,497
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,744
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/197,083
; PRIOR FILING DATE: 2000-04-13
```

```
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/224,157
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,744
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/197,083
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/233,405
; PRIOR FILING DATE: 2000-09-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-409-92

Query Match          98.2%; Score 1368; DB 14; Length 256;
Best Local Similarity 99.6%; Pred. No. 1.6e-124;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  5  IVGQEARSKWPQVSLRVHGPVYMHFCGSLIHPQWLTAAACVGPDKDLAALRVQL 64
Db  12  IVGQEARSKWPQVSLRVHGPVYMHFCGSLIHPQWLTAAACVGPDKDLAALRVQL 71

Qy  65  REQLHYQDQLLPVSRILVHPQFYTAQIGADIALLELEPVPKVSSSHVHTVTLPPASETFP 124
Db  72  REQLHYQDQLLPVSRILVHPQFYTAQIGADIALLELEPVPKVSSSHVHTVTLPPASETFP 131

Qy  125  PGMPCWWTGWDVNDRLPPFPPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDML 184
Db  132  PGMPCWWTGWDVNDRLPPFPPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDML 191

Qy  185  CAGNTRDSCQSGGGLVCKVNGTWTQAGVWSWGEGCAQPNRPGIYTRVYILDWIIHY 244
Db  192  CAGNTRDSCQSGGGLVCKVNGTWTQAGVWSWGEGCAQPNRPGIYTRVYILDWIIHY 251

Qy  245  VPKKP 249
Db  252  VPKKP 256

RESULT 8
US-10-150-811-92
; Sequence 92, Application US/10150811
; Publication No. US20040010120A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar et al.
; TITLE OF INVENTION: No. US20040010120A1el Polypeptides and Nucleic Acids Encoding Sam
; FILE REFERENCE: 15966-675CIP2CON1
; CURRENT APPLICATION NUMBER: US/10/150,811
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 09/970,607
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/182,733
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/182,724
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/183,896
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/184,497
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/224,157
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,744
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/197,083
; PRIOR FILING DATE: 2000-04-13
```

```
; PRIOR APPLICATION NUMBER: 60/233,405
; PRIOR FILING DATE: 2000-09-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-150-811-92

Query Match      98.2%; Score 1368; DB 15; Length 256;
Best Local Similarity 99.6%; Pred. No. 1.6e-124;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 IVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWVLTAAACVGPDKDLAALRVQL 64
      |||
Db      12 IVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWVLTAAACVGPDKDLAALRVQL 71
      |||

QY      65 REQLHYQDQLLPVSRILVHPQFYTAQICADIALLELEBPVKVSSHVHTVTLPPASETFP 124
      |||
Db      72 REQLHYQDQLLPVSRILVHPQFYTAQICADIALLELEBPVKVSSHVHTVTLPPASETFP 131
      |||

QY      125 PMPQWVTGWDVNDERLPPFPPLKQVKVPTMENHICDAKYHLGAYTGDDVRIVRDDML 184
      |||
Db      132 PMPQWVTGWDVNDERLPPFPPLKQVKVPTMENHICDAKYHLGAYTGDDVRIVRDDML 191
      |||

QY      185 CAGNTRRSDSCGDSGGLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYYLDDWIHY 244
      |||
Db      192 CAGNTRRSDSCGDSGGLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYYLDDWIHY 251
      |||

QY      245 VPKKP 249
      ||||
Db      252 VPKKP 256
      ||||

RESULT 9
US-10-150-813-104
; Sequence 104, Application US/10150813
; Publication No. US20030224367A1
; GENERAL INFORMATION:
; APPLICANT: Majumder
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-675CIPCON2
; CURRENT APPLICATION NUMBER: US/10/150,813
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: 09/898,954
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/182,733
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/182,724
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/183,896
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/184,497
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/224,157
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,744
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/184,497
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/197,083
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/233,405
; PRIOR FILING DATE: 2000-09-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-150-813-104

Query Match      98.2%; Score 1368; DB 12; Length 264;
Best Local Similarity 99.6%; Pred. No. 1.6e-124;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 IVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWVLTAAACVGPDKDLAALRVQL 64
      |||
Db      20 IVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWVLTAAACVGPDKDLAALRVQL 79
      |||

QY      65 REQLHYQDQLLPVSRILVHPQFYTAQICADIALLELEBPVKVSSHVHTVTLPPASETFP 124
      |||
Db      80 REQLHYQDQLLPVSRILVHPQFYTAQICADIALLELEBPVKVSSHVHTVTLPPASETFP 139
      |||

QY      125 PMPQWVTGWDVNDERLPPFPPLKQVKVPTMENHICDAKYHLGAYTGDDVRIVRDDML 184
      |||
Db      140 PMPQWVTGWDVNDERLPPFPPLKQVKVPTMENHICDAKYHLGAYTGDDVRIVRDDML 199
      |||

QY      185 CAGNTRRSDSCGDSGGLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYYLDDWIHY 244
      |||
Db      200 CAGNTRRSDSCGDSGGLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYYLDDWIHY 259
      |||

QY      245 VPKKP 249
      ||||
Db      260 VPKKP 264
      ||||

RESULT 10
US-10-139-854-104
; Sequence 104, Application US/10139854
; Publication No. US20030202971A1
; GENERAL INFORMATION:
; APPLICANT: Majumder, Kumud
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-675CON2
; CURRENT APPLICATION NUMBER: US/10/139,854
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 09/783,429
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,733
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/182,724
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/183,896
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/184,497
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/224,157
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,744
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/197,083
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/233,405
; PRIOR FILING DATE: 2000-09-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-854-104

Query Match      98.2%; Score 1368; DB 12; Length 264;
Best Local Similarity 99.6%; Pred. No. 1.6e-124;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 IVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWVLTAAACVGPDKDLAALRVQL 64
      |||
Db      20 IVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWVLTAAACVGPDKDLAALRVQL 79
      |||
```

QY 65 REQHLYYQDQLLPVSRIRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
Db |||||
QY 80 REQHLYYQDQLLPVSRIRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 139
Db |||||
QY 125 PGMPCWVTGWDVNDRLPPFPFLKQVKVPIIMENHICDAKYHLGAYTGDDVIRVDDML 184
Db |||||
QY 140 PGMPCWVTGWDVNDRLPPFPFLKQVKVPIIMENHICDAKYHLGAYTGDDVIRVDDML 199
QY 185 CAGNTRDSCQDGGGLPVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYYLDDWIHHY 244
Db |||||
QY 200 CAGNTRDSCQDGGGLPVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYYLDDWIHHY 259
QY 245 VPKKP 249
Db |||||
QY 260 VPKKP 264

RESULT 11

US-10-131-409-104
; Sequence 104, Application US/10131409
; Publication No. US20030199465A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar et al.
; TITLE OF INVENTION: No. US20030199465A1el Polypeptides and Nucleic Acids Encoding Sam
; FILE REFERENCE: 15966-675CIP1CON1
; CURRENT APPLICATION NUMBER: US/10/131,409
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/898,954
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/182,733
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/182,724
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/183,896
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/184,497
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/224,157
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/197,083
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/233,405
; PRIOR FILING DATE: 2000-09-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-409-104

Query Match 98.2%; Score 1368; DB 14; Length 264;
Best Local Similarity 99.6%; Pred. No. 1.6e-124;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IVGGQAPRSKWPQVSLRVHGPYMMHFCGSLIHPQWLTAAACVGPDPVKDLAALRVOL 64
Db |||||
QY 65 REQHLYYQDQLLPVSRIRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
Db |||||
QY 80 REQHLYYQDQLLPVSRIRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 139
QY 125 PGMPCWVTGWDVNDRLPPFPFLKQVKVPIIMENHICDAKYHLGAYTGDDVIRVDDML 184
Db |||||
QY 140 PGMPCWVTGWDVNDRLPPFPFLKQVKVPIIMENHICDAKYHLGAYTGDDVIRVDDML 199

QY 185 CAGNTRDSCQDGGGLPVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYYLDDWIHHY 244
Db |||||
QY 200 CAGNTRDSCQDGGGLPVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYYLDDWIHHY 259
QY 245 VPKKP 249
Db |||||
QY 260 VPKKP 264

RESULT 12

US-10-150-811-104
; Sequence 104, Application US/10150811
; Publication No. US20040010120A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar et al.
; TITLE OF INVENTION: No. US20040010120A1el Polypeptides and Nucleic Acids Encoding Sam
; FILE REFERENCE: 15966-675CIP2CON1
; CURRENT APPLICATION NUMBER: US/10/150,811
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 09/970,607
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/182,733
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/182,724
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/183,896
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/184,497
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/224,157
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,744
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/197,083
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/233,405
; PRIOR FILING DATE: 2000-09-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 104
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-150-811-104

Query Match 98.2%; Score 1368; DB 15; Length 264;
Best Local Similarity 99.6%; Pred. No. 1.6e-124;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IVGGQAPRSKWPQVSLRVHGPYMMHFCGSLIHPQWLTAAACVGPDPVKDLAALRVOL 64
Db |||||
QY 65 REQHLYYQDQLLPVSRIRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 124
Db |||||
QY 80 REQHLYYQDQLLPVSRIRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFP 139
QY 125 PGMPCWVTGWDVNDRLPPFPFLKQVKVPIIMENHICDAKYHLGAYTGDDVIRVDDML 184
Db |||||
QY 140 PGMPCWVTGWDVNDRLPPFPFLKQVKVPIIMENHICDAKYHLGAYTGDDVIRVDDML 199
QY 185 CAGNTRDSCQDGGGLPVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYYLDDWIHHY 244
Db |||||
QY 200 CAGNTRDSCQDGGGLPVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYYLDDWIHHY 259
QY 245 VPKKP 249
Db |||||
QY 260 VPKKP 264

RESULT 13

US-09-813-432-44
; Sequence 44, Application US/09813432
; Publication No. US20030148485A1
; GENERAL INFORMATION:
; APPLICANT: Taupier Jr., Raymond J
; APPLICANT: Majmuder, Kamud
; APPLICANT: Spaderna, Steven K
; APPLICANT: Smithson, Glenda
; APPLICANT: Mezes, Peter S
; APPLICANT: Vernet, Corine A. M.
; TITLE OF INVENTION: No. US20030148485A1el Polypeptides and Amino Acids Encoding Same
; FILE REFERENCE: 15966-729
; CURRENT APPLICATION NUMBER: US/09/813,432
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,836
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/193,843
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-432-44

Query Match 98.2%; Score 1368; DB 10; Length 275;
Best Local Similarity 99.6%; Pred. No. 1.7e-124;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 IVGGQAPRSKWPQVSLRVHGPYMMHFCGSLIHPQWLTAAACVGPDKDLAALRVQL 64
Db 31 IVGGQAPRSKWPQVSLRVHGPYMMHFCGSLIHPQWLTAAACVGPDKDLAALRVQL 90
QY 65 REQHLYYQDQLLPVSRILVHPQFYTAQIGADIALLEPEPVKVVSHVHTVTLPPASETFP 124
Db 91 REQHLYYQDQLLPVSRILVHPQFYTAQIGADIALLEPEPVKVVSHVHTVTLPPASETFP 150
QY 125 PGMPCWVTGWGDVNDERLPPFPPLKQVKVPMENHICDAKYHLGAYTGDDVRIVRDDML 184
Db 151 PGMPCWVTGWGDVNDERLPPFPPLKQVKVPMENHICDAKYHLGAYTGDDVRIVRDDML 210
QY 185 CAGNTRRSDSCQDSGGPLVCKVNGTWLQAGVVSWECEGCAQPNRPGIYTRVTYLDWIHY 244
Db 211 CAGNTRRSDSCQDSGGPLVCKVNGTWLQAGVVSWECEGCAQPNRPGIYTRVTYLDWIHY 270
QY 245 VPKKP 249
Db 271 VPKKP 275

RESULT 14

US-10-246-583-44
; Sequence 44, Application US/10246583

; Publication No. US20040058862A1

; GENERAL INFORMATION:
; APPLICANT: Majmuder
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-729CIP2CON1
; CURRENT APPLICATION NUMBER: US/10/246,583
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/174,364
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-246-583-44

Query Match 98.2%; Score 1368; DB 12; Length 275;
Best Local Similarity 99.6%; Pred. No. 1.7e-124;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 IVGGQAPRSKWPQVSLRVHGPYMMHFCGSLIHPQWLTAAACVGPDKDLAALRVQL 64
Db 31 IVGGQAPRSKWPQVSLRVHGPYMMHFCGSLIHPQWLTAAACVGPDKDLAALRVQL 90
QY 65 REQHLYYQDQLLPVSRILVHPQFYTAQIGADIALLEPEPVKVVSHVHTVTLPPASETFP 124
Db 91 REQHLYYQDQLLPVSRILVHPQFYTAQIGADIALLEPEPVKVVSHVHTVTLPPASETFP 150
QY 125 PGMPCWVTGWGDVNDERLPPFPPLKQVKVPMENHICDAKYHLGAYTGDDVRIVRDDML 184
Db 151 PGMPCWVTGWGDVNDERLPPFPPLKQVKVPMENHICDAKYHLGAYTGDDVRIVRDDML 210
QY 185 CAGNTRRSDSCQDSGGPLVCKVNGTWLQAGVVSWECEGCAQPNRPGIYTRVTYLDWIHY 244
Db 211 CAGNTRRSDSCQDSGGPLVCKVNGTWLQAGVVSWECEGCAQPNRPGIYTRVTYLDWIHY 270
QY 245 VPKKP 249
Db 271 VPKKP 275

RESULT 15

US-10-352-684A-48
; Sequence 48, Application US/10352684A
; Publication No. US20030215452A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; APPLICANT: Weich, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,

; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
; FILE REFERENCE: MPI02-019P1RNONNIM
; CURRENT APPLICATION NUMBER: US/10/352,684A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/364,476
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-10-352-684A-48

Query Match 98.2%; Score 1368; DB 15; Length 275;
Best Local Similarity 99.6%; Pred. No. 1.7e-124;
Matches 244; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 IVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWLTAAACVGPDVKDLAALRVQL 64
Db 31 IVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWLTAAHCVGPDVKDLAALRVQL 90
Qy 65 REQHLYYQDQLLPVSRILIVHPQFYTAIGADIALLEBEPVKVSSHVHTVTLPPASETFP 124
Db 91 REQHLYYQDQLLPVSRILIVHPQFYTAIGADIALLEBEPVKVSSHVHTVTLPPASETFP 150
Qy 125 PGMPCWVTGWDVNDRLPPPELPKQVKPIMENHICDAKYHLGAYTGDDVRIVRDDML 184
Db 151 PGMPCWVTGWDVNDRLPPPELPKQVKPIMENHICDAKYHLGAYTGDDVRIVRDDML 210
Qy 185 CAGNTRDSCQSGGSLVCKVNGTWLQAGVWSNGEGCAQFNRPFIYTRYTYLDWIHHY 244
Db 211 CAGNTRDSCQSGGSLVCKVNGTWLQAGVWSNGEGCAQFNRPFIYTRYTYLDWIHHY 270
Qy 245 VPKKP 249
Db 271 VPKKP 275

Search completed: July 22, 2004, 15:54:31
Job time : 941 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 22, 2004, 15:27:32 ; Search time 4800 Seconds
(without alignments)
2248.420 Million cell updates/sec

Title: US-09-598-982-21

Perfect score: 1393

Sequence: 1 LEKRIVGQAEPRSKWQV.....IYTRVTYVLDWIHYVKKP 249

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xl
-Q=/cgn2_1/USPTO_spool_p/US09598982/runat_20072004_064409_6487/app_query.fasta_1.391
-DB=GenEmbl -QWMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09598982.qcgn_1_1_7406@runat_20072004_064409_6487 -NCPU=6 -ICPU=3
-NO_WMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hcg.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sv.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_on.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rnd.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1393	100.0	771	6	AX347853 Sequence
2	1388	99.6	771	6	AX347869 Sequence
3	1387	99.6	771	6	AR165112 Sequence
4	1387	99.6	771	6	AX347841 Sequence
5	1387	99.6	771	6	BD211490 Enzymatic
6	1384	99.4	771	6	AX347857 Sequence
7	1384	99.4	771	6	AX347859 Sequence
8	1382	99.2	771	6	AX347838 Sequence
9	1379	99.0	771	6	AX347855 Sequence
10	1379	99.0	771	6	AX347873 Sequence
11	1379	99.0	771	6	AX347875 Sequence
12	1374	98.6	735	6	AX347861 Sequence
13	1374	98.6	735	6	AX347871 Sequence
14	1369	98.3	735	6	AX347877 Sequence
15	1368	98.2	735	6	AR165109 Sequence
16	1368	98.2	735	6	AX347843 Sequence
17	1368	98.2	735	6	BD211487 Enzymatic
18	1368	98.2	1128	6	AR080461 Sequence
19	1368	98.2	1128	9	HUMTRY2A
20	1368	98.2	1143	9	HUMBTYP
21	1368	98.2	1145	9	S55551
22	1368	98.2	1194	9	BC029356 Homo sapi
23	1368	98.2	1235	9	BC038416 Homo sapi
24	1365	98.0	735	6	AX347865 Sequence
25	1365	98.0	735	6	AX347867 Sequence
26	1363	97.8	735	6	AX347834 Sequence
27	1363	97.8	1137	6	AR080460 Sequence
28	1363	97.8	1137	9	HUMTRY1A
29	1360	97.6	735	6	AX347863 Sequence
30	1360	97.6	735	6	AX347881 Sequence
31	1360	97.6	735	6	AX347883 Sequence
32	1355	97.3	735	6	AX347879 Sequence
33	1344	96.5	1081	6	AR080462 Sequence
34	1344	96.5	1081	6	AX329646 Sequence
35	1344	96.5	1081	6	AX330205 Sequence
36	1344	96.5	1081	6	AX334644 Sequence
37	1344	96.5	1081	6	AX375047 Sequence
38	1344	96.5	1081	9	HUMTRY3A
39	1341	96.3	1221	6	AX014344 Sequence
40	1341	96.3	1221	6	BD222223 Human nuc
41	1329	95.4	2662	6	AX338508 Sequence
42	1286	92.3	884	9	AF206665 Homo sapi
43	1286	92.3	1206	9	BC028059 Homo sapi
44	1286	92.3	1207	9	BC051852 Homo sapi
45	1274	91.5	1154	6	AR080459 Sequence

ALIGNMENTS

RESULT 1

AX347853
LOCUS 771 bp DNA linear PAT 01-FEB-2000
DEFINITION Sequence 20 from Patent WO0198470.
ACCESSION AX347853
VERSION AX347853.1 GI:18495660
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Maffit, M., Niles, A. L. and Haak-Prendoscho, M.
TITLE Recombinant proteolytic trypases, active site mutants thereof, and
methods of making same
JOURNAL Patent: WO 0198470-A 20 27-DEC-2001;
PROMEGA CORPORATION (US)
FEATURES
source Location/Qualifiers
1..771
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
<1..756
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD22420.1"
/db_xref="GI:18495661"
/db_xref="RETRMBL:CAD22420"
/translation="GPLEKRIVGGQAPRSKWPQVLSLRVHGPPWHFCGGSLLHPQW
VLTAAACVGFVDKLAALRQLRREQLHYQDQLLVSRILVHPQFYTAQIGADIALLE
LIEPDKVSHGHTVTLTPASSETPPGMCVWTGMDVNDRLRPPPLKQVKPVTME
NHICDKYHLGATGDDVIRVDMLCAGNTRDSCQGDGGLVKVNGTWLQAGVW
SWEGCAQNPNRGIYTRVTYYLDWIHHVPKK"

ORIGIN
Alignment Scores:
Pred. No.: 1,77e-122 Length: 771
Score: 1393.00 Matches: 249
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-598-982-21 (1-249) x AX347853 (1-771)

Qy 1 LeuGluYsArgIleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20
Db 7 CTCGAGAAAGATCGTCGGGGTCAGGAGCCCCCAGAGCAAGTGGCCCTGGCAGTG 66
Qy 21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40
Db 67 AGCCTGAGAGTCACGGCCCATCTGATGCATCTCTCGCGGGGCTCCCTCATCCACCCC 126
Qy 41 GlnTrpValLeuThrAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeu 60
Db 127 CAGTGGGTGCTGACCCCGCGGGTGGTGGGACCGGACGTCAGAGATCTGGCGCCCTC 186
Qy 61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80
Db 187 AGGCTGCAACTCGGGGAGCAGCACTCTACTACGAGACCAGCTGCTGCGGTCAGCAGG 246
Qy 81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuGlu 100
Db 247 ATCATGTGTGACCCACAGTGTCTACCGCCAGATCGGAGCGGACATGCGCCCTGCTGGAG 306
Qy 101 LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer 120
Db 307 CTGGAGAGCCGGTGAAGGCTCCAGCACAGTCCACACGGTCAACCTGCGCCCTGCCTCA 366
Qy 121 GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsn 140
Db 367 GAGACCTTCCCCCGGGATGCGGTGCTGGGTCACTGGCTGGGCGGATGGACAATGAT 426
Qy 141 GluArgLeuProProPheProLeuLeuGlnValLysValProIleMetGluAsnHis 160

```

Db      67 AGCTGAGAGTCCACGGCCCATCTGGATGCATCTTCTGCGGGGCTCCCTCATCCACCCC 126
QY      41 GlnTrpValLeuThrAlaAlaAAlaCysValGlyProAspValLysAspLeuAlaAlaLeu 60
Db      127 CAGGGGTGTGTGACCGCGCGGGTGTGGTGGACCGGACGTCACAGGATCTGGCGCCCTC 186
QY      61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80
Db      187 AGGTGCACTGCGGGAGCAGCACCTCTACTACAGGACCGAGCTGTGCCGTGAGCAGG 246
QY      81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100
Db      247 ATCATGTGCACCCACAGTTCTACACGCCCCAGATCCGAGCGGACATCGCCCTGCTGGAG 306
QY      101 LeuGluGlnProValLysValSerSerHisValHisThrValThrLeuProAlaSer 120
Db      307 CTGGAGAGCGGGTGAACGTCTCCAGCCACGTCACACGGGTCAACCGCTGCCCTGCCTCA 366
QY      121 GluThrPheProGlyMetProCysTyrValThrGlyTyrGlyAspValAspAsnAsp 140
Db      367 GAGACCTTCCCCCGGGATGCGGTGCTGGGTCACTGGCTGGGGCGATGTGGACATGAT 426
QY      141 GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160
Db      427 GAGCGCTCCACCGCCATTTCTCTGAAGCAGGTGAAGGTCCCATTAATGGAAAAACAC 486
QY      161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArg 180
Db      487 ATTTGTGACGCAAAATACCACTTGGCGCCTACACGGGAGACGACGTCCGATCGTCCGT 546
QY      181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200
Db      547 GACGACATGTGTGTGCGGGAAACACCGGAGGACATCATGCCAGGGCGATCTCCGGAGG 606
QY      201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220
Db      607 CCCCTGTGTGCAAGGTGAATGGCACCTGGCTGCGAGCGGGCGTGTGTCAGCTGGGGCGAG 666
QY      221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240
Db      667 GGCTGTGCCAGCCCAACCGGCTGGCATCTACACCGCTGTACACCGCTGTACCTACTTGGACTGG 726
QY      241 IleHisHisTyrValProLysLysPro 249
Db      727 ATCCACCACCTATGTCCCCAAAAGCCG 753

RESULT 3
AR165112
LOCUS      AR165112
DEFINITION Sequence 4 from patent US 6274366.
ACCESSION AR165112
VERSION    AR165112.1 GI:16238527
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 771)
AUTHORS   Maffitt,M.A., Niles,A.L. and Haak-Frendscho,M.
TITLE     Enzymatically-active recombinant human .beta.-tryptase and method
          of making same
JOURNAL    Patent: US 6274366-A 4 14-AUG-2001;
FEATURES   Location/Qualifiers
            source          1..771
                        /organism="unknown"
                        /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      6.53e-122      Length:      771
Score:          1387.00      Matches:      248
Percent Similarity: 99.60%      Conservative: 0
Best Local Similarity: 99.60%      Mismatches: 1

```

```

Query Match:      99.57%      Indels:      0
DB:               6          Gaps:      0

US-09-598-982-21 (1-249) x AR165112 (1-771)

QY      1 LeuGluLysArgIleValGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20
Db      7 CTCAGAAAAGAAATCGTGGGGGTTCAGAGAGCCCCCAGGACCAAGTGGCCCTGGCAGGTG 66
QY      21 SerLeuArgValHisGlyProTyrTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40
Db      67 AGCTGAGAGTCCACGGCCCATCTGGATGCATCTTCTGCGGGGCTCCCTCATCCACCCC 126
QY      41 GlnTrpValLeuThrAlaAlaAAlaCysValGlyProAspValLysAspLeuAlaAlaLeu 60
Db      127 CAGGGGTGTGTGACCGCGCGGCTGCTGGTGGACCGGACGTCACAGGATCTGGCGCCCTC 186
QY      61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80
Db      187 AGGTGCACTGCGGGAGCAGCACCTCTACTACAGGACCGAGCTGTGCCGTGAGCAGG 246
QY      81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100
Db      247 ATCATGTGCACCCACAGTTCTACACGCCCCAGATCCGAGCGGACATCGCCCTGCTGGAG 306
QY      101 LeuGluGlnProValLysValSerSerHisValHisThrValThrLeuProAlaSer 120
Db      307 CTGGAGAGCGGGTGAAGGTCTCCAGCCACGTCACACGGGTCAACCGCTGCCCTGCCTCA 366
QY      121 GluThrPheProGlyMetProCysTyrValThrGlyTyrGlyAspValAspAsnAsp 140
Db      367 GAGACCTTCCCCCGGGATGCGGTGCTGGGTCACTGGCTGGGGCGATGTGGACATGAT 426
QY      141 GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160
Db      427 GAGCGCTCCACCGCCATTTCTCTGAAGCAGGTGAAGGTCCCATTAATGGAAAAACAC 486
QY      161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArg 180
Db      487 ATTTGTGACGCAAAATACCACTTGGCGCCTACACGGGAGACGACGTCCGATCGTCCGT 546
QY      181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200
Db      547 GACGACATGTGTGTGCGGGAAACACCGGAGGACATCATGCCAGGGCGATCTCCGGAGG 606
QY      201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220
Db      607 CCCCTGTGTGCAAGGTGAATGGCACCTGGCTGCGAGCGGGCGTGTGTCAGCTGGGGCGAG 666
QY      221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240
Db      667 GGCTGTGCCAGCCCAACCGGCTGGCATCTACACCGCTGTACACCGCTGTACCTACTTGGACTGG 726
QY      241 IleHisHisTyrValProLysLysPro 249
Db      727 ATCCACCACCTATGTCCCCAAAAGCCG 753

RESULT 4
AX347841
LOCUS      AX347841
DEFINITION Sequence 8 from Patent WO0198470.
ACCESSION AX347841
VERSION    AX347841.1 GI:18495648
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Maffitt,M., Niles,A.L. and Haak-Frendscho,M.
TITLE     Recombinant proteolytic tryptases, active site mutants thereof, and
          methods of making same
JOURNAL    Patent: WO 0198470-A 8 27-DEC-2001;

```

```

PROMEGA CORPORATION (US)
FEATURES
  source
    1..771
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
    <7..756
    /notes="unnamed protein product"
    /codon_start=1
    /protein_id="CAD22418.1"
    /db_xref="GI:18495649"
    /translation="LEKRIVGQEAEPKRWQVSLRVHGYPMWHFGGSLIHPQWVL
    TAAHCVGPDPVQLAARLVQLREQLYYQDLFPVRIIVHPQFYTAIGADIALLELE
    EPKVSVSHVHTVLTLPASETFPPGMPQWVTGWDGVNDRLPPFPPLKQVKVPIEMNH
    ICDKYLHGLAYTGDDVRIIVDDMLCAGNTERDSCQDGGSGPLCKVNGTWLQAGVSW
    GEGCAGQNRPGIITRYTYLIDWIHHVYPKKP"
  CDS
    1..771
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
    <7..756
    /notes="unnamed protein product"
    /codon_start=1
    /protein_id="CAD22418.1"
    /db_xref="GI:18495649"
    /translation="LEKRIVGQEAEPKRWQVSLRVHGYPMWHFGGSLIHPQWVL
    TAAHCVGPDPVQLAARLVQLREQLYYQDLFPVRIIVHPQFYTAIGADIALLELE
    EPKVSVSHVHTVLTLPASETFPPGMPQWVTGWDGVNDRLPPFPPLKQVKVPIEMNH
    ICDKYLHGLAYTGDDVRIIVDDMLCAGNTERDSCQDGGSGPLCKVNGTWLQAGVSW
    GEGCAGQNRPGIITRYTYLIDWIHHVYPKKP"
  RESULT 5
  LOCUS
    BD2111490
  DEFINITION
    Enzymatically-active recombinant human beta-tryptase and method of
    making same.
  ACCESSION
    BD2111490
  VERSION
    BD2111490.1 GI:33021260
  KEYWORDS
    JP 2002515254-A/4.
  SOURCE
    Homo sapiens (human)
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1 (bases 1 to 771)
  AUTHORS
    Maffitt M.A., Niles, A.L. and Frendtscho, M.H.
  TITLE
    Enzymatically-active recombinant human beta-tryptase and method of
    making same
  JOURNAL
    Patent: JP 2002515254-A 4 28-MAY-2002;
    PROMEGA CORP
  COMMENT
    OS Homo sapiens (human)
    PN JP 2002515254-A/4
    PD 28-MAY-2002
    PF 29-OCT-1998 JP 2000549745
    PR 15-MAY-1998 US 09/079970
    PI MARK A MAFFITT, ANDREW L NILES, MARY HAAK FRENDTSCHO PC
    (C12N15/09, C07K16/40, C12N1/19, C12N9/64, C12P21/08, C12Q1/37// PC
    (C12N9/64, C12R1/645), C12N15/00
    CC Strandedness: Single;
    CC Topology: Linear;
    CC Enzymatically-active recombinant human beta-tryptase and CC
    method of making
    CC same
    FH Key Location/Qualifiers
    FT CDS 7..753
    FT misc_signal 7..18.
    FT Location/Qualifiers
    source
      1..771
      /organism="Homo sapiens"
      /mol_type="genomic DNA"
      /db_xref="taxon:9606"
    ORIGIN
    Alignment Scores:
    Pred. No.: 6.53e-122 Length: 771
    Score: 1387.00 Matches: 248
    Percent Similarity: 99.60% Conservative: 0
    Best Local Similarity: 99.60% Mismatches: 1
    Query Match: 99.57% Indels: 0
    DB: Gaps: 6
    US-09-598-982-21 (1-249) x BD211490 (1-771)
    QY 1 LeuGluLysArgIleValGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20
    DB 7 CTCGAGAAAAGATCGTCGGGGTTCAGGAGCCCGCCAGGAGCAAGTGGCCCTGGCAGGTG 66
    QY 21 SerLeuArgValHisGlyProTyTrpMetHisPheCysGlyGlySerLeuIleHisPro 40
    DB 67 AGCTGTAGAGTCCAGCGCCCATACTGTGATGCATCTTCGGGGGCTCCCTCATCCACCC 126
    QY 41 GlnTrpValLeuThrAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeu 60
    DB 127 CAGTGGTGTCTGACCGCAGCGCACTGCTGGAGCGGACGTCAGGATCTGGCGCCCTC 186
    QY 61 ArgValGlnLeuArgGluGlnHisLeuTyTrpGlnAspGlnLeuLeuProValSerArg 80
    DB 187 AGGTGCACTGCGGGAGCAGCACCCTCTACTACAGGACCAGCTGCTGCGCGTCCAGCAGG 246
    QY 81 IleIleValHisProGlnPheTyThrAlaGlnIleGlyAlaAspIleAlaLeuGlu 100
    DB 247 ATCATCTGTGACCCACAGTTCTACACCGCCAGATCGAGCGGACATCGCCCTGCTGGAG 306
    QY 101 LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer 120
    DB 307 CTGGAGAGCGCGTGAAGTCTCCAGGCACGTCACACCGGTACCCCTGCCCTGCTCA 366
    QY 121 GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsp 140
    DB 367 GAGACCTTCCCGCGGGATGCCGTGCTGGGTCTACGCGGAGACGATGGCAATGAT 426
    QY 141 GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160
    DB 427 GAGGCGCTCCACCGCCATTTCTCTGAGCAGGTGAAGTCCCATATGGAACAC 486
    QY 161 IleCysAspAlaIysTyHisLeuGlyValaTyThrGlyAspValArgIleValArg 180
    DB 487 ATTGTGACGCAAAATACCACTTGGCGCTTACACGGGAGACGATCGCATCGTCCGT 546
    QY 181 AspAspMetLeuCysAlaGlyAsnThrArgAspSerCysGlnGlyAspSerGlyGly 200
    DB 547 GACACATGTGTGTGCGGGAAACCCCGAGGAGACTCATGCCAGGCGCATCCGAGGGG 606
    QY 201 ProLeuValCysIysValAsnGlyTyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220
    DB 607 CCCCTGTGTGCAAGGTGAATGGACCTGGTGTGAGCGGGCGTGGTCAGCTGGGGCGAG 666
  
```

```

Db      187 AGGGTCAACTCGGGAGCAGCACCTTACTACAGGACCGAGCTGCTGCGGTTCAGCAGG 246
QY      81 llelleValHisProGlnPheTyrThrAlaGlnlleGlyAlaAspIleAlaLeuLeuGlu 100
Db      247 ATCATCGTGCACCCACAGTTCTACACGCCCGCAGATCGGAGCGGACATCGCCCTGCTGGAG 306
QY      101 LeuGluGluProValLysValSerHisValHisThrValThrLeuProAlaSer 120
Db      307 CTGGAGGAGCGGTGAAGTCTCCAGCCACGCTCCACACGGTCAACCTGCCCCCTGCTCTCA 366
QY      121 GluThrPheProGlyMetProCysTyrThrValThrGlyTyrGlyAspValAspAsnAsp 140
Db      367 GAGACCTTCCCCCGGGGATGCGTGGCTGCTGGCTGCTGGCTGCTGGCTGCTGGCTGCTGG 426
QY      141 GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160
Db      427 GAGCGCTTCCCCCGGGGATGCGTGGCTGCTGGCTGCTGGCTGCTGGCTGCTGGCTGCTGG 486
QY      161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArg 180
Db      487 ATTGTGACGCAAAATACCACTTGGCGCTTACCGGGAGAGCGTCCGCGATCGTCCGT 546
QY      181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200
Db      547 GAGGACATGCTGTGTCGGGGAACACCGGAGGAGCTCATGCGAGGGGACTCCGAGGG 606
QY      201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220
Db      607 CCCCCTGGTGTGCAAGGTGATGGCACTGGCTGCGAGCGGGCGTGGTCACTGCTGGGCGAG 666
QY      221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTrpLeuAspTrp 240
Db      667 GGCTGTGCGCCAGCCCAACCGGCTGGCATCTACACCGGTGTCACCTACTACTTGGACTGG 726
QY      241 lleHisHisTyrValProLysPro 249
Db      727 ATCCACCACTATGTCCTCCCAAAAGCCG 753

RESULT 6
AX347857
LOCUS      AX347857              771 bp      DNA      linear      PAT 01-FEB-2002
DEFINITION Sequence 24 from Patent WO0198470.
ACCESSION  AX347857
VERSION     AX347857.1   GI:18495664
KEYWORDS    Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
  AUTHORS   Maffit,M., Niles,A.L. and Haak-Frendscho,M.
  TITLE     Recombinant proteolytic tryptases, active site mutants thereof, and
            methods of making same
  JOURNAL   Patent: WO 0198470-A 24 27-DEC-2001;
            PROMEGA CORPORATION (US)
FEATURES    Location/Qualifiers
            1..771
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"
             <7..756
             /note="unnamed protein product"
             /codon_start=1
             /protein_id="CAD22422.1"
             /db_xref="GI:18495664"
             /translation="LEKRIVGQAPRSKPQWVSLRVHGFYMMHFCGSLIHPQWVL
            TAACVGPDPVLDLAALRVQLREOHLVYODLLPVSRIVHVPQFTYTAQIAGDIALLELE
            EPVKVSHVHTVTLPPASETPPGMPCWVTGWGDVNDERLPPFPPLKQVKVPMENH
            ICDAKYHLGATGDDVRLVRDMLCANKTRRDSQGDAGGFLVCKVINGTLMQAGVWSW
            GEGCAQNPRLPIYRTVYLDWIHHYVPRKP"

CDS
ORIGIN

```

```

Alignment Scores:
Pred. No.:      1,266-121      Length:      771
Score:          1384.00      Matches:      247
Percent Similarity: 99.60%      Conservative: 1
Best Local Similarity: 99.20%      Mismatches: 1
Query Match:      99.35%      Indels:      0
DB:              6           Gaps:      0

US-09-598-982-21 (1-249) x AX347857 (1-771)

QY      1 LeuGluLysArgIleValGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20
Db      7 CTCGAGAAAAGAAATCGTGGGGGTTCAGGAGGCCGCCAGAGCAAGTGGCCCTGGCAGGTG 66
QY      21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40
Db      67 AGCCTGAGAGTCCACGGGCCCATCTACTGGATGCATCTTCTGCGGGGGTCTCCCTCATCCACCC 126
QY      41 GlnTrpValLeuThrAlaAlaAlaCysValGlyProAspValLysAspLeuAlaLeu 60
Db      127 CAGTGGGTGCTGACCGCAGCGCACTGCGTGGGACCGAGCTCAAGATCTGGCGGCCCTC 186
QY      61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80
Db      187 AGGGTGAACATGCGGAGCAGCACCTCTACTACAGGACCACCTGCTGCGGTTCAGCAGG 246
QY      81 llelleValHisProGlnPheTyrThrAlaGlnlleGlyAlaAspIleAlaLeuLeuGlu 100
Db      247 ATCATCGTGCACCCACAGTTCTACACGCCCGCAGATCGGAGCGGACATCGCCCTGCTGGAG 306
QY      101 LeuGluGluProValLysValSerHisValHisThrValThrLeuProProAlaSer 120
Db      307 CTGGAGGAGCGGTGAAGTCTCCAGCCACGTCACACGTCACGCTGACCTGCCCCCTGCTCTCA 366
QY      121 GluThrPheProProGlyMetProCysTrpValThrGlyTyrGlyAspValAspAsnAsp 140
Db      367 GAGACCTTCCCCCGGGGATGCGTGGTGGTCACTGGCTGGGGCGATGTGGACATGAT 426
QY      141 GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160
Db      427 GAGCGCTTCCCCCGGGGATGCGTGGTGGTCACTGGCTGGGGCGATGTGGACATGAT 486
QY      161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArg 180
Db      487 ATTGTGACGCAAAATACCACTTGGCGCTTACCGGGAGAGCGTCCGCACTGCTCCGT 546
QY      181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200
Db      547 GAGGACATGCTGTGTCGGGGAACACCGGAGGAGCTCATGCGAGGGGACTCCGAGGG 606
QY      201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220
Db      607 CCCCCTGGTGTGCAAGGTGATGGCACTGGCTGCGAGCGGGCGTGGTCACTGCTGGGCGAG 666
QY      221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTrpLeuAspTrp 240
Db      667 GGCTGTGCGCCAGCCCAACCGGCTGGCATCTACACCGGTGTCACCTACTACTTGGACTGG 726
QY      241 lleHisHisTyrValProLysPro 249
Db      727 ATCCACCACTATGTCCTCCCAAAAGCCG 753

RESULT 7
AX347859
LOCUS      AX347859              771 bp      DNA      linear      PAT 01-FEB-2002
DEFINITION Sequence 26 from Patent WO0198470.
ACCESSION  AX347859
VERSION     AX347859.1   GI:18495666
KEYWORDS    Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE	1	ProLeuValCysLysValAsnGlyThrTriPLeuGlnAlaGlyValValSerTyrGlyGlu	220
AUTHORS	Maffit, M., Niles, A.L. and Haak-Frendscho, M.		
TITLE	Recombinant proteolytic tryptases, active site mutants thereof, and methods of making same		
JOURNAL	Patent: WO 0198470-A 26 27-DEC-2001;		
FEATURES	PROMEGA CORPORATION (US)		
source	Location/Qualifiers		
	1..771		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
	<7..756		
	/note="unnamed protein product"		
	/codon_start=1		
	/protein_id="CAD22423.1"		
	/db_xref="GI:18495667"		
	/db_xref="REMTREMBL:CAD22423"		
	/translation="LEKRIVGQEPAPSKWQVSLRVHGPYMHFPGGSLIHPQWVL		
	TAACVGPVDKDLAALVQREQLHYQDQLPVSRIVHPQFYTAQIGADIALLELE		
	EPNVSSHVHTVLPASSETPPGMPGVTGWDVNDRLPPFPPLKQVKVPMENH		
	ICDAKYLHGLAYTGDDVRIVRDMLCAGNTRDSCQDAGGFLVCKVNGTWLQAGVWSW		
	GGCAQPNRPGIYTRVITYLDWIHHYVKKP"		
ORIGIN			
Alignment Scores:			
Pred. No.:	1.26e-121	Length:	771
Score:	1384.00	Matches:	247
Percent Similarity:	99.60%	Conservative:	1
Best Local Similarity:	99.20%	Mismatches:	1
Query Match:	99.35%	Indels:	0
DB:	6	Gaps:	0
US-09-598-982-21 (1-249) x AX347859 (1-771)			
Qy	1	LeuGluLysArgIleValGlyGlnGluAlaProArgSerLysTyrProTriPLeuVal	20
Db	7	CTCGAGAAAGAAATCGTCGGGGGTGAGGAGCCCGGAGCAAGTGGCCCTGGCAGGTG	66
Qy	21	SerLeuArgValHisGlyProTyrTriPLeuHisPheCysGlyGlySerLeuIleHisPro	40
Db	67	AGCCTGAGAGTCCACGGCCCATCTGGATGACATCTCTCGGGGGTCCCTCATCACCCC	126
Qy	41	GlnTrpValLeuThrAlaAlaCysValGlyProAspValLysAspLeuAlaLeu	60
Db	127	CAGTGGGTGCTGACCGCAGCGCACTGCTGGGACCGGACGTCAGGATCTGGCCGCTC	186
Qy	61	ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg	80
Db	187	AGGCTGCAACTGCGGGAGCAGCACTCTACTACGAGGACCACTGCTCCCGTCAAGCAGG	246
Qy	81	IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu	100
Db	247	ATCATCTGTCACCAAGTCTTACACCCCGGAGATCGGAGCGGACATCGCCCTGCTGGAG	306
Qy	101	LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer	120
Db	307	CTGGAGGAGCGGTGAAGTCTCCAGCCACGTCACACGGTCACCGCTGCCCTGCCCTCA	366
Qy	121	GlnThrPheProGlyMetProCysTrpValThrGlyTyrGlyAspValAspAsnAsp	140
Db	367	GAGACCTTCCCGGGGATCCGCTGGGTGCTGGGTGCTGGGTGCTGGGTGCTGGGTGCT	426
Qy	141	GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis	160
Db	427	GAGCGCTCCACCGCCATTCCTCTGAAGCAGGTGAAGTCCCATATGGAACACAC	486
Qy	161	IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArg	180
Db	487	ATTTGTGCGCAAAATACACCTTGGCGCTTACACGGGAGACGAGTCCGATCTCGGT	546
Qy	181	AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly	200
Db	547	GACGACATGCTGTGTGCCGGGAACACCGGAGGAGTCTATGCAAGGAGACCGCGGCA	606


```

QY      81  IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100
Db      247  ATCATCGTGGTCCACCAAGTCTTACACCGCCGATCGGAGCGGACATGCGCTGTGTGGAG 306
QY      101  LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer 120
Db      307  CTGGAGAGCGCGGTGAAGCTCTCCAGCCACGTCACACGCGTCAACCGTCCCGCTCCCTCA 366
QY      121  GluThrPheProGlyMetProCysTrpValThrGlyTyrGlyAspValAspAsnAsp 140
Db      367  GAGACCTTCCCGCCGGGATGCGGTGCTGGGTGCTGCGTGGGCGATGTGGACAAATGAT 426
QY      141  GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160
Db      427  GAGCGCTTCCACCGCCATTCCTCTGAAGCAGGTGAAGTCCCATATATGGAARACAC 486
QY      161  IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArg 180
Db      487  ATTTGTGACGCAAAATACACCTTGGCGCTACACCGCGTGTACACCGTGTACCTACTTGGACTGG 546
QY      181  AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200
Db      547  GACGACATGCTGTGTGCGCGAACCACCGAGGAGTCTATGCGAGGCGGACTCCGAGCGG 606
QY      201  ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220
Db      607  CCGCTGTGTGTCGCGGATGCGGTGCTGCGTGGCGGCGTGGTGGTGGGCGGAG 666
QY      221  GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240
Db      667  GGCTGTGCGCCAGCCACCGGCTGGCATACACCGGTGTACACCGGTGTACCTACTTGGACTGG 726
QY      241  IleHisHisTyrValProLysLysPro 249
Db      727  ATCCACCACTATGTCCTCCCAAAAGCCG 753

RESULT 9
AX347855
LOCUS      AX347855              771 bp    DNA          linear      PAT 01-FEB-2002
DEFINITION Sequence 22 from Patent WO0198470.
ACCESSION  AX347855
VERSION    AX347855.1  GI:18495662
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1
  AUTHORS   Maffit,M., Niles,A.L. and Haak-Frendscho,M.
  TITLE     Recombinant proteolytic trypsinases, active site mutants thereof, and
            methods of making same
  JOURNAL   Patient: WO 0198470-A 22 27-DEC-2001;
            PROMESA CORPORATION (US)
FEATURES    Location/Qualifiers
            1..771
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"
             <7..756
             /note="unnamed protein product"
             /codon_start=1
             /protein_id="CAD22421.1"
             /db_xref="GI:18495663"
             /db_xref="REFSEQ:CAD22421"
             /translation="LEKRIVGGQAPRSKWPQVSLRVHGYPMWHFQCGSLHPQWVL
            TAAHCVGSDVTDLAALRVQLREQLHYQDQLLPVSRIVHPQFYTAQTGAIALLLE
            EPVKVSHVTVLTPPASSETPPGWPVQWTCWGDVNDRLPPPPPLKQVKVPMENH
            ICDAKYLHGYTGDVRIVRDMLCAGNTRDSQGDSSGGLVCKVNGTWLQGVVSW
            GEGCAQNPRLPIYTRVYIYLDIHHVYKPK"

ORIGIN
Alignment Scores:

```

```

Pred. No.:      3.73e-121      Length:      771
Score:          1379.00      Matches:      247
Percent Similarity: 99.20%      Conservative: 0
Best Local Similarity: 99.20%      Mismatches: 2
Query Match:      98.99%      Indels:      0
DB:              6      Gaps:      0

US-09-598-982-21 (1-249) x AX347855 (1-771)

QY      1  LeuGluLysArgIleValGlyGlnGlnAlaProArgSerLysTrpProTrpGlnVal 20
Db      7  CTCGAGAAAGAAATCGTCGGGGTTCAGGAGGCCCGCAGGAGCAAGTGCGCTGGCAGGTG 66
QY      21  SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40
Db      67  AGCCTGAGAGTCCACGCGCCATCTCTGGATGACATTTCTGCGGGGGCTCCCTCATCCACCCC 126
QY      41  GlnTrpValLeuThrAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeu 60
Db      127  CAGTGGGTGTCGACCGCAGCGCACCTGCGTGGAGCCGAGCGTCAAGGATCTGGCGCCCTC 186
QY      61  ArgValGlnLeuArgGluGlnHisLeuTyrTrpGlnAspGlnLeuLeuProValSerArg 80
Db      187  AGGCTGCAACTGCGGGAGCAGCACCTCTACTACCGAGGACCACTGCTGCTCGCGTCAGCAGG 246
QY      81  IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100
Db      247  ATCATGTGTCACCCACAGTTCTACACCGCCAGATCGGAGCGGCAATCGCCCTGTCTGGAG 306
QY      101  LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer 120
Db      307  CTGGAGGAGCGGTGAAGTCTCCAGCCACCTCCACACGGTCAACCTGCCCGCTGCCTCA 366
QY      121  GluThrPheProGlyMetProCysTrpValThrGlyTyrGlyAspValAspAsnAsp 140
Db      367  GAGACCTTCCCGCCGGGATGCGGTGCTGGTCACTGGCTGGGCGATGTGGACAAATGAT 426
QY      141  GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160
Db      427  GAGCGCTTCCCGCCCATTTCTCTGAAGCAGGTGAAGTCCCATATATGGAARACAC 486
QY      161  IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArg 180
Db      487  ATTTGTGACGCAAAATACCACTTGGCGCTACACGGGAGACGCTCCGATCGTCCGT 546
QY      181  AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200
Db      547  GACGACATGCTGTGTGCGCGAACCACCGAGGAGTCTATGCGAGGCGGACTCCGAGCGG 606
QY      201  ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220
Db      607  CCGCTGTGTGTCGCGGATGCGGTGCTGCGTGGCGGCGTGGTGGTGGGCGGAG 666
QY      221  GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240
Db      667  GGCTGTGCGCCAGCCACCGGCTGGCATACACCGGTGTACACCGGTGTACCTACTTGGACTGG 726
QY      241  IleHisHisTyrValProLysLysPro 249
Db      727  ATCCACCACTATGTCCTCCCAAAAGCCG 753

RESULT 10
AX347873
LOCUS      AX347873              771 bp    DNA          linear      PAT 01-FEB-2002
DEFINITION Sequence 40 from Patent WO0198470.
ACCESSION  AX347873
VERSION    AX347873.1  GI:18495680
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE   1

```

AUTHORS	Maffit,M., Niles,A.L. and Haak-Frendscho,M.
TITLE	Recombinant proteolytic trypsinases, active site mutants thereof, and methods of making same
JOURNAL	Patent: WO 0198470-A 40 27-DEC-2001;
	PROMEGA CORPORATION (US)
FEATURES	Location/Qualifiers
source	1..771
	/organism="Homo sapiens"
	/mol_type="unassigned DNA"
	/db_xref="taxon:9606"
CDS	<1..756
	/note="unnamed protein product"
	/codon_start=1
	/protein_id="CAD22430.1"
	/db_xref="GI:18495681"
	/db_xref="REMTREMBL:CAD22430"
	/translations="GPLEKRIVGGEAPRSKPMQVSLRVHGPYMHVFCGSLHHPQW VLTAAHCNVGPDVDAALAEVLRQLEHLYQDQLPVSRILIVHPQFTAQIGADIALLE LEEPYNVSHVHTVTLPPASSTPRGMPCWTKGWDVNDRLPFPPLKQVXPVIME NHICDAKHGATGDDVRIVRDMLCAGNTRRDSQGDAGGFLVCKVNGTWLQAGVV SWGEGCAQPNRPNGIYTRVITYLNDIHHYVPKP"
ORIGIN	
Alignment Scores:	
Pred. No.:	3,73e-121
Score:	1379.00
Percent Similarity:	99.20%
Best Local Similarity:	98.80%
Query Match:	98.99%
DB:	6
	Length: 771
	Matches: 246
	Conservative: 1
	Mismatches: 2
	Indels: 0
	Gaps: 0
US-09-598-982-21 (1-249) x AX347873 (1-771)	
Qy	1 LeuGluIysArgIleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20
Db	7 CTCGAGAAAGAAATCGTCGGGGTFCAGAGGCCCCCAGGAGCAAGTGCCTTGCAGGTG 66
Qy	21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40
Db	67 AGCCTGAGATGTCACGGCCCATCTGATGATGACTTCTCGCGGGGCTCCCTCAITCACCCC 126
Qy	41 GlnTrpValLeuThrAlaAlaCysValGlyProAspValIysAspLeuAlaAlaLeu 60
Db	127 CAGTGGGTGCTGACCGCAGGCACCTGCTGGGACCGGACGTCAAGGATCTGGCGGCCCTC 186
Qy	61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80
Db	187 AGGGTGCAACTCGGGGAGCAGCACTCTACTACCAGGACCAGCTGTCTGCCGTGAGCAGG 246
Qy	81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100
Db	247 ATCATCTGTGACCACCACTTCTACACGCCCCAGATCGGAGCGGACATCGCCCTGCTCGAG 306
Qy	101 LeuGluGluProValIysValSerSerHisValHisThrValThrLeuProProAlaSer 120
Db	307 CTGGAGAGCGCGTGAACGTCTCCAGCCACGTCCACAGGTCAACCTTGCCTTGCCTCA 366
Qy	121 GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp 140
Db	367 GAGACCTTCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGCGCATGTGGACAATGAT 426
Qy	141 GluArgLeuProProProPheProLeuIysGlnValIysValProIleMetGluAsnHis 160
Db	427 GAGCGCTTCCACCGCCATTTCCTCTGAAGCAGGTGAAGGTCCCCCAATAATGGAANAAC 486
Qy	161 IleCysAspAlaIaIysTyrHisLeuGlyAlaIaTyrThrGlyAspAspValArgIleValArg 180
Db	487 ATTGTGACGCAAAATACCACTTGGCGCTTACACGGGAGACGCTCGCATGCTCGGT 546
Qy	181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200
Db	547 GACGACATGCTGTGCGCGGAAACACCGGAGGACTCATGTCAAGGCGACGCGCGGGA 606

QY 81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyValaAspIleAlaLeuLeuGlu 100
 Db 247 ATCATCGTGCACCCACAGTTCTACACCGCCAGATCGGAGCGGACATCGCCCTGCTGGAG 306
 QY 101 LeuGluGluProValIysValSerSerHisValHisThrValThrLeuProAlaSer 120
 Db 307 CTGGAGGAGCCGGTGAACCTCTCCAGCCACGTCACACACGCTCACCTGCGCCCTGCTCA 366
 QY 121 GluThrPheProGlyMetProCysTrpValThrGlyTrpGlyValAspValAspAsp 140
 Db 367 GAGACCTTCCCCCGGGGATGCGTCTGGTCTACCTGGCTGGCGGATGTGACAAATGAT 426
 QY 141 GluArgLeuProProPheProLeuIysGlnValIysValProIleMetGluAsnHis 160
 Db 427 GAGCGCTCCACCGCCATTCTCTGAAGCAGGTGAAGGTCCCATATATGGAACACAC 486
 QY 161 IleCysAspAlaIysTyrHisLeuGlyAlaTyrThrGlyValAspValArgIleValArg 180
 Db 487 ATTGTGAGCAAAATACACCTTGGCGCTTACCGGAGACGATCGCGCATCGTCCGT 546
 QY 181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyValSerGlyGly 200
 Db 547 GAGCAGATCTGTGTCGGGACACCCCGAGGACTCATGCCAGGAGACCGCCGCGGA 606
 QY 201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220
 Db 607 CCACCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGCGGGCGTGGTCACTGGGCGAG 666
 QY 221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTrpLeuAspTrp 240
 Db 667 GGCTGTGCGCCAGCCCAACCGGCTGGCATCTACCCCGTGTACCTACTACTTGGACTGG 726
 QY 241 IleHisHisTyrValProIysLysPro 249
 Db 727 ATCCACCACTATGTCCTCCCAAAAGCCG 735
 RESULT 12
 AX347861 735 bp DNA linear PAT 01-FEB-2002
 LOCUS Sequence 28 from Patent WO0198470.
 DEFINITION AX347861
 ACCESSION AX347861
 VERSION AX347861.1 GI:18495668
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Maffit, M., Niles, A.L. and Haak-Frendscho, M.
 TITLE Recombinant proteolytic trypsinases, active site mutants thereof, and methods of making same
 JOURNAL Patent: WO 0198470-A 28 27-DEC-2001;
 PROMEGA CORPORATION (US)
 FEATURES Location/Qualifiers
 source 1..735
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 <1..>735
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAD22424.1"
 /db_xref="GI:18495669"
 /db_xref="REMBL:CAD22424"
 /translation="TVGQEARSPKWPQVSLRVHGPYWMFPCGSLIHPQWVLTAA
 CVGPDVLDALRLVQLRQHLVYQDLPLVSRILVHPQFYTAQIGADTALDELEPVK
 VSSHVHTVLLPASPETFPFGMCWVTGMDVNDRLPPFPPLKQKVPIMENHICDA
 KYHLGAYTGDVIRVIRDMCLCAGNTRDRSCQDGGPLVCKVNGTQLQAGVVSNGEG
 AQPNRPGIYTRVTYLDWIHHVVKP"
 CDS
 ORIGIN
 Alignment Scores: 1.05e-120 Length: 735
 Pred. No.:

Score: 1374.00 Matches: 245
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.64% Indels: 0
 DB: 6 Gaps: 0
 US-09-598-982-21 (1-249) x AX347861 (1-735)
 QY 5 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24
 Db 1 ATCTGTCGGGGTTCAGGAGGCGCCCGCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 60
 QY 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
 Db 61 CAGGCCCATATCTGGATGCATCTTCGGGGGCTCCCTCATCCACCCAGTGGGTGCTG 120
 QY 45 ThrAlaAlaCysValGlyProAspValIysAspLeuAlaAlaLeuArgValGlnLeu 64
 Db 121 ACCGCGCGCGTGGTGGGACCGGACGTCAGAGATCTGGCCGCTCAGGGTGGACTG 180
 QY 65 ArgGluGlnHisLeuTyrTrpGlnAspGlnLeuLeuProValSerArgIleIleValHis 84
 Db 181 CGGGAGCAGCCTCTACTTACCAGACCCAGCTGCTGCCGTCCAGAGGATCATCGTGCAC 240
 QY 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluPro 104
 Db 241 CCACAGTTCTACCGCGCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGAGCGG 300
 QY 105 ValIysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
 Db 301 GTGAAGGTCTCCAGCCACGTCACACGTCACCTGCCCTGCCCTCAGAGACCTTCCCC 360
 QY 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
 Db 361 CGGGGATGCGGTGCTGGGTCACTGGCTGGGCGCATGTGGCAATGATGAGCGCTCCCA 420
 QY 145 ProProPheProLeuIysGlnValIysValProIleMetGluAsnHisIleCysAspAla 164
 Db 421 CGCCATTTCTCTGAAGCAGTGAAGTCCCCATAATGGAACCAACATTTGTGACGCA 480
 QY 165 LysTyrHisLeuGlyValaTyrThrGlyAspValArgIleValArgAspAspMetLeu 184
 Db 481 AAATACCACTTGGCGCTACACGGGAGACGAGCTCGCATCTGCTCGTGGACGACATGCTG 540
 QY 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
 Db 541 TGTGCGGGAAACACCGGAGGAGTCTATGCCAGGCGACTCCCGAGGGCCCTCGGTGTGC 600
 QY 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlyCysAlaGln 224
 Db 601 AAGTGAATGACCTTGGCTGACGCGGGCGTGGTCACTGGGCGGAGGGCTGTGCCAG 660
 QY 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTrpLeuAspTrpIleHisHisTyr 244
 Db 661 CCCAACCGCGCTGGCATCTACACCGGTGTCACTACTTGGACTGGATCCACCATAT 720
 QY 245 ValProIysLysPro 249
 Db 721 GTCCCCAAAAGCCG 735
 RESULT 13
 AX347871
 LOCUS Sequence 38 from Patent WO0198470.
 DEFINITION AX347871
 ACCESSION AX347871
 VERSION AX347871.1 GI:18495678
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Maffit, M., Niles, A.L. and Haak-Frendscho, M.

TITLE Recombinant proteolytic trypsinases, active site mutants thereof, and methods of making same
 JOURNAL Patent: WO 0198470-A 38 27-DEC-2001;
 PROMEGA CORPORATION (US)
 FEATURES Location/Qualifiers
 source 1..771
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 CDS 1..771
 /note="unnamed protein product"
 /protein_id="CAD22429.1"
 /db_xref="GI:18495679"
 /db_xref="EMBL:CAD22429"
 /translation="LEKRIVGQEAPEKWPQVSLRVHGFYWMHFCGSLIHPQWVL
 TAACHGPDVDAALRLVQREQLHYQDQLPVSRILVHPQFYTAQIGADIALLELEPEVN
 EPNVSHVHTLPPASETPPCMPGVTGWDVNDRLPPPLPKQVKVIMENH
 ICAKAYHLGATGDDVRIVRDMCLCATNRDSCQSDSGGLVCKVNGTWLQAGVWSM
 GEGCAQPNRPGIVTRVITYLTDHIIHVPKKP"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1,11e-120 Length: 771
 Score: 1374.00 Matches: 246
 Percent Similarity: 98.80% Conservatives: 0
 Best Local Similarity: 98.80% Mismatches: 3
 Query Match: 98.64% Indels: 0
 DB: 6 Gaps: 0
 US-09-598-982-21 (1-249) x AX347871 (1-771)
 QY 1 LeuGluLysArgIleValGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20
 Db 7 CTCGAGAAAGATCGTCGGGGGTCAGAGAGCCCGCCAGAGCAAGTGCCTCGCAGGTG 66
 QY 21 SerLeuArgValHisGlyProTrpTrpMetHisPheCysGlyGlySerLeuIleHisPro 40
 Db 67 AGCCTGAGAGTCCACGGCCCATCTACTGATGACCTTCTCGGGGGGTCCTCATCCACCCC 126
 QY 41 GlnTrpValLeuThrAlaAlaAlaCysValGlyProAspValLysAspLeuAlaLeu 60
 Db 127 CAGTGGGTGCTGACCGCAGCGACCTGCGTGGAGCCGACGTCAGAGATCTCGCGCCCTC 186
 QY 61 ArgValGlnLeuArgGlnHisLeuTrpTrpGlnAspGlnLeuLeuProValSerArg 80
 Db 187 AGGTGCAACTCGGGAGCAGACCTCTACTACAGGACGAGTCTCGCGGTGAGCAGG 246
 QY 81 IleIleValHisProGlnPheTrpThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100
 Db 247 ATCATCGTGCACCCACAGTCTTACACCCGCCAGATCGGAGCGCAATCGCCTGCTGGAG 306
 QY 101 LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProAlaSer 120
 Db 307 CTGAGGAGCGCGTGAACGTCCTCCAGCAGCAGTCCACGCTGACCTGCCCCCTCCCTCA 366
 QY 121 GluThrPheProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp 140
 Db 367 GAGACTTCCCCCGGGGATGCGTGGTGGTCACTGGCTGGGGGATGTGGACATGAT 426
 QY 141 GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160
 Db 427 GAGCGCTCCACCGCCATTTCTCTGAAGCAGGTGAAGTCCCCCATATATGAAACCCAC 486
 QY 161 IleCysAspAlaLysTrpHisLeuGlyAlaTrpThrGlyAspValArgIleValArg 180
 Db 487 ATTGTGAGCGAAATACCATCTTGCGCTTACCGGAGACGAGTCCGCACTGCTCCGT 546
 QY 181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200
 Db 547 GACGACATGCTGTGCGCGGGAACACCCGAGGAGCTCATGCCAGGCGACTCCGAGGG 606
 QY 201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220

Db 607 CCCTCGTGTGCAAGTGTAATGACCTGCTGACGCGCGCTGGTTCAGCTGGGGCGAG 666
 QY 221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTrpLeuAspTrp 240
 Db 667 GGCTGTGCGCCGACCCCAACCGGCTGGCATCTACACCGTGTCACTACTACTTGGACTGG 726
 QY 241 IleHisHisTyrValProLysLysPro 249
 Db 727 ATCCACCACCTATGTCCCAAAAAGCCG 753
 RESULT 14
 AX347877 735 bp DNA linear PAT 01-FEB-2002
 LOCUS AX347877
 DEFINITION Sequence 44 from Patent WO0198470.
 ACCESSION AX347877
 VERSION AX347877.1 GI:18495684
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Maffit, M., Niles, A.L. and Haak-Frendscho, M.
 TITLE Recombinant proteolytic trypsinases, active site mutants thereof, and methods of making same
 JOURNAL Patent: WO 0198470-A 44 27-DEC-2001;
 PROMEGA CORPORATION (US)
 FEATURES Location/Qualifiers
 source 1..735
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 CDS <1..>735
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAD22432.1"
 /db_xref="GI:18495685"
 /translation="IVLQGEAPRSKWPQVSLRVHGFYWMHFCGSLIHPQWVLTAAAC
 CVGPDVDAALRLVQREQLHYQDQLPVSRILVHPQFYTAQIGADIALLELEPEVN
 VSHVHTLPPASETPPCMPGVTGWDVNDRLPPPLPKQVKVIMENHICDA
 KYHLGATGDDVRIVRDMCLCATNRDSCQSDSGGLVCKVNGTWLQAGVSMGEGC
 AQPNRPGIVTRVITYLTDHIIHVPKKP"
 ORIGIN
 Alignment Scores:
 Pred. No.: 3,12e-120 Length: 735
 Score: 1369.00 Matches: 244
 Percent Similarity: 99.59% Conservatives: 0
 Best Local Similarity: 99.59% Mismatches: 1
 Query Match: 98.28% Indels: 0
 DB: 6 Gaps: 0
 US-09-598-982-21 (1-249) x AX347877 (1-735)
 QY 5 IleValGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24
 Db 1 ATCGTGGGGTCCAGAGCGCCCGCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 60
 QY 25 HisGlyProTrpTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
 Db 61 CACGCCCATCTACTGATGATCTTCTCGGGGGGCTCCCTCATCCACCCCGAGGTGCTG 120
 QY 45 ThrAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 64
 Db 121 ACCGCCGCGGCTGCGTGGACCGCGACGTCAGAGATCTGGCGCTCAGGGTGAACATG 180
 QY 65 ArgGluGlnHisLeuTrpTrpGlnAspGlnLeuLeuProValSerArgIleIleValHis 84
 Db 181 CGGAGCAGCAGCTCTACTTACCGAGCAGCTGCTGCCGCTGAGGAGATCATCTGTCAC 240
 QY 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluPro 104

```

Db      241  CCACAGTTCTACACGCCAGATCGAGCGGACATCGCCCTCTGGAGTGGAGGCGC 300
Qy      105  VallysValSerSerHisValHisThrValThrLeuProAlaSerGluThrPhePro 124
Db      301  GTGAACGCTCTCAGCACGCTCCACACGGTCAACCTGCCCTCGCTCAGAGACCTTCCCC 360
Qy      125  ProGlyMetProCysTrpValThrGlyTrpGlyAspValAlaAsnAspGluArgLeuPro 144
Db      361  CCGGGATGCGGTCTGCTGGTCACTGGCTGGGCGGATGTGGCAATGATGAGGCGCTCCCA 420
Qy      145  ProProPheProLeuLysGlnValLysValProLeuMetGluAsnHisIleCysAspAla 164
Db      421  CCGCATTTCTCTGAAGCAGGTGAAGTCCCATATATGTAATGTAATGTAATGTAATGTA 480
Qy      165  LysTyrHisLeuGlyAlaTyrThrGlyAspValAlaArgIleValArgAspMetLeu 184
Db      481  AAATACCACTTGGCGCTACACGGGAGACGCTCCGCTCGCTCGGACGACATGCTG 540
Qy      185  CysAlaGlyAsnThrArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
Db      541  TGTGCGGGAAACACCGGAGGACTCATGCGAGGCGACTCCGGAGGCGCCCTGGTGTG 600
Qy      205  LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224
Db      601  AAGGTGAATGGACCTGCTGCGCGCGGCGTGTGCTCAGCTGGGCGAGGCTGTGCCAG 660
Qy      225  ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisTyr 244
Db      661  CCCAACCGCGCTGGCATCTACACCGTGTACCTACTACTTGGACTGGATCCACCACTAT 720
Qy      245  ValProLysLysPro 249
Db      721  GTCCCCAAAAAGCGC 735

RESULT 15
AR165109
LOCUS      AR165109              735 bp      DNA      linear      PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6274366.
ACCESSION AR165109
VERSION    AR165109.1  GI:16238522
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 735)
AUTHORS    Maffitt, M.A., Niles, A.L. and Haak-Frendscho, M.
TITLE      Enzymatically-active recombinant human .beta.-tryptase and method
of making same
JOURNAL    Patent: US 6274366-A 14-AUG-2001;
FEATURES   Location/Qualifiers
            source          1..735
                        /organism="unknown"
                        /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.:      3.88e-120      Length:      735
Score:          1368.00      Matches:    244
Percent Similarity: 99.59%      Conservative: 0
Best Local Similarity: 99.59%      Mismatches: 1
Query Match:    98.21%      Indels:    0
DB:             6      Gaps:      0

US-09-598-982-21 (1-249) x AR165109 (1-735)

Qy      5  IleValGlyGlyGlnGlnAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24
Db      1  ATCGTCGGGGGTGAGAGGCGCCCGAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 60
Qy      25  HisGlyProTyrTrpMetHisPheCysGlySerLeuIleHisProGlnTrpValLeu 44
Db      61  CACGCCCACTACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCGCAGTGGGTGCTG 120

```

```

Qy      45  ThrAlaAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 64
Db      121  ACCGAGCGCACTGCGTGGGACCGGACGCTCAAGGATCTGGCCGCTCAGGGTGAACCTG 180
Qy      65  ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuProValSerArgIleIleValHis 84
Db      181  CGGAGCAGCACCTCTACTACAGGACCGAGTGTGCTGCCGTGAGGATCATCTGTGCAC 240
Qy      85  ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluPro 104
Db      241  CCACAGTTCTACACCGCCAGATCGAGCGGACATCGCCCTCTGGAGTGGAGGAGCG 300
Qy      105  VallysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
Db      301  GTGAAGGTCTCCAGCCCGTCCACACGCTCACCTGCCCTCGCTCGCTCAGAGACCTTCCC 360
Qy      125  ProGlyMetProCysTrpValThrGlyTrpGlyAspValAlaAsnAspGluArgLeuPro 144
Db      361  CCGGGATGCGGTCTGCTGGTCACTGGCTGGGCGGATGTGGCAATGATGAGGCGCTCCCA 420
Qy      145  ProProPheProLeuLysGlnValLysValProLeuMetGluAsnHisIleCysAspAla 164
Db      421  CCGCATTTCTCTGAAGCAGGTGAAGTCCCATATATGTAATGTAATGTAATGTAATGTA 480
Qy      165  LysTyrHisLeuGlyAlaTyrThrGlyAspValAlaArgIleValArgAspMetLeu 184
Db      481  AAATACCACTTGGCGCTACACGGGAGACGCTCCGCTCGCTCGGACGACATGCTG 540
Qy      185  CysAlaGlyAsnThrArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
Db      541  TGTGCGGGAAACACCGGAGGACTCATGCGAGGCGACTCCGGAGGCGCCCTGGTGTG 600
Qy      205  LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224
Db      601  AAGGTGAATGGACCTGCTGCGCGCGGCGTGTGCTCAGCTGGGCGAGGCTGTGCCAG 660
Qy      225  ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisTyr 244
Db      661  CCCAACCGCGCTGGCATCTACACCGTGTACCTACTACTTGGACTGGATCCACCACTAT 720
Qy      245  ValProLysLysPro 249
Db      721  GTCCCCAAAAAGCGC 735

```

Search completed: July 22, 2004, 17:22:57
Job time : 4805 secs

This Page Blank (usp10)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 22, 2004, 15:38:42 ; Search time 86 Seconds
(without alignments)
1606.776 Million cell updates/sec

Title: US-09-598-982-21

Perfect score: 1393

Sequence: 1 LEKRIVGQAEPRSKWQV.....IYTRVTYLDWIHHVVKPK 249

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Fgapop 10.0 , Ygapext 0.5
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09598982/runat_20072004_064410_6521/app_query.fasta_1.391
-DB-Issued_Patents_NA -QWnt-fastcap -SUFFIX=rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09598982 @CGN 1 1.128 @runat_20072004_064410_6521 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DEEXT=7

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1387	99.6	771	3	US-09-079-970A-4
2	1368	98.2	735	3	US-09-079-970A-1
3	1368	98.2	1128	2	US-09-016-366A-20
4	1368	98.2	1128	2	US-08-978-404B-15
5	1363	97.8	1137	2	US-09-016-366A-18
6	1363	97.8	1137	2	US-08-978-404B-13
7	1344	96.5	1081	2	US-09-016-366A-22
8	1344	96.5	1081	2	US-08-978-404B-17
9	1274	91.5	1154	2	US-09-016-366A-16
10	1274	91.5	1154	2	US-08-978-404B-11
11	1091	78.3	1108	2	US-09-016-366A-14
12	1091	78.3	1108	2	US-08-978-404B-20

13	1075	77.2	1219	2	US-08-978-404B-7	Sequence 7, Appli
14	1054	75.7	1031	2	US-08-978-404B-1	Sequence 1, Appli
15	1051	75.4	1097	2	US-08-978-404B-4	Sequence 4, Appli
16	1051	75.4	1103	2	US-09-016-366A-24	Sequence 24, Appli
17	1000.5	71.8	2259	2	US-08-845-998-3	Sequence 3, Appli
18	1000.5	71.8	2259	3	US-09-206-537-3	Sequence 3, Appli
19	1000.5	71.8	2259	3	US-09-430-854-3	Sequence 3, Appli
20	979	70.3	3757	2	US-09-016-366A-13	Sequence 13, Appli
21	979	70.3	3757	2	US-08-978-404B-19	Sequence 19, Appli
22	961.5	69.0	2218	3	US-08-845-998-5	Sequence 5, Appli
23	961.5	69.0	2218	3	US-09-206-537-5	Sequence 5, Appli
24	961.5	69.0	2218	3	US-09-430-854-5	Sequence 5, Appli
25	836.5	60.1	2397	2	US-08-978-404B-2	Sequence 2, Appli
26	684.5	49.1	1095	2	US-08-978-404B-9	Sequence 9, Appli
27	563.5	40.5	980	4	US-09-023-942A-30	Sequence 30, Appli
28	563.5	40.5	1110	4	US-09-386-653A-1	Sequence 1, Appli
29	561.5	40.3	1212	4	US-09-620-312D-431	Sequence 431, App
30	554.5	39.8	1130	4	US-09-386-653A-8	Sequence 8, Appli
31	552	39.6	933	4	US-09-023-942A-29	Sequence 29, Appli
32	536.5	38.5	1613	4	US-09-387-375-1	Sequence 1, Appli
33	527.5	37.9	1130	4	US-09-387-375-8	Sequence 8, Appli
34	507	36.4	1142	4	US-09-386-642-8	Sequence 8, Appli
35	507	36.4	1169	4	US-09-386-642-7	Sequence 7, Appli
36	501.5	36.0	1165	4	US-09-023-942A-28	Sequence 28, Appli
37	501.5	36.0	1378	4	US-09-907-794A-262	Sequence 262, App
38	501.5	36.0	1378	4	US-09-905-125A-262	Sequence 262, App
39	501.5	36.0	1378	4	US-09-902-775A-262	Sequence 262, App
40	501.5	36.0	1430	4	US-09-386-629-1	Sequence 1, Appli
41	499.5	35.9	1094	4	US-09-023-942A-3	Sequence 3, Appli
42	493.5	35.4	1081	3	US-09-008-271A-15	Sequence 15, Appli
43	493.5	35.4	1100	4	US-09-907-794A-256	Sequence 256, App
44	493.5	35.4	1100	4	US-09-905-125A-256	Sequence 256, App
45	493.5	35.4	1100	4	US-09-902-775A-256	Sequence 256, App

ALIGNMENTS

RESULT 1

US-09-079-970A-4

; Sequence 4, Application US/09079970A

; Patent No. 6274366

; GENERAL INFORMATION:

; APPLICANT: Maffitt, Mark A.

; APPLICANT: Niles, Andrew L.

; APPLICANT: Haak-Frendscho, Mary

; TITLE OF INVENTION: Enzymatically-Active Recombinant Human

; TITLE OF INVENTION: Beta-Tryptase and Method of Making Same

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Intellectual Property Department

; STREET: 8000 Excelsior Drive, Suite 401

; CITY: Madison

; STATE: WISCONSIN

; COUNTRY: U.S.A.

; ZIP: 53717-1914

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/079,970A

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Leone, Joseph T.

; REGISTRATION NUMBER: 37,170

; REFERENCE/DOCKET NUMBER: 34506.073

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (608) 831-2100

; TELEFAX: (608) 831-2106

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

```

; LENGTH: 771 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7..753
; FEATURE:
; NAME/KEY: misc signal
; LOCATION: 7..18
; US-09-079-970A-4
Alignment Scores:
Pred. No.: 1.71e-144 Length: 771
Score: 1387.00 Matches: 248
Percent Similarity: 99.60% Conservatives: 0
Best Local Similarity: 99.60% Mismatches: 1
Query Match: 99.57% Indels: 0
DB: 3 Gaps: 0

US-09-598-982-21 (1-249) x US-09-079-970A-4 (1-771)
QY 1 LeuGluLysArgIleValGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20
DB 7 CTCGAGAAAGAAATCGTCGGGGGTCAGAGAGCCGCCAGGAGCAAGTGGCCCTGCAGGTG 66
QY 21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40
DB 67 AGCTGAGAGTCCACGCCCACTATCGATGATGCTTCGCGGGGCTCCCTCATCCACCC 126
QY 41 GlnTrpValLeuThrAlaAlaAlaCysValGlyProAspValLysAspLeuAlaLeu 60
DB 127 CAGTGGGTGTCACCGCAGCGCACTGCGTGGAGCCGACGTCAGAGTCTGGCGGCCCTC 186
QY 61 ArgValGlnLeuArgGluGlnHisLeuTyrTrpGlnAspGlnLeuLeuProValSerArg 80
DB 187 AGGTGGAACATCGCGGAGCAGCACTCTACTACCAGGACCGAGTCTGCGCGGTGAGCAGG 246
QY 81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuGlu 100
DB 247 ATCATGTGCACCCACAGTTCTACCGCCCGACATCGAGGGGACATCGCCCTGCTGGAG 306
QY 101 LeuGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer 120
DB 307 CTGGAGGAGCGGTGAAGGTCTCCAGGCACCTCCACACGCGTCAACCCCTGCCCTGCCTCA 366
QY 121 GluThrPheProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp 140
DB 367 GAGACCTTCCCGCGGAGTCCGCTGCTGGGTCTACTGCTGGGGGAGTGGACAATGAT 426
QY 141 GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160
DB 427 GAGCGCTCCACCGCCATTTCTCTGAAGCAGGTGAAGTCCCAATATGAAACCCAC 486
QY 161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArg 180
DB 487 ATTTGTACGCAAAATACCACTTGGCGCCTACACGGGAGACGACGTCGCGATCGTCCGT 546
QY 181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200
DB 547 GACGACATGCTGTGTGCGCGGAAACCCCGGAGGACTCATCCAGGGGCACTCCGAGGG 606
QY 201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220
DB 607 CCCCTGTGTGCAAGGTGAATGGACCTTGGCTGCGAGCGGGCGTGGTCAAGTGGGGCGAG 666
QY 221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrLeuAspTrp 240

```

667 GGCTGTGCCAGCCCAACCGGCTGGCATACACACCGTGTCACTACTACTTTGGACTGG 726

241 IleHisHisTyrValProLysLysPro 249

727 ATCCACCACCTATGTCCCCAAAAGCCG 753

RESULT 2

US-09-079-970A-1

; Sequence 1, Application US/09079970A

; Patent No. 6274366

; GENERAL INFORMATION:

; APPLICANT: Mafitt, Mark A.

; APPLICANT: Niles, Andrew L.

; APPLICANT: Haak-Frendscho, Mary

; TITLE OF INVENTION: Enzymatically-Active Recombinant Human

; TITLE OF INVENTION: Beta-Tryptase and Method of Making Same

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Intellectual Property Department

; STREET: 8000 Excelsior Drive, Suite 401

; CITY: Madison

; STATE: WISCONSIN

; COUNTRY: U.S.A.

; ZIP: 53717-1914

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/079,970A

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Leone, Joseph T.

; REGISTRATION NUMBER: 37,170

; REFERENCE/DOCKET NUMBER: 34506.073

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (608) 831-2100

; TELEFAX: (608) 831-2106

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 735 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..735

US-09-079-970A-1

Alignment Scores:

Pred. No.: 2.04e-142 Length: 735

Score: 1369.00 Matches: 244

Percent Similarity: 99.59% Conservatives: 0

Best Local Similarity: 99.59% Mismatches: 1

Query Match: 98.21% Indels: 0

DB: 3 Gaps: 0

US-09-598-982-21 (1-249) x US-09-079-970A-1 (1-735)

QY 5 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24

DB 1 ATCTCGGGGTGAGAGGCCGCCAGGAGTGGCCCTGGAGGTGAGCTGAGAGTC 60

QY 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44

DB 61 CACGGCCCACTACTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCGAGTGGGTGCTG 120

45 ThrAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 64
121 ACCGACGCGCACTGCTGGGACCGGACGCTCAAGATCTGGCGCCCTCAGGGTGCAACTG 180
65 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleLeuValHis 84
181 CGGGAGCAGCAGCTTACTACCAAGACCACTGCTGCCGCTCAGCAGGATCATCGTGCAC 240
85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlnLeuPro 104
241 CCACAGTTCTACACCGCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCGG 300
105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
301 GTGAAGGTCTCCAGCACCGTCCACACGCTCACCTGCCCTGCCCTCAGAGACCTTCCCC 360
125 ProGlyMetProCysTyrValThrGlyTyrGlyAspValAspAsnAspGluArgLeuPro 144
361 CGGGGATCGCTGGGTCTACTGGCTGGGCGATGTGCAATGATGAGCGCTCCCA 420
145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
421 CGCCCATTTCTCTGAAGCAGGTGAAGTCCCATTAATGGAACCAACATTTGTGACGCA 480
165 LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspAspMetLeu 184
481 AATATACCACTTGGCGCTTACACGGGAGACGCTCGCATCTGCTGGACCACTGCTG 540
185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
541 TGTGCGGGGAAACACCGGAGGACTCATGCCAGGCGCACTCCGAGGGCCCTCGTGTGC 600
205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluCysAlaGln 224
601 AAGTGATGGCACTGCTGCGGCGGCGGTGTCAGTGGGGGAGGGGTGTGCCAG 660
225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisTyr 244
661 CCCAACCGGCTGGCATCTACACCGTGTCACTACTACTACTACTACTACTACTACTAT 720
245 ValProLysLysPro 249
721 GTCCCCCAAAAGCGG 735

RESULT 3

US-09-016-366A-20
Sequence 20, Application US/09016366A
Patent No. 5955431
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESS: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090

FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1128 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-016-366A-20
Alignment Scores:
Pred. No.: 3,84e-142 Length: 1128
Score: 1368.00 Matches: 244
Percent Similarity: 99.59% Conservative: 0
Best Local Similarity: 99.59% Mismatches: 1
Query Match: 98.21% Indels: 0
DB: 2 Gaps: 0
US-09-598-982-21 (1-249) x US-09-016-366A-20 (1-1128)
QY 5 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24
Db 89 ATCTGTTGGGGTTCAGGAGCGCCCGGAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 148
QY 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
Db 149 CACGCCCATATGATGATGACCTTCTGCGGGGCTCCCTCATCCACCCCGAGTGGTGTG 208
QY 45 ThrAlaAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 64
Db 209 ACCGAGCGCACTGCTGGGACCGGACGCTCAAGGATCTGGCGGCTCAGGAGTATCTGTGCAC 268
QY 65 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleLeuValHis 84
Db 269 CGGAGCAGCACTTACTACTACGAGCAGCTGCTGCGGTCAGCAGGATCATCTGTGCAC 328
QY 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluGluPro 104
Db 329 CCACAGTTCTACACCGCCAGATCGGAGCGACATCGCCCTGCTGGAGCTGGAGGAGCG 388
QY 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
Db 389 GTGAAGGTCTCCAGCGCACTCCACCGTCACTGCGCCCTGCGCCCTCAGAGACCTTCCCC 448
QY 125 ProGlyMetProCysTyrTrpValThrGlyTyrGlyAspValAspAsnAspGluArgLeuPro 144
Db 449 CCGGGGATGCGGTCTGGGTCACTGGCTGGGCGCATGTGGCAATGATGAGCGCTCCCA 508
QY 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
Db 509 CCGCCATTTCTCTGAAGCAGGTGAAGTCCCATTAATGGAACCAACATTTGTGACGCA 568
QY 165 LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspAspMetLeu 184
Db 569 AATATACCACTTGGCGCTTACACGGGAGACGCTCGCATCTGCTGGAGTGCATGCTG 628
QY 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
Db 629 TGTGCGGGAAACACCGGAGGACTCATGCGAGGCGACTCCCGAGGGCCCTCGTGTGC 688
QY 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224
Db 689 AAGTGAATGGCACCTGGCTGCGAGGCGGCTGTGTCAGTGGGCGAGGGCTGTGCCAG 748
QY 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisTyr 244

```

Db      749  CCACACGGCGCTGGCACTACACCGCGTGCACCTACTTGTGACTGGATCCACCACTAT 808
      245  ValProLysLysPro 249
      809  GTCCCAAAAAGCGG 823

RESULT 4
US-08-978-404B-15
; Sequence 15, Application US/08978404B
; Patent No. 5968782
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
; TITLE OF INVENTION: FIBRINOGEN
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,404B
; FILING DATE: 25-NOV-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/032,354
; FILING DATE: 04-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1128 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-978-404B-15

Alignment Scores:
Pred. No.: 3.84e-142 Length: 1128
Score: 1368.00 Matches: 244
Percent Similarity: 99.59% Conservative: 0
Best Local Similarity: 99.59% Mismatches: 1
Query Match: 98.21% Indels: 0
DB: 2 Gaps: 0

US-09-598-982-21 (1-249) x US-08-978-404B-15 (1-1128)

QY      5  IleValGlyGlyGlnGluAlaProArgSerLysTrpTrpGlnValSerLeuArgVal 24
Db      89  ATCGTGGGGTTCAGAGAGCCCGCCAGGACAGTGGCCCTGGCAGGTGAGCGCTGAGAGTC 148

QY      25  HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
Db      149  CACGCCCATACCTGGATGCACTTCTCGGGGGCTCCCTCATCCACCCCGAGTGGGTGCTG 208

QY      45  ThrAlaAlaAlaCysValGlyProValLysAspLeuAlaAlaLeuArgValGlnLeu 64
Db      209  ACCGACGCGCACTGGCGTGGGACCGGACGTCAGAGATCTGGCCGCCCTCGGGTGCACCTG 268

```

```

QY      65  ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 84
Db      269  CGGGAGCAGCACCTCTACTACACAGGACCACTGTCGCGGTGACGAGGATCATCTGTGCAC 328

QY      85  ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluGluPro 104
Db      329  CCACAGTTCTACACCGCCGAGATCGGAGCGGAGCATGCGCCCTGTGGAGCTGGAGGAGCGG 388

QY      105  ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
Db      389  GTGAGGTCTCCAGCCACGTCACACGGTCACTGCGCCCTGCTCAGAGACCTTCCCC 448

QY      125  ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
Db      449  CCGGGGATGCGGTGCTGGGTCACTGGCTGGGGGCGATGTGACAAATGATGAGCGCCTCCCA 508

QY      145  ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
Db      509  CCGCCATTTCTCTGAAGCAGGTGAGGTCCCAATATGGAACCAACATTTGTGACGCA 568

QY      165  LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspAspMetLeu 184
Db      569  AATACCACTTGGCGCTACACGGGAGACGACGTCCGTCATCGTCGTCGACGACATGCTG 628

QY      185  CysAlaGlyAsnThrArgArgAspSerCysGlnClyAspSerGlyGlyProLeuValCys 204
Db      629  TGTGCCGGGAACACCCGGAGGAGCTCATGCGAGGGCGACTCCGGAGGGCCCTGCTGTGTC 688

QY      205  LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224
Db      689  AAGGTGAATGGCACTGCTGCTGCGAGCGCGGCTGTGCTGAGCTGGGGCGGGGCTGTGCCAG 748

QY      225  ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisTyr 244
Db      749  CCCAACCGCGCTGGCACTACACCCGTGTACCTACTACTTGGACTGGATCCACCACTAT 808

QY      245  ValProLysLysPro 249
Db      809  GTCCCAAAAAGCGG 823

RESULT 5
US-09-016-366A-18
; Sequence 18, Application US/09016366A
; Patent No. 5955431
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; APPLICANT: Huang, Chifu
; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,366A
; FILING DATE: January 30, 1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,090
; FILING DATE: 05-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7093

```

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 1137 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

US-09-016-366A-18

Alignment Scores:

Pred. No.: 1.39e-141 Length: 1137
Score: 1363.00 Matches: 243
Percent Similarity: 99.18% Conservative: 0
Best Local Similarity: 99.18% Mismatches: 2
Query Match: 97.85% Indels: 0
DB: 2 Gaps: 0

US-09-598-982-21 (1-249) x US-09-016-366A-18 (1-1137)

QY 5 IleValGlyGlyGlnGlnAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24
DB 87 ATCGTCGGGGGTTCAGGAGGCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 146
QY 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
DB 147 CACGGCCCATACTGATGACATCTTCGGGGGGCTCCCTCATCCACCCCGAGTGGTGTCTG 206
QY 45 ThrAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 64
DB 207 ACCGAGCGCACTGCTGGGACCGGAGCTCAAGATCTGGCGGCTCGCCCTCAGGTCGACTG 266
QY 65 ArgGlnGlnHisLeuTyrTyrGlnAspGlnLeuProValSerArgIleIleValHis 84
DB 267 CGGAGGAGCAGCACTCTACTACGAGGACAGCTGTGCGGGTCTGCGGATCATCGTGAC 326
QY 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluGluPro 104
DB 327 CCACAGTTTACACGCCCCAGATCGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCG 386
QY 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
DB 387 GTGAACGTCTCCAGCCACGTCCACACGCTCACCCCTGCTGCTGCTGCTGCTGCTGCTG 446
QY 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
DB 447 CCGGGGATGCGCTGCTGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCTCCCA 506
QY 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
DB 507 CCGCATTTCTCTGAGAGGAGTGAAGTCCCATATATGGAACCAATTTGAGCGCA 566
QY 165 LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspMetLeu 184
DB 567 AAATPACCACTTGGCGCTACACGGGAGACGACGTCCGATCGTCCGTGAGCATGCTG 626
QY 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
DB 627 TGTCCGGGGAACACCCGGAGGAGTCTATGCGAGGGGACTCCGAGGGGCGCCCTGGTGTGC 686
QY 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlyGlyCysAlaGln 224
DB 687 AAGGTGAATGGCACCTGGCTGACGGGGGGTGTGTGAGCTGGGGCGAGGGCTGFGCCAG 746
QY 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 244
DB 747 CCAACCGGCTGGCATCTACACCCGCTGCTACCTACTTGGATCTGGATCCACCATAT 806
QY 245 ValProLysLysPro 249
|||||

Db 807 GTCCCCAAAAGCCG 821

RESULT 6

US-08-978-404B-13

; Sequence 13, Application US/08978404B

; Patent No. 5968782

; GENERAL INFORMATION:

; APPLICANT: Stevens, Richard L.

; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES

; TITLE OF INVENTION: FIBRINOGEN

; NUMBER OF SEQUENCES: 74

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

; STREET: 600 Atlantic Avenue

; CITY: Boston

; STATE: MA

; COUNTRY: U.S.A.

; ZIP: 02210-2211

; COMPUTER READABLE FORM:

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/978,404B

; FILING DATE: 25-NOV-97

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/032,354

; FILING DATE: 04-DEC-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Plumer, Elizabeth R.

; REGISTRATION NUMBER: 36,637

; REFERENCE/DOCKET NUMBER: B0801/7090

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-720-3500

; TELEFAX: 617-720-2441

; TELEX:

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1137 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-978-404B-13

Alignment Scores:

Pred. No.: 1.39e-141 Length: 1137
Score: 1363.00 Matches: 243
Percent Similarity: 99.18% Conservative: 0
Best Local Similarity: 99.18% Mismatches: 2
Query Match: 97.85% Indels: 0
DB: 2 Gaps: 0

US-09-598-982-21 (1-249) x US-08-978-404B-13 (1-1137)

QY 5 IleValGlyGlyGlnGlnAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24
DB 87 ATCGTCGGGGGTTCAGGAGGCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 146
QY 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
DB 147 CACGGCCCATACTGATGACATCTTCGGGGGGTCTTCCTATCCACCCCGAGTGGTGTCTG 206
QY 45 ThrAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 64
DB 207 ACCGAGCGCACTGCTGGGACCGGAGCTCAGGATCTGGCCCTCAGGTCGAACTG 266
QY 65 ArgGlnGlnHisLeuTyrTyrGlnAspGlnLeuProValSerArgIleIleValHis 84
DB 267 CGGAGGAGCAGCACTCTACTACGAGGACAGCTGTGCGGCTGACGAGATCCTGTCGAC 326
QY 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluGluPro 104

Db 327 CCACAGTCTACACCCAGATCGAGCGGACATCGCCCTGCTGAGCTGGAGGACCG 386
QY 105 VallyValSerSerHisValHisThrValThrLeuProAlaSerGluThrPhePro 124
Db 387 GTGAAGCTCTCAGACGACGCTCCACACGGGTCAACCTGCGCCCTGCCTCAGAGACCTTCCCC 446
QY 125 ProGlyMetProCysTrpValThrGlyTrpGlyValAspValAspAsnAspGluArgLeuPro 144
Db 447 CCGGGGATGCGGTGCTGGGTGCTGCTGGGGGATGTGGACAAATGATGAGCGCCCTCCCA 506
QY 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
Db 507 CCGCCATTCCTCTGAAGCAGGTGAAGGTCCCAATATGAAACCAACCAATTTGTGAGCA 566
QY 165 LysTyrHisLeuGlyAlaTyrThrGlyAspValAlaGlyValArgIleValArgAspMetLeu 184
Db 567 AAATACCACTTGGCGCTACACGGGAGACGAGCTCCGATCGTCCGTGACGACATGCTG 626
QY 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
Db 627 TGTGCCGGGAACACCGGAGGACTCATGTCAGGGGACTCCGGAGGGGCCCTGGTGTGC 686
QY 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224
Db 687 AGGTGAATGCGACCTGGCTGCAGGGGGGCTGTGTCAAGCTGGGGGCGAGGCTGTGCCAG 746
QY 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisTyr 244
Db 747 CCCAACCGGCTGCGATCATCACCCGTGTCACTACTTGGACTGGATCCACCACTAT 806
QY 245 ValProLysLysPro 249
Db 807 GTCCCCAAAAAGCG 821

RESULT 7

US-09-016-366A-22
; Sequence 22, Application US/09016366A
; Patent No. 5955431
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; APPLICANT: Huang, Chifu
; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
; TITLE OF INVENTION: INHIBITORS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,366A
; FILING DATE: January 30, 1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,090
; FILING DATE: 05-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1081 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-016-366A-22

Alignment Scores:

Pred. No.: 1,65e-139 Length: 1081
Score: 1344.00 Matches: 241
Percent Similarity: 98.37% Conservatives: 0
Best Local Similarity: 98.37% Mismatches: 4
Query Match: 96.48% Indels: 0
DB: Gaps: 0

US-09-598-982-21 (1-249) x US-09-016-366A-22 (1-1081)

QY 5 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24
Db 68 ATCGTTGGGGGTCCAGGAGGCCCCCAGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 127
QY 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
Db 128 CGCAGCCGATACCTGATGACACTTCTGCGGGGGCTCCCTCATCCACCCAGTGGGTGCTG 187
QY 45 ThrAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 64
Db 188 ACCGAGCGCACTGCTGGGACCGGAGCTCAGAGATCTGGCCGCCCTCAGGGTGCAACTG 247
QY 65 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuProValSerArgIleIleValHis 84
Db 248 CCGGAGCAGCACCTCTACTACAGGACCACTGCTGCCGGTCCAGGATCATCGTGAC 307
QY 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluGluPro 104
Db 308 CCACAGTCTACACCGCCCGAGATCGGAGCGGACATCGCCCTGTGGAGCTGGAGAGCGG 367
QY 105 ValLysValSerSerHisValHisThrValThrLeuProAlaSerGluThrPhePro 124
Db 368 GTGAGGTCTCCAGCCACGCTCCACCGTCCACCGTCCCGCTGCCCTCAGAGACCTTCCCC 427
QY 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
Db 428 CCGGGGATGCGTCTGCTGGTCACTGCTGGGGGATGTGGACAAATGATGAGCGCTCCCA 487
QY 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
Db 488 CCGCCATTTCTCTGAAGCAGGTGAGGTCCCCATATGGAACCAACCAATTTGTGAGCA 547
QY 165 LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspMetLeu 184
Db 548 AAATACCACTTGGCGCTTACCGGAGACGAGCTCCGATCGTCCGTGACGACATGCTG 607
QY 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
Db 608 TGTCCGGGAACACCGGAGGACTCATGCGAGGGGCGACTCCGGAGGGGCCCTGGTGTGC 667
QY 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224
Db 668 AAGGTGAATGACCACTGGCTGACGCGGGGCTGGTCACTGGGGGAGGGCTGTGCCAG 727
QY 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisTyr 244
Db 728 CCCAACCGGCTGCGATCATCACCCGTGTCACTACTACTTGGAGTGGATCCACCACTAT 787
QY 245 ValProLysLysPro 249
Db 788 GTCCCCAAAAAGCG 802

RESULT 8

US-08-978-404B-17
; Sequence 17, Application US/08978404B

Patent No. 5958782
 GENERAL INFORMATION:
 APPLICANT: Stevens, Richard L.
 TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
 NUMBER OF SEQUENCES: 74
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 STREET: 600 Atlantic Avenue
 CITY: Boston
 STATE: MA
 COUNTRY: U.S.A.
 ZIP: 02210-2211
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/978,404B
 FILING DATE: 25-NOV-97
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/032,354
 FILING DATE: 04-DEC-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Plumer, Elizabeth R.
 REGISTRATION NUMBER: 36,637
 REFERENCE/DOCKET NUMBER: B0801/7090
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-720-3500
 TELEFAX: 617-720-2441
 TELEX:
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1081 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-978-404B-17
 Alignment Scores:
 Pred. No.: 1.65e-139 Length: 1081
 Score: 1344.00 Matches: 241
 Percent Similarity: 98.37% Conservativity: 0
 Best Local Similarity: 98.37% Mismatches: 4
 Query Match: 96.48% Indels: 0
 DB: 2 Gaps: 0

US-09-598-982-21 (1-249) x US-08-978-404B-17 (1-1081)

QY 5 IleValGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24
 DB 68 ATCTTGGGGTTCAGAGGCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCTCAGAGTC 127
 QY 25 HisGlyProTyrTrpMetHisPheCysGlySerLeuIleHisProGlnTrpValLeu 44
 DB 128 CGCGACCGATCTGGATGCACTTCTGGGGGGCTCCCTCATCCACCCCACTGGTGTG 187
 QY 45 ThrAlaAlaCysValGlyProAspValLysAspLeuAlaLeuArgValGlnLeu 64
 DB 188 ACCGACGGCACTCGGGGGAGCCGAGCTCAAGGATCTGGCCGCCCTCAGGGTCAACTG 247
 QY 65 ArgGluGlnHisLeuTyrTrpGlnAspGlnLeuProValSerArgIleLeuValHis 84
 DB 248 CGGAGCAGCACCTCTACTACAGACCCAGCTGCTGGGGTCAAGGATCATCGTGAC 307
 QY 85 ProGlnPheTyrThrAlaGlnIleClyAlaAspIleAlaLeuLeuGluLeuPro 104
 DB 308 CCACAGTTCTACACCGCCAGATCGGAGCGACATCGCCCTGCTGGAGCTGGAGAGCCG 367
 QY 105 ValLysValSerSerHisValHisThrValThrLeuProAlaSerGluThrPhePro 124

DB 368 GTGAAGGTCTCCAGCACGTCACACGGTACCCCTGCCCTCCCTCAGAGACCTTCCCC 427
 QY 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
 DB 428 CCGGGGATGCCGTGTGGTCTACTGGCTGGGGCGATGTGGACAATGATGAGCGCTCCCA 487
 QY 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
 DB 488 CGGCCATTTCCTCTGAGCAGGTGAAGGTCCCAATATGAAACACCAATTTGTGACGCA 547
 QY 165 LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspAspMetLeu 184
 DB 548 AATATCACCTTGGCGCTTACACGGGAGAGCGATCGTCGGTACGACATGTGTG 607
 QY 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
 DB 608 TGTGCGGGAAACACCGGAGGACTCATGCCAGGCGACTCCGAGGGCGCTCGGTGTGC 667
 QY 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224
 DB 668 AAGTGAATGGCACCCTGGCTGCAGCGGGCGTGGTGCAGTGGGGCGAGGGCTGTCC 727
 QY 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisTyr 244
 DB 728 CCCAACCGGCTGGCATCTACACCGGTGTACCTACTTGGACTGGATCCACCATAT 787
 QY 245 ValProLysLysPro 249
 DB 788 GTCCCCAAAAAGCCG 802
 RESULT 9
 US-09-016-366A-16
 Sequence 16, Application US/09016366A
 Patent No. 5955431
 GENERAL INFORMATION:
 APPLICANT: Stevens, Richard L.
 APPLICANT: Huang, Chifu
 TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
 TITLE OF INVENTION: INHIBITORS
 NUMBER OF SEQUENCES: 65
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 STREET: 600 Atlantic Avenue
 CITY: Boston
 STATE: MA
 COUNTRY: U.S.A.
 ZIP: 02210-2211
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/016,366A
 FILING DATE: January 30, 1998
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/037,090
 FILING DATE: 05-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Plumer, Elizabeth R.
 REGISTRATION NUMBER: 36,637
 REFERENCE/DOCKET NUMBER: B0801/7093
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-720-3500
 TELEFAX: 617-720-2441
 TELEX:
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1154 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

; MOLECULE TYPE: cdna
US-09-016-366A-16

Alignment Scores:

Alignment Scores:					
Pred. No.:	1.05e-131	Length:	1154		
Score:	1274.00	Matches:	226		
Percent Similarity:	94.6%	Conservative:	6		
Best Local Similarity:	92.24%	Mismatches:	13		
Query Match:	91.46%	Indels:	0		
DB:	2	Gaps:	0		

US-09-598-982-21 (1-249) x US-09-016-366A-16 (1-1154)

Qy	5	IleValGlyGlnGlnAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal	24
Db	108	ATCGTCGGGGTCAGGAGGCCCCAGAGAGCAAGTGGCCCTGGCAGTGCAGCTGAGATC	167
Qy	25	HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu	44
Db	168	CGGACCGGATCTGGATGCATCTTCGCGGGGCTCCCTCATCCACCCAGTGGGTGCTG	227
Qy	45	ThrAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu	64
Db	228	ACCGGGCGCACTGCTGGHACGGACGCTCAAGGATCTGGCCACCCTCAGGGTGCAACTG	287
Qy	65	ArgGluGlnHisLeuTyrTrpGlnAspGlnLeuLeuProValSerArgIleIleValHis	84
Db	288	CGGAGCAGCACCTCTACTACAGACCAGCTGCTGCCAGTCAGCAGGATCATCTGTCAC	347
Qy	85	ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGlnPro	104
Db	348	CCACAGTTCTACATCATCCAGACTGGAGCGGATATCGCCCTGCTGGAGCTGGAGAGCC	407
Qy	105	ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro	124
Db	408	GTGAACATCTCCAGCGCGTCCACACGGTCATGCTGCCCTGCCTCGGAGACCTCCCC	467
Qy	125	ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro	144
Db	468	CGGGGATCGCGTGCTGGTCACTGGCTGGGCGCATGTGCAACAATCATGAGCCCTCCCA	527
Qy	145	ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla	164
Db	528	CGCCATTTCCTCGAAGCAGGTGAAGTGCCTCCATATGAAACACCAATTTGTGACGCA	587
Qy	165	LysTyrHisLeuGlyValatyrThrGlyAspAspValArgIleValArgAspAspMetLeu	184
Db	588	AAATACCACCTTGGGCGCTACACGGGAGACGAGCCGCGATCATCTCGTGCAGCATGCTG	647
Qy	185	CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys	204
Db	648	TGTGCGGGAAACAGCCAGAGGGACTCTCTCAAGGGGCGACTCTGGAGGGGCCCTGGTGTG	707
Qy	205	LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln	224
Db	708	AAGGTGAATGGCACTTGGCTACAGGCGGCGGTGGTCAAGTCAGGAGCGGCTGTGCCAG	767
Qy	225	ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr	244
Db	768	CCCAACCGGCTGGGCATCTACACCCGTGTCTACTACTTGGACTGGATCCACCCTAT	827
Qy	245	ValProLysLysPro	249
Db	828	GTCCGCAAAAAGCCG	842

RESULT 10

```

RESULT 10
US-08-978-404B-11
; Sequence 11, Application US/08978404B
; Patent No. 5968782
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
; TITLE OF INVENTION: FIBRINOGEN

```

QY 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
 Db 528 CGCCATTTCCCTCAAGCAGGTGAAGTCCCATTAATGGAAACCACTTTGTGACGCA 587
 QY 165 LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspMetLeu 184
 Db 588 AATACCACTTGGCGCTACACGGGAGACGACGTCCGCATCATCCGTGACGACATGCTG 647
 QY 185 CysAlaGlyAsnThrArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
 Db 648 TGTGCGGGAACAGCAGGAGACTCCCTGCAAGGGCGACTCTGGAGGGCCCTGTGTGTC 707
 QY 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224
 Db 708 AAGTGAATGGCACCTGCTACAGCGGGGGTGGTGGTGGGAGGGCTGTGCCAG 767
 QY 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisTyr 244
 Db 768 CCCAACCGGCTGGCATCTACACCGTGTCACTACTTGGACTGGATCCACCATAT 827
 QY 245 ValProLysLysPro 249
 Db 828 GTCCCCAAAAGCCG 842

RESULT 11

US-09-016-366A-14
 ; Sequence 14, Application US/09016366A
 ; Patent No. 5955431
 ; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; APPLICANT: Huang, Chifu
 ; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
 ; TITLE OF INVENTION: INHIBITORS
 ; NUMBER OF SEQUENCES: 65
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: U.S.A.
 ; ZIP: 02210-2211
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016.366A
 ; FILING DATE: January 30, 1998
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/037,090
 ; FILING DATE: 05-FEB-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Plumer, Elizabeth R.
 ; REGISTRATION NUMBER: 36,637
 ; REFERENCE/DOCKET NUMBER: B0801/7093
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-720-3500
 ; TELEFAX: 617-720-2441
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1108 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cdna
 ; US-09-016-366A-14

Alignment Scores:

Pred. No.: 1.91e-111 Length: 1108

Score: 1091.00 Matches: 190
 Percent Similarity: 86.01% Conservative: 19
 Best Local Similarity: 78.19% Mismatches: 34
 Query Match: 78.32% Indels: 0
 DB: 2 Gaps: 0

US-09-598-982-21 (1-249) x US-09-016-366A-14 (1-1108)

QY 5 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24
 Db 127 ATCTGGGAGACATGAGGCTTCTGAGAGTAAGTGGCCCTGGCAGGTGAGCCTGAGATT 186
 QY 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
 Db 187 AATTAACACTACTGGATACATTTCTGGAGGCTCTCTCATCCACCCACAGTGGGTGCTC 246
 QY 45 ThrAlaAlaCysValGlyProAspValLysAspLeuAlaLeuArgValGlnLeu 64
 Db 247 ACTCGGCACACTGTGTGGGACCGCACATCAAAAGCCACAGCTTCTCCGGGTGCAGCTT 306
 QY 65 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuProValSerArgIleIleValHis 84
 Db 307 CGTGAGCAGTATCTATATCTATGGGACCGAGCTCTCTTTCAACCGGATCGTGGTGAC 366
 QY 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluPro 104
 Db 367 CCCCACTATTACCGCGGAGGTGGGCGACAGCTTGCCTGTGGAGCTTGAGGTCCCT 426
 QY 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
 Db 427 GTGAATGTCTCCACCCATATCCACCCCATATCCCTGCTGCCCTGCTCGAGACCTTCCCC 486
 QY 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
 Db 487 CCTGGACATCTGCTGGGTGACAGGTGGGCGACATTGATTAATGACGACCTCTCCCA 546
 QY 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
 Db 547 CCTCTTATCTCTGAAGCAAGTGAAGTTCCTTGTGGAAACAGCCTGTGTGACCGG 606
 QY 165 LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspMetLeu 184
 Db 607 AAGTACCACACTGGCTCTCTACACGGAGATGATTTTCCCATGTCCATGATGGCATGCTG 666
 QY 185 CysAlaGlyAsnThrArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
 Db 667 TGTCTGGAAATACCGAGGAGACTCTCTGCGAGGCGATTTCAGGGGGGCCACTGTGTCTGC 726
 QY 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224
 Db 727 AAGTGAAGGGTACTCTGGCTGCAGGCGAGGTGGTGTGAGTGGGTGAGGGCTGGCAG 786
 QY 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisTyr 244
 Db 787 CCCAACAAAGCTGGCATCTACACCGGCTGACATCTACTACTAGACTGATGATCCACCGCTAT 846
 QY 245 ValProLys 247
 Db 847 GTCCCTGAG 855

RESULT 12

US-08-978-404B-20
 ; Sequence 20, Application US/08978404B
 ; Patent No. 5968782
 ; GENERAL INFORMATION:
 ; APPLICANT: Stevens, Richard L.
 ; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
 ; TITLE OF INVENTION: FIBRINOGEN
 ; NUMBER OF SEQUENCES: 74
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston

QY	165	LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspMetLeu	184
Db	607	AAGTACCACATGGCCTCTACAGGAGATGATTTCCATGTCCATGATGGCATGCTG	666
QY	185	CysAlaGlyAsnThrArgAspSerCysGlnGlyAspSerGlyProLeuValCys	204
Db	667	TGTGCTGGAATACACAGGAGACTCTCTGCCAGGCGGATTCAGGGGGCCACTGGTCTGC	726
QY	205	LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlyCysAlaGln	224
Db	727	AAAGTGAAGGGTACCTGGCTGCAGGAGAGTGGTGCAGTGGGGTGGGGTGGGCACAG	786
QY	225	ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisTyr	244
Db	787	CCACAGACCCCTGGCATCTACACCCGGGTGACATCTACTTACTTAGACTGGATCCACCGCTAT	846
QY	245	ValProLys 247	
Db	847	GTCCCTGAG 855	
RESULT 13			
US-08-978-404B-7			
; Sequence 7, Application US/08978404B			
; Patent No. 5968782			
; GENERAL INFORMATION:			
; APPLICANT: Stevens, Richard L.			
; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES			
; TITLE OF INVENTION: FIBRINOGEN			
; NUMBER OF SEQUENCES: 74			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.			
; STREET: 600 Atlantic Avenue			
; CITY: Boston			
; STATE: MA			
; COUNTRY: U.S.A.			
; ZIP: 02210-2211			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Diskette			
; COMPUTER: IBM Compatible			
; OPERATING SYSTEM: DOS			
; SOFTWARE: FastSEQ for Windows Version 2.0			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/978,404B			
; FILING DATE: 25-NOV-97			
; CLASSIFICATION: 435			
; PRIORITY APPLICATION DATA:			
; APPLICATION NUMBER: 60/032,354			
; FILING DATE: 04-DEC-1996			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Plumer, Elizabeth R.			
; REGISTRATION NUMBER: 36,637			
; REFERENCE/DOCKET NUMBER: B0801/7090			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 617-720-3500			
; TELEFAX: 617-720-2441			
; TELEX:			
; INFORMATION FOR SEQ ID NO: 7:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1219 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
US-08-978-404B-7			
Alignment Scores:			
Pred. No.:	1,31e-109	Length:	1219
Score:	1075.00	Matches:	188
Percent Similarity:	84.77%	Conservative:	18
Best Local Similarity:	77.37%	Mismatches:	37
Query Match:	77.17%	Indels:	0
DB:	2	Gaps:	0
US-09-598-982-21 (1-249) x US-08-978-404B-7 (1-1219)			


```

QY 5 IleValGlyGlyGlnGluAlaProArgSerLysTyrProTyrGlnValSerLeuArgVal 24
Db 273 ATTGTGGGGGACAGAGCAGCCTGGGAACAAGTGGCCCTGGCAGGTGAGCCCTTCGTGCC 332
QY 25 HisGlyProTyrTyrMetHisPheCysGlyGlySerLeuIleHisProGlnTyrValLeu 44
Db 333 AATGAACACTTCTGGAGGCAATTCGCGGGGCTCCCTCATCCACCACAGTGGGTGCTC 392
QY 45 ThrAlaAlaCysValGlyProAspValValValValValValValValValValVal 64
Db 393 ACCGGGGACACTGTGTGGGACCGACTATGTGTATCCCAACAAGGTGACAGTACAGCTT 452
QY 65 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 84
Db 453 CGAAGACAGTACTCTATTACACGACCACTGCTGGCTGTGAGCGGATCATCACAC 512
QY 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluPro 104
Db 513 CCGACATTCATGCCACCAGGAATGGGGCGGACATCGCCCTACTTGAGCTCAAGAACCT 572
QY 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
Db 573 GTAACATTCGAGCAATGTCACCCCGTCTCCCTGCTCCCTGCTCCCTCAGAGACCTTC 632
QY 125 ProGlyMetProCysTyrPyrValThrGlyTyrGlyAspValValAspAsnArgLeuPro 144
Db 633 TCAGGAACATTCGTGGGTGACAGCTGGGGGAACATCGACAATGATGTGAGCCTGCCA 692
QY 145 ProProPheProLeuLysGlnValValValProIleMetGluAsnHisIleCysAspAla 164
Db 693 CCGCCATTCCTCGAAGAGGTGCAAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 752
QY 165 LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspMetLeu 184
Db 753 AAGTATCAACAAGGTGTCTACACAGGGGACACATCCCATTTGTCGAGACGACATGCTG 812
QY 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
Db 813 TGTGCTGGGAAGGACAGACGACTCTCTCCAGGGTGACTCCGAGGACCTCTGCTGCTG 872
QY 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224
Db 873 AAGTAAACGGTACTGCTGCTGAGCAGAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCT 932
QY 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTyrIleHisTyr 244
Db 933 CCCAACAGGCTGCACTACACTCGGTACCTTACTTACTTGGTGGTGGTGGTGGTGGT 992
QY 245 ValProLys 247
Db 993 GTCCCAAG 1001

```

RESULT 14

```

US-08-978-404B-1
; Sequence 1, Application US/08978404B
; Patent No. 5968782
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
; TITLE OF INVENTION: FIBRINOGEN
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

```

```

; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,404B
; FILING DATE: 25-NOV-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/032,354
; FILING DATE: 04-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:

```

INFORMATION FOR SEQ ID NO: 1:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1031 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-978-404B-1

```

Alignment Scores:

```

Pred. No.: 2,17e-107 Length: 1031
Score: 1054.00 Matches: 186
Percent Similarity: 83.54% Conservative: 17
Best local Similarity: 76.54% Mismatches: 40
Query Match: 75.66% Indels: 0
DB: 2 Gaps: 0

```

US-09-598-982-21 (1-249) x US-08-978-404B-1 (1-1031)

```

QY 5 IleValGlyGlyGlnGluAlaProArgSerLysTyrProTyrGlnValSerLeuArgVal 24
Db 111 ATTGTGGGGGACAGAGGACATGGGAACAAGTGGCCCTGGCAGGTGAGCCCTTCGTGCC 170
QY 25 HisGlyProTyrTyrMetHisPheCysGlyGlySerLeuIleHisProGlnTyrValLeu 44
Db 171 AATGACACTTCTGGATGCAATTCGCGGTGGTCTCCCTCATCCACCACAGTGGGTGCTC 230
QY 45 ThrAlaAlaCysValGlyProAspValValValValValValValValValValVal 64
Db 231 ACTCGGCACACTGTGTGGGACCGGATGTCTGCTGACCCCAAGGTGAGGTGAGTACAGCTC 290
QY 65 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuProValSerArgIleIleValHis 84
Db 291 CGTAAGCAGTACTCTATTACCATGACCCCTGATGCTGTGAGCCAGATCATCACAC 350
QY 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluPro 104
Db 351 CCCGACTTCTACATCGTCCAGGATGGGCGACATTCGCTGTGTAACCTCACAACCTC 410
QY 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
Db 411 GTGAACATTTCTGACTATGTCACCCCTGTCCCCCTACCTCTCTGCTCAGAGACCTTC 470
QY 125 ProGlyMetProCysTyrPyrValThrGlyTyrGlyAspValValAspAsnArgLeuPro 144
Db 471 TCAGGAACGTTGTGCTGGGTGACAGGCTGGGGTAACTGACATGCTGTAAACCTTC 530
QY 145 ProProPheProLeuLysGlnValValProIleMetGluAsnHisIleCysAspAla 164
Db 531 CCACCATTTCTTGAAGGAGGTGCAAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 590
QY 165 LysTyrHisLeuGlyAlaTyrThrGlyAspValValValValValValValValVal 184
Db 591 AAGTATCAACAAGGTCTCATCAGGTTGACATGTCCACATTTGTCCGAGATGACATGCTG 650
QY 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
Db 651 TGTGCTGGGATGAAGGACATGACTCTCTGCGGGGACTCCCGAGGACCTCTGGTCTGC 710

```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 22, 2004, 15:26:22 ; Search time 474 Seconds
(without alignments)
2231.648 Million cell updates/sec

Title: US-09-598-982-21

Perfect score: 1393

Sequence: 1 LKRIUGQAPRKPWMOV.....IYTRVTYLDWIHYVKKP 249

Scoring table:

BLOSUM62	Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5	
Fgapop 6.0	Fgapext 7.0	
Delop 6.0	Delext 7.0	

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2 1/USPTO spool p/US09598982/runat_20072004_064409_6476/app.query.fasta_1.391
-DB=N Geneseq 29Jan04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPTXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09598982.cgn 1.1 885 @runat_20072004_064409_6476 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq 29Jan04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002s:*
- 7: Geneseqn2003as:*
- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1393	100.0	771	6	AAS20775 DNA encod
2	1388	99.6	771	6	AAS20783 DNA encod
3	1387	99.6	771	6	AAS20783 DNA encod
4	1387	99.6	771	6	AAS20783 DNA encod
5	1384	99.4	771	6	AAS20783 DNA encod
6	1384	99.4	771	6	AAS20783 DNA encod
7	1382	99.2	771	6	AAS20783 DNA encod
8	1379	99.0	771	6	AAS20786 DNA encod

9	1379	99.0	771	6	AAS20785	DNA encod
10	1379	99.0	771	6	AAS20776	DNA encod
11	1374	98.6	735	6	AAS20779	DNA encod
12	1374	98.6	771	6	AAS20784	DNA encod
13	1369	98.3	735	6	AAS20787	DNA encod
14	1368	98.2	735	6	AAS20787	DNA encod
15	1368	98.2	735	6	AAS20787	DNA encod
16	1368	98.2	735	6	AAS20787	DNA encod
17	1368	98.2	735	6	AAS20787	DNA encod
18	1368	98.2	735	6	AAS20787	DNA encod
19	1368	98.2	735	6	AAS20787	DNA encod
20	1368	98.2	735	6	AAS20787	DNA encod
21	1368	98.2	735	6	AAS20787	DNA encod
22	1368	98.2	735	6	AAS20787	DNA encod
23	1368	98.2	735	6	AAS20787	DNA encod
24	1368	98.2	735	6	AAS20787	DNA encod
25	1368	98.2	735	6	AAS20787	DNA encod
26	1368	98.2	735	6	AAS20787	DNA encod
27	1365	98.0	735	6	AAS20782	DNA encod
28	1365	98.0	735	6	AAS20782	DNA encod
29	1363	97.8	735	6	AAS20781	DNA encod
30	1363	97.8	735	6	AAS20781	DNA encod
31	1363	97.8	735	6	AAS20781	DNA encod
32	1363	97.8	735	6	AAS20781	DNA encod
33	1363	97.8	735	6	AAS20781	DNA encod
34	1363	97.8	735	6	AAS20781	DNA encod
35	1360	97.6	735	6	AAS20789	DNA encod
36	1360	97.6	735	6	AAS20789	DNA encod
37	1360	97.6	735	6	AAS20789	DNA encod
38	1355	97.3	735	6	AAS20788	DNA encod
39	1344	96.5	1081	2	AAV44331	Human mas
40	1344	96.5	1081	2	AAV44331	Human mas
41	1344	96.5	1081	2	AAV44331	Human mas
42	1344	96.5	1081	3	AAV44331	Human mas
43	1344	96.5	1081	3	AAV44331	Human mas
44	1344	96.5	1081	6	ABL66816	Colon ade
45	1344	96.5	1081	6	ABL66816	Colon ade

ALIGNMENTS

RESULT 1

AAS20775

ID AAS20775 standard; DNA; 771 BP.

XX AAS20775;

AC AAS20775;

XX AAS20775;

DT 09-APR-2002 (first entry)

XX DNA encoding human beta-II tryptase active site mutant H44A #1.

XX Human; proteolytic tryptase; protease; recombinant beta-II tryptase;

XX enzyme; mutant; ds.

XX Homo sapiens.

OS Synthetic.

XX WO200198470-A2.

XX 27-DEC-2001.

XX 20-JUN-2001; 2001WO-US019681.

XX 21-JUN-2000; 2000US-00598982.

XX (PROM-) PROMEGA CORP.

XX Maffit M, Niles AL, Haak-Frendscho M;

XX WPI; 2002-114578/15.

XX P-PSDB; AAU12009.

XX DNA construct for producing enzymatically-inactive proteolytic tryptase, PT

PT comprises DNA sequence encoding proteolytic trypsin having an active site mutation.

XX Claim 7; Page 83-84; 126pp; English.

XX The present invention relates to recombinant human proteolytic trypsin, active site mutants of these trypsin and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic trypsin with an active site mutation (the construct drives expression of a mature proteolytic trypsin that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II trypsin. The active site mutants of proteolytic trypsin provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic trypsin produced are useful as an antigen to generate anti-human trypsin antibodies and in drug screening for compounds which act as trypsin inhibitors, antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant human beta-II trypsin active site mutants

XX Sequence 771 BP; 147 A; 256 C; 244 G; 124 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.04e-121	Length:	771
Score:	1393.00	Matches:	249
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-598-982-21 (1-249) x AAS20775 (1-771)

QY 1 LeuGluValHisArgLeuValGlyGlnGlnAlaProArgSerLysTrpProTrpGlnVal 20

DB 7 CTCGAGAAAGATCTGTCGGGGTTCAGAGAGCCCGCCAGAGCAAGTGCGCCCTGGCAGGTG 66

QY 21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuLeuHisPro 40

DB 67 AGCCTGAGAGTCCACGGGCCCATCTATGATGACATCTCTCGGGGGCTCCCTCATCCACCC 126

QY 41 GlnTrpValLeuThrAlaAlaCysValGlyProAspValLysAspLeuAlaLeu 60

DB 127 CAGTGGGTCGTGACCGCGCGGTGGTGGACCGGACGTCAGAGATCTGGCGCCCTC 186

QY 61 ArgValGlnLeuArgGluGlnHisLeuTyrTrpGlnAspGlnLeuLeuProValSerArg 80

DB 187 AGGGTGCACTCGGGAGCAGCACCTCTTACACAGGACAGCTCTGCGCGTCAAGCAGG 246

QY 81 IleLeuValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspLeuLeuGlu 100

DB 247 ATCATCGTGCACCCACAGTCTTACACCGCCAGATCGGAGCGGACATCGCCCTGCTGGAG 306

QY 101 LeuGluGluProValLysValSerHisValHisThrValLeuLeuProProAlaSer 120

DB 307 CTGAGGAGCGGTGAGGTCTCCAGCCACGTCACACGGTCAACCTGCCCCCTGCCICA 366

QY 121 GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspLeu 140

DB 367 GAGACCTTCCCCCGGGATGCGTGTGGTCACTGGTGGGGGATGTGGACATGAT 426

QY 141 GluArgLeuProProPheProLeuLysGlnValLysValProLeuMetGluAsnHis 160

DB 427 GAGCGCTCCACCGCATTTCTCTGAAGCAGGTGAAGTCCCCATATGGAACACAC 486

QY 161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArg 180

DB 487 ATTGTGAGCGAAATACACCTTGGCGCTACACGGAGACGACGTCCGCTCGCTCG 546

QY 181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200

DB 547 GACGACATCTGTGTCCCGGGAACACCCGAGGGACTCATGCGAGGCGACTCCGAGGG 606

QY 201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220

DB 607 CCCCTGGTGTCAAGGTGATGGACCTGGCTGCGAGCGGGCTGTCTAGCTGGGCGAG 666

QY 221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTrpLeuAspTrp 240

DB 667 GGCTGTGCGCAGCCCAACCGGCTGGCATCTACACCGCTGTCCACTACTACTTGGACTGG 726

QY 241 IleHisHisTyrValProLysLysPro 249

DB 727 ATCCACCACTATGTGCCCCAAAAGCCG 753

RESULT 2

AAS20783

ID AAS20783 standard; DNA; 771 BP.

XX AAS20783;

AC AC

XX 09-APR-2002 (first entry)

DT

XX DNA encoding human beta-II trypsin active site mutant H44A #3.

DE

XX Human; proteolytic trypsin; protease; recombinant beta-II trypsin;

KW enzyme; mutant; ds.

XX Homo sapiens.

OS Synthetic.

XX WO200198470-A2.

FN

XX 27-DEC-2001.

PD

XX 20-JUN-2001; 2001WO-US019681.

PF

XX 21-JUN-2000; 2000US-00598982.

PR

XX (PROM-) PROMEGA CORP.

PA

XX Maffit M, Niles AL, Haak-Frendscho M;

PI

XX WPI; 2002-114578/15.

DR P-PSDB; AAU12017.

XX

PT DNA construct for producing enzymatically-inactive proteolytic trypsin,

PT comprises DNA sequence encoding proteolytic trypsin having an active

PT site mutation.

XX Claim 7; Page 104-105; 126pp; English.

XX The present invention relates to recombinant human proteolytic trypsin, active site mutants of these trypsin and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic trypsin with an active site mutation (the construct drives expression of a mature proteolytic trypsin that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II trypsin. The active site mutants of proteolytic trypsin provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic trypsin produced are useful as an antigen to generate anti-human trypsin antibodies and in drug screening for compounds which act as trypsin inhibitors, antagonists, agonists, etc. AAS20775-AAS20790 encode for recombinant human beta-II trypsin active site mutants

XX Sequence 771 BP; 147 A; 257 C; 243 G; 124 T; 0 U; 0 Other;

Alignment Scores: 6.02e-121 Length: 771

Pred. No.:

Score: 1388.00 Matches: 248
 Percent Similarity: 99.60% Conservative: 0
 Best Local Similarity: 99.60% Mismatches: 1
 Query Match: 99.64% Indels: 0
 DB: 6 Gaps: 0

US-09-598-982-21 (1-249) x AAS20783 (1-771)

QY 1 LeuGluLysArgIleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20
 DB 7 CTCGAGAAAGATCGTGGGGTTCAGAGGCCCCAGAGCAAGTGGCCCTGGCAGGTG 66
 QY 21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuLeuHisPro 40
 DB 67 AGCCTGAGAGTCCACGGGCCATCTACTGGATGCACTTCTCGGGGGCTCCCTCATCCACCCC 126
 QY 41 GlnTrpValLeuThrAlaAlaCysValGlyProAspValLysAspLeuAlaLeu 60
 DB 127 CAGTGGGTGCTGACCGCGCGGTGCGTGGAGCCGACGTCAAGGATCTGGCCGCCCTC 186
 QY 61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80
 DB 187 AGGTGCACTGCGGAGCAGCACCTCTACTACAGACCACTCTGCGGTTCAGCAGG 246
 QY 81 IleLeuValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGlu 100
 DB 247 ATCATCGTGCACCCACAGTCTACACCGCCAGATCGGAGCGGACATCGCCCTGCTGGAG 306
 QY 101 LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer 120
 DB 307 CTGGAGGAGCGGGTGAACGTCTCCAGCCACGTCCACACGGTCAACCTGCCCTGCCCTCA 366
 QY 121 GluThrPheProProGlyMetProCysTrpValThrGlyTyrGlyAspValAspAsnAsp 140
 DB 367 GAGACCTTCCCCCGGGATGCCGTGCTGGGTCACTGGCTGGGGGATGTGGACAATGAT 426
 QY 141 GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160
 DB 427 GAGCGCTCCACCGCCATTTCTCTGAAGCAGGTGAAGTCCCATATATGMAAACAC 486
 QY 161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArg 180
 DB 487 ATTTGTGACGCAAAATACCACTTGGCCCTTACACGGGAGACGACGTCCGATCGTCCGT 546
 QY 181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200
 DB 547 GACGACATGTGTGTGCGGGAACACCGGAGGACTCATCCAGGGCGACTCCCGAGGG 606
 QY 201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220
 DB 607 CCCCTGGTGTGCAAGGTGAATGGCACTGCTGGTGGAGCGGCGGTGTCAGTGGGGCGAG 666
 QY 221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTrpLeuAspTrp 240
 DB 667 GGCTGTGCCAGCCCAACCGGCCCTGGCATCTACACCGGTGTACCTACTACTTGGACTGG 726
 QY 241 IleHisHisTyrValProLysLysPro 249
 DB 727 ATCCACCACTATGTCCTCCCAAAAGCCG 753

RESULT 3

ID AAZ40175 standard; DNA; 771 BP.

XX AC AAZ40175;

DT 18-FEB-2000 (first entry)

XX Human beta-tryptase coding sequence.

DE Beta-tryptase; human; DNA expression construct; protein production;
 XX combinatorial library screening; X ray crystallography; antigen;
 KW antibody generation; ss.

XX Homo sapiens.
 OS WO9960139-Al.
 PN 25-NOV-1999.
 PD
 PF 29-OCT-1998; 98WO-US022994.
 PR 15-MAY-1998; 98US-00079970.
 XX (PROM-) PROMEGA CORP.

PI Maffitt MA, Niles AL, Haak-Frendscho M;

XX WPI; 2000-053300/04.

DR P-PSDB; AAY55011.

PT New DNA expression construct for production of enzymatically active

PS recombinant human beta-tryptase.

XX Disclosure; Page 43-44; 50pp; English.

CC This sequence encodes the human beta-tryptase. The invention relates to a
 CC DNA expression construct comprising (5' to 3') a promoter linked to a
 CC signal sequence which is linked to a sequence encoding human beta-
 CC tryptase. The DNA construct is useful for transforming host cells to
 CC express, post translationally process and secrete enzymatically active
 CC human tryptase. The method is useful for the production of large amounts
 CC of tryptase with defined specifications. The transformant is useful for
 CC pharmacological studies, combinatorial library screens and X ray
 CC crystallographic studies. The tryptase produced allows for the
 CC development of tryptase agonists and/or antagonists, is useful as an
 CC antigen to generate antihuman tryptase antibodies in various animals, can
 CC be used in screening for compounds which act as tryptase inhibitors,
 CC antagonists, agonists etc. and to assay for the presence of tryptase in
 CC biological or other solutions. Tryptase inhibitors, antagonists, agonists
 CC etc. may be useful as therapeutics. The tryptase does not require any
 CC post-expression or post-purification modifications or manipulations to
 CC initiate tryptase activity and it has enzymatic activity which compares
 CC favourably with cadaveric tryptase. The availability of enzymatically
 CC active tryptase facilitates the large scale screening of combinatorial
 CC libraries for specific tryptase inhibitors as potential therapeutics and
 CC advances the understanding of the biological significance of tryptase in
 CC mast cell mediated diseases. The tryptase can be used to detect low
 CC levels of tryptase

SQ Sequence 771 BP; 149 A; 256 C; 242 G; 124 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 7.47e-121 Length: 771
 Score: 1387.00 Matches: 248
 Percent Similarity: 99.60% Conservative: 0
 Best Local Similarity: 99.60% Mismatches: 1
 Query Match: 99.57% Indels: 0
 DB: 3 Gaps: 0

US-09-598-982-21 (1-249) x AAZ40175 (1-771)

QY 1 LeuGluLysArgIleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20
 DB 7 CTCGAGAAAGATCGTGGGGTTCAGAGGCCCCAGAGCAAGTGGCCCTGGCAGGTG 66
 QY 21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuLeuHisPro 40
 DB 67 AGCCTGAGAGTCCACGGGCCATCTACTGGATGCACTTCTCGGGGGCTCCCTCATCCACCCC 126
 QY 41 GlnTrpValLeuThrAlaAlaCysValGlyProAspValLysAspLeuAlaLeu 60
 DB 127 CAGTGGGTGCTGACCGCGCGGTGCGTGGAGCCGACGTCAAGGATCTGGCCGCCCTC 186
 QY 61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80

QY 181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200
 DB 547 GACGACATGCTGTGCGGGAAACACCGGAGGACTCTGCGAGGGGAGCTCCGGAGGG 606
 QY 201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220
 DB 607 CCCCTGGTGTGCAAGGTGAATGGACCTGGCTGTCAGGCGGGCGTGTGAGTGGGGCGAG 666
 QY 221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrIleuAspTrp 240
 DB 667 GGCTGTGCGCCAGCCCAACCGGCGTGGCATCTACACCGGTGTCACTACTTGGACTGG 726
 QY 241 IleHisHisTyrValProLysLysPro 249
 DB 727 ATCCACCACTATGTCCTCCCAAAAGCGG 753
 RESULT 5
 AAS20778
 ID AAS20778 standard; DNA; 771 BP.
 XX AC AAS20778;
 XX DT 09-APR-2002 (first entry)
 XX DNA encoding human beta-II tryptase active site mutant S194A #2.
 XX Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
 XX enzyme; mutant; ds.
 XX KW Homo sapiens.
 XX OS Synthetic.
 XX PN WO200198470-A2.
 XX DT 27-DEC-2001.
 XX PD 20-JUN-2001; 2001WO-US019691.
 XX PF 21-JUN-2000; 2000US-00598992.
 XX PR (PROM-) PROMEGA CORP.
 XX PA Maffit M, Niles AL, Haak-Frendscho M;
 XX PI WPI; 2002-114578/15.
 XX DR P-PSDB; AAU12012.
 XX PT DNA construct for producing enzymatically-inactive proteolytic tryptase,
 XX PT comprises DNA sequence encoding proteolytic tryptase having an active
 XX PT site mutation.
 XX PS Claim 7; Page 91-92; 126pp; English.
 XX The present invention relates to recombinant human proteolytic tryptases,
 CC active site mutants of these tryptases and the methods for producing
 CC these. The method involves the production of a DNA expression construct
 CC comprising a promoter operably linked to a secretion signal sequence
 CC which is operably linked to a DNA sequence encoding a proteolytic
 CC tryptase with an active site mutation (the construct drives expression of
 CC a mature proteolytic tryptase that lacks enzymatic activity due to the
 CC active site mutation, in hosts transformed to contain the construct). The
 CC method is useful for producing enzymatically-active beta-II tryptase. The
 CC active site mutants of proteolytic tryptase provide a tool to investigate
 CC the structural and functional properties of the protease and its
 CC enzymatic activity, and for modelling studies. The enzymatically-active,
 CC recombinant proteolytic tryptase produced are useful as an antigen to
 CC generate anti-human tryptase antibodies and in drug screening for
 CC compounds which act as tryptase inhibitors, antagonists, agonists, etc.
 CC AAS20775-AAS20790 encode for recombinant human beta-II tryptase active
 XX site mutants
 XX SQ Sequence 771 BP; 152 A; 255 C; 241 G; 123 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1,43e-120 Length: 771
 Score: 1384.00 Matches: 247
 Percent Similarity: 99.60% Conservative: 1
 Best Local Similarity: 99.20% Mismatches: 1
 Query Match: 99.35% Indels: 0
 DB: 6 Gaps: 0
 US-09-598-982-21 (1-249) x AAS20778 (1-771)
 QY 1 LeuGluLysArgIleValGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20
 DB 7 CTCGAGAAAGAAATCGTCGGGGTCAGGAGGCCCCAGAGCAAGTGCCTCGGAGGTG 66
 QY 21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40
 DB 67 AGCCTGAGAGTCCACGCGCCCATACTGGATGCACATCTGCGGGGGCTCCTCATCCACCCC 126
 QY 41 GlnTrpValLeuThrAlaAlaAlaCysValGlyProAspValLysAspLeuAlaLeu 60
 DB 127 CAGTGGGTGCTGACCGGAGCGCCTGCGTGGGACCGGACGTCAAAGGATCTCGCGCCCTC 186
 QY 61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80
 DB 187 AGGTGCAACTGCGGAGCAGCACCTCTACTACAGGACAGCTGCTGCCGTGAGCAGG 246
 QY 81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuGlu 100
 DB 247 ATCATCGTGCACCCACAGTTCTACACGCGCCAGATCGGAGCGGACATCGCCCTGCTGGAG 306
 QY 101 LeuGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer 120
 DB 307 CTGAGGAGCGGTGAAGGTCTCCAGCCACGTCCACACGCTCACCGTCCCGCTGCCCTCA 366
 QY 121 GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp 140
 DB 367 GAGACCTTCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGCGGATGTGGCAATGAT 426
 QY 141 GluArgLeuProProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160
 DB 427 GAGCGCTCCCGCCCATTTCTCTGAAGCAGGTGAAGGTCCCATTAATGAAACCCAC 486
 QY 161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspValAlaIleValArg 180
 DB 487 ATTGTGACGCAAAATACCACTTTGGCGCTTACCGGAGACGACGTCCGCTCGCTCGGT 546
 QY 181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200
 DB 547 GACGACATGCTGTGCGGGAAACACCGGAGGAGCTCATGCCAAGGAGAGCGCGGCGGA 606
 QY 201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220
 DB 607 CCACTGTGTGCAAGGTGAATGGCACCTGCGTGGCGGCGGTGGTCAAGTGGGGCGAG 666
 QY 221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTrpLeuAspTrp 240
 DB 667 GGCTGTGCGCCAGCCCAACCGGCGTGGCATCTACACCGGTGTCACTACTTGGACTGG 726
 QY 241 IleHisHisTyrValProLysLysPro 249
 DB 727 ATCCACCACTATGTCCTCCCAAAAGCGG 753
 RESULT 6
 AAS20777
 ID AAS20777 standard; DNA; 771 BP.
 XX AC AAS20777;
 XX DT 09-APR-2002 (first entry)
 XX DNA encoding human beta-II tryptase active site mutant S194A #1.

KW Human; proteolytic triptase; protease; recombinant beta-II triptase;
 KW enzyme; mutant; ds.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200198470-A2.
 XX
 PD 27-DEC-2001.
 XX
 PF 20-JUN-2001; 2001WO-US019681.
 XX
 PR 21-JUN-2000; 2000US-00598982.
 XX
 PA (PROM-) PROMEGA CORP.
 XX
 PI Maffit M, Niles AL, Haak-Frendscho M;
 XX WPI; 2002-114578/15.
 DR P-PSDB; AAU12011.
 XX
 PT DNA construct for producing enzymatically-inactive proteolytic triptase,
 PT comprises DNA sequence encoding proteolytic triptase having an active
 PT site mutation.
 XX
 PS Claim 7; Page 88-90; 126pp; English.
 XX
 CC The present invention relates to recombinant human proteolytic triptases,
 CC active site mutants of these triptases and the methods for producing
 CC these. The method involves the production of a DNA expression construct
 CC comprising a promoter operably linked to a secretion signal sequence
 CC which is operably linked to a DNA sequence encoding a proteolytic
 CC triptase with an active site mutation (the construct drives expression of
 CC a mature proteolytic triptase that lacks enzymatic activity due to the
 CC active site mutation, in hosts transformed to contain the construct). The
 CC method is useful for producing enzymatically-active beta-II triptase. The
 CC active site mutants of proteolytic triptase provide a tool to investigate
 CC the structural and functional properties of the triptase and its
 CC enzymatic activity, and for modelling studies. The enzymatically-active,
 CC recombinant proteolytic triptase produced are useful as an antigen to
 CC generate anti-human triptase antibodies and in drug screening for
 CC compounds which act as triptase inhibitors, antagonists, agonists, etc.
 CC AAS20775-AAS20790 encode for recombinant human beta-II triptase active
 CC site mutants
 XX
 SQ Sequence 771 BP; 150 A; 255 C; 241 G; 125 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.43e-120 Length: 771
 Score: 1384.00 Matches: 247
 Percent Similarity: 99.60% Conservative: 1
 Best Local Similarity: 99.20% Mismatches: 1
 Query Match: 99.35% Indels: 0
 DB: 6 Gaps: 0

US-09-598-982-21 (1-249) x AAS20777 (1-771)

QY 1 LeuGluValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuGlu 20
 DB 7 CTCGAGAAAGATCTGCGGGGTCAGAGAGCCCGCCAGGACAAAGTGGCCCTGGCAGGTG 66
 QY 21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40
 DB 67 AGCTGAGATCCACGCCCATCTGGATGCATCTCTGCGGGGCTCCCTCATCCACCCC 126
 QY 41 GlnTrpValLeuThrAlaAlaCysValGlyProAspValLysAspLeuAlaLeu 60
 DB 127 CAGTGGGTGTGACCGCAGCGCACTGGGTGGGACCGGACGTCACAGGATCTGGCGCCCTC 186
 QY 61 ArgValGlnLeuArgGluGlnHisLeuTyrTrpGlnAspGlnLeuProValSerArg 80
 DB 187 AGGTGCACTGGCGGGAGCAGCACCTCTACTACAGGACCAAGCTGCTGCCGTGAGCAGG 245

QY 81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuGlu 100
 DB 247 ATCATGTCACCCACAGTTCACACGCCACAGATCGGAGCGACATCGCCCTGCTGGAG 306
 QY 101 LeuGluGluProValLysValSerHisValHisThrValThrLeuProProAlaSer 120
 DB 307 CTGGAGGAGCGGTGAAGGTCTCCAGCCAGTCCACCGGTACCCCTGCCCTGCTCA 366
 QY 121 GluThrPheProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp 140
 DB 367 GAGACCTTCCCCCGGGGATGCCGTGCTGGTCACTGGCTGGGCGCATGTGGCAATGAT 426
 QY 141 GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160
 DB 427 GAGCGCTCCCCACCGCCATTTCTCTGAAGCAGGTGAAGGTCCCATATATGGAACAC 486
 QY 161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspValAlaGlnIleValArg 180
 DB 487 ATTTGTGACGCAAAATACCACTTGGCGCTACACGGGACACCGTCCCATCTGCTCGT 546
 QY 181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200
 DB 547 GACGACATGCTGTGTGCGGGAACACCCGGAGGACTCATGTCAAGCGGACGCCGCGGA 606
 QY 201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220
 DB 607 CCTCTGTGTGCAAGGTGAATGGACCTGTGCTGAGGGCGGCGTGTGTGCTGCTGCTG 666
 QY 221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240
 DB 667 GGTGTGCGGAGCCCAACCGCGCTGGCATCTACACCGGTGTACACCGGTGTACCTACTTGGACTGG 726
 QY 241 IleHisHisTyrValProLysLysPro 249
 DB 727 ATCCACCACTATGTCCCAAAAGCCG 753

RESULT 7
 AAS20763
 ID AAS20763 standard; DNA; 771 BP.
 XX
 AC AAS20763;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE DNA encoding human beta-I triptase.
 XX
 KW Human; proteolytic triptase; protease; beta-I triptase; enzyme; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 CDS 7..756
 FT /*tag= a
 FT /partial
 FT /product= "Beta-I triptase"
 FT /note= "This sequence lacks a start codon"
 XX
 PN WO200198470-A2.
 XX
 PD 27-DEC-2001.
 XX
 PF 20-JUN-2001; 2001WO-US019681.
 XX
 PR 21-JUN-2000; 2000US-00598982.
 XX
 PA (PROM-) PROMEGA CORP.
 XX
 PI Maffit M, Niles AL, Haak-Frendscho M;
 XX WPI; 2002-114578/15.
 DR P-PSDB; AAU12006.
 XX
 PT DNA construct for producing enzymatically-inactive proteolytic triptase,

PT comprises DNA sequence encoding proteolytic tryptase having an active
 PT site mutation.

PS Disclosure; Page 72-74; 126pp; English.

XX The present invention relates to recombinant human proteolytic tryptases,
 CC active site mutants of these tryptases and the methods for producing
 CC these. The method involves the production of a DNA expression construct
 CC comprising a promoter operably linked to a secretion signal sequence
 CC which is operably linked to a DNA sequence encoding a proteolytic
 CC tryptase with an active site mutation (the construct drives expression of
 CC a mature proteolytic tryptase that lacks enzymatic activity due to the
 CC active site mutation, in hosts transformed to contain the construct). The
 CC method is useful for producing enzymatically-active beta-II tryptase. The
 CC active site mutants of proteolytic tryptase provide a tool to investigate
 CC the structural and functional properties of the protease and its
 CC enzymatic activity, and for modelling studies. The enzymatically-active,
 CC recombinant proteolytic tryptase produced are useful as an antigen to
 CC generate anti-human tryptase antibodies and in drug screening for
 CC compounds which act as tryptase inhibitors, antagonists, agonists, etc.
 CC The present sequence encodes for human beta-I tryptase

SQ Sequence 771 BP; 149 A; 257 C; 241 G; 124 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.2e-120 Length: 771
 Score: 1382.00 Matches: 247
 Percent Similarity: 99.20% Conservative: 0
 Best Local Similarity: 99.20% Mismatches: 2
 Query Match: 99.21% Indels: 0
 DB: 6 Gaps: 0

US-09-598-982-21 (1-249) x AAS20763 (1-771)

QY 1 LeuGluTyrArgIleValGlyGlyClnGlnAlaProArgSerLysTyrProTyrGlnVal 20
 DB 7 CTCGAGAAAGAAATCGTGGGGGTCAGAGAGCCCGCCAGGAGCAAGTGGCCCTGGCAGGTG 66
 QY 21 SerLeuArgValHisGlyProTyrTyrMetHisPheCysGlyGlySerLeuIleHisPro 40
 DB 67 AGCCTGAGAGTCCAGGGCCCATCTGGATGACATCTCTCGGGGGCTCCCTCATCCACCCC 126
 QY 41 GlnTyrValLeuThrAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeu 60
 DB 127 CAGTGGGTGCTGACCGCAGCAGTCTGCTGGGACCGGACGTCAGGATCTGGCGCCCTC 186
 QY 61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArg 80
 DB 187 AGGTGGCACTGCGGGAGCAGCACCCTCTACTACCAGGACCCAGCTGCTCGCGGTCCAGCAGG 246
 QY 81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuGlu 100
 DB 247 ATCATGTGTCACCCACAGTCTTACACGCCCAGATCGAGGGGACATCGCCCTGCTGGAG 306
 QY 101 LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProProAlaSer 120
 DB 307 CTGAGGAGCGGTGAAGCTCTCCAGCCAGCTCCACACGGTCACCTGCGCCCTGCCCTCA 366
 QY 121 GluThrPheProProGlyMetProCysTyrValThrGlyTyrGlyAspValAspAsnAsp 140
 DB 367 GAGACCTTCCCGGGGATCCGCTGCTGGGTCTACTGCTGGGCGATGTGGACAATGAT 426
 QY 141 GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160
 DB 427 GAGCGCTCCACCGCCATTTCTCTGAGCAGGTGAGGTCCTCCCATATGGAACACAC 486
 QY 161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArg 180
 DB 487 ATTTGTACGCAAAATACCACTTGGCGCTTACACGGGAGACGACGTCGATCGTCGT 546
 QY 181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200
 DB 547 GACGACATGCTGTGCGGGGAACACCGGAGGAGACTCATGCCAGGGCGACTCCGGAGGG 606

QY 201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220
 DB 607 CCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCAGGGGGGCTGTGCTCAGCTGGGGCGAG 666
 QY 221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTyr 240
 DB 667 GGCTGTGCCAGCCCAACCGGCTGGCATCTACACCCGCTGTCACCTACTTGGACTGG 726
 QY 241 IleHisHisTyrValProLysLysPro 249
 DB 727 ATCCACCATATGTCCCCAAAAGCG 753

RESULT 8

AAS20786

ID AAS20786 standard; DNA; 771 BP.

XX AAS20786;

AC AAS20786;

XX 09-APR-2002 (first entry)

XX

DE DNA encoding human beta-II tryptase active site mutant SI94A #6.

XX Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
 KW enzyme; mutant; ds.

XX Homo sapiens.

OS Synthetic.

XX WO200198470-A2.

XX 27-DEC-2001.

XX

XX 20-JUN-2001; 2001WO-US019681.

XX 21-JUN-2000; 2000US-00598982.

XX (PROM-) PROMEGA CORP.

XX Maffit M, Niles AL, Haak-Frendscho M;

XX WPI; 2002-114578/15.

XX P-PSDB; AAU12020.

PT DNA construct for producing enzymatically-inactive proteolytic tryptase,
 PT comprises DNA sequence encoding proteolytic tryptase having an active
 PT site mutation.

PS Claim 7; Page 113-114; 126pp; English.

XX The present invention relates to recombinant human proteolytic tryptases,
 CC active site mutants of these tryptases and the methods for producing
 CC these. The method involves the production of a DNA expression construct
 CC comprising a promoter operably linked to a secretion signal sequence
 CC which is operably linked to a DNA sequence encoding a proteolytic
 CC tryptase with an active site mutation (the construct drives expression of
 CC a mature proteolytic tryptase that lacks enzymatic activity due to the
 CC active site mutation, in hosts transformed to contain the construct). The
 CC method is useful for producing enzymatically-active beta-II tryptase. The
 CC active site mutants of proteolytic tryptase provide a tool to investigate
 CC the structural and functional properties of the protease and its
 CC enzymatic activity, and for modelling studies. The enzymatically-active,
 CC recombinant proteolytic tryptase produced are useful as an antigen to
 CC generate anti-human tryptase antibodies and in drug screening for
 CC compounds which act as tryptase inhibitors, antagonists, agonists, etc.
 CC AAS20775-AAS20790 encode for recombinant human beta-II tryptase active
 CC site mutants

SQ Sequence 771 BP; 152 A; 256 C; 240 G; 123 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.21e-120 Length: 771
 Score: 1379.00 Matches: 246

101 LeuGluGluProValLysValSerSerHisValHisThrValThrLeuProAlaSer 120
 307 CTGGAGAGCGGTGAACGTCTCCAGCAGCTCCACACGGTCAACCTGCCCTGCCTCA 366
 121 GluThrPheProProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsp 140
 367 GAGACCTTCCCGCGGGATGCCGTGCTGGGTCACTGGCTGGGCGATGTGGCAATGAT 426
 141 GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160
 427 GAGCGCTCCACCGCCCATTTCTCTGAAGCAGGTGAAGGTCCCAATATGGAAACAC 486
 161 IleCysAspAlaLysTyrHisLeuGlyValatyrThrGlyAspValArgIleValArg 180
 487 ATTTGTGACGCAAAATACCACTTGGCGCTTACACGGGAGACGCTCCGATGCTCGT 546
 181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200
 547 GAGCAGATGCTGTGTGCCGGGAACACCGGAGGACTCATGTCAAGGCGAGCGCGCGGA 606
 201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220
 607 CCTGTGTGTGCAAGGTGAATGGCACTGGCTGCAGCGGGCGTGGTCAAGTGGGGGAG 666
 221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240
 667 GGCTGTGCCAGCCACCGCGCTGGCATCTACACCGGTGTCACTACTTGGACTGG 726
 241 IleHisHisTyrValProLysLysPro 249
 727 ATCCACCACTATGTCCCAAAAGCCG 753

RESULT 10

AAS20776
 ID AAS20776 standard; DNA; 771 BP.

XX AC AAS20776;

XX DT 09-APR-2002 (first entry)

XX DE DNA encoding human beta-II tryptase active site mutant D91A #1.

XX KW Human; proteolytic tryptase; protease; recombinant beta-II tryptase;

XX KM enzyme; mutant; ds.

XX XX Homo sapiens.

OS Synthetic.

XX XX WO200198470-A2.

XX PD 27-DEC-2001.

XX PF 20-JUN-2001; 2001WO-US019681.

XX PR 21-JUN-2000; 2000US-00598982.

XX PA (PROM-) PROMEGA CORP.

XX PI Maffit M, Niles AL, Haak-Frendscho M;

XX DR WPI; 2002-114578/15.

XX DR P-PSDB; AAU12010.

XX PT DNA construct for producing enzymatically-inactive proteolytic tryptase,

PT comprises DNA sequence encoding proteolytic tryptase having an active

PT site mutation.

XX PS Claim 7; Page 86-87; 126pp; English.

XX CC The present invention relates to recombinant human proteolytic tryptases,

CC active site mutants of these tryptases and the methods for producing

CC these. The method involves the production of a DNA expression construct

CC comprising a promoter operably linked to a secretion signal sequence

CC which is operably linked to a DNA sequence encoding a proteolytic

CC tryptase with an active site mutation (the construct drives expression of

CC a mature proteolytic tryptase that lacks enzymatic activity due to the

CC active site mutation, in hosts transformed to contain the construct). The

CC method is useful for producing enzymatically-active beta-II tryptase. The

CC active site mutants of proteolytic tryptase provide a tool to investigate

CC the structural and functional properties of the protease and its

CC enzymatic activity, and for modelling studies. The enzymatically-active,

CC recombinant proteolytic tryptase produced are useful as an antigen to

CC generate anti-human tryptase antibodies and in drug screening for

CC compounds which act as tryptase inhibitors, antagonists, agonists, etc.

CC AAS20775-AAS20790 encode for recombinant human beta-II tryptase active

CC site mutants

XX SQ Sequence 771 BP; 149 A; 256 C; 242 G; 124 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4,21e-120 Length: 771

Score: 1379.00 Matches: 247

Percent Similarity: 99.20% Conservative: 0

Best Local Similarity: 99.20% Mismatches: 2

Query Match: 98.99% Indels: 0

DB: 6 Gaps: 0

US-09-598-982-21 (1-249) x AAS20776 (1-771)

Qy 1 LeuLulysArgIleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnVal 20

Db 7 CTCGAGAAAGAAATCGTCGGGGGTGAGAGGCCCGCCAGGAGCAAGTGGCCCTGGCAGGTG 66

Qy 21 SerLeuArgValHisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisPro 40

Db 67 AGCTGAGAGTCCACGCCCCATCTGGATGCACCTCTCGGGGGCTCCCTCATCCACCC 126

Qy 41 GlnTrpValLeuThrAlaAlaCysValGlyProAspValLysAspLeuAlaLeu 60

Db 127 CAGTGGTGTGACCGCAGCGCACTGGGTGGAGCCGACGCTCAAGGATCTGGCGCCCTC 186

Qy 61 ArgValGlnLeuArgGluGlnHisLeuTyrTyrGlnAspGlnLeuProValSerArg 80

Db 187 AGGTGTCACTGGCGGAGCAGCACCTCTACTACAGGACGAGCTGCTGCCGTGAGCAGG 246

Qy 81 IleIleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuGlu 100

Db 247 ATCATCTGTGACCCACAGTTCACACGCCCAGATCGAGCGGCAATCGCCCTGCTGGAG 306

Qy 101 LeuGluProValLysValSerSerHisValHisThrValThrLeuProAlaSer 120

Db 307 CTGGAGGAGCGGTGAAGGTCTCCAGCCACGTCACACGGGTCAACCTGCCCTGCCCTCA 366

Qy 121 GluThrPheProGlyMetProCysTrpValThrGlyTyrGlyAspValAspAsp 140

Db 367 GAGACCTTCCCGCGGGATGCCGTGCTGGGTCACTGGCTGGGGCGAGTGGCAATGAT 426

Qy 141 GluArgLeuProProPheProLeuLysGlnValLysValProIleMetGluAsnHis 160

Db 427 GAGCGCTCCACCGCCATTTCTCTGAAGCAGGTGAAGGTCCCAATATGGAAACAC 486

Qy 161 IleCysAspAlaLysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArg 180

Db 487 ATTTGTGACGCAAAATACCACTTGGCGCTTACACGGGAGACGCTCCGATGCTCCGT 546

Qy 181 AspAspMetLeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGly 200

Db 547 GACACATGCTGTGTGCCGGGAACACCGGAGGACTCATGCCAGGGCGATCTCGGAGGG 606

Qy 201 ProLeuValCysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlu 220

Db 607 CCTGTGTGTGCAAGGTGAATGGCACCTGGCTGAGGGGGCGTGGTCAGTGGGGCGAG 666

Qy 221 GlyCysAlaGlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrp 240

Db 667 GGCTGTGCCAGCCCAACCGGCTGGCATCTACACCGGTGTCACTACTACTGACTGG 726

QY 241 IleHisHisTyrValProLysLysPro 249
 Db 727 ATCCACCACTATGTCCCAAAAGCCG 753

RESULT 11
 AAS20779
 ID AAS20779 standard; DNA; 735 BP.
 XX
 AC AAS20779;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE DNA encoding human beta-II tryptase active site mutant H44A #2.
 XX
 KW Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
 KW enzyme; mutant; ds.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200198470-A2.
 XX
 XX 27-DEC-2001.
 XX
 XX 20-JUN-2001; 2001WO-US019681.
 PF
 XX 21-JUN-2000; 2000US-00598982.
 PR
 XX (PROM-) PROMEGA CORP.
 PA
 XX Maffit M, Niles AL, Haak-Frendscho M;
 PI WPI; 2002-114578/15.
 DR
 DR P-PSDB; AAU12013.
 XX
 PT DNA construct for producing enzymatically-inactive proteolytic tryptase,
 PT comprises DNA sequence encoding proteolytic tryptase having an active
 PT site mutation.
 XX
 PS Example 1c; Page 94-95; 126pp; English.
 XX
 CC The present invention relates to recombinant human proteolytic tryptases,
 CC active site mutants of these tryptases and the methods for producing
 CC these. The method involves the production of a DNA expression construct
 CC comprising a promoter operably linked to a secretion signal sequence
 CC which is operably linked to a DNA sequence encoding a proteolytic
 CC tryptase with an active site mutation (the construct drives expression of
 CC a mature proteolytic tryptase that lacks enzymatic activity due to the
 CC active site mutation, in hosts transformed to contain the construct). The
 CC method is useful for producing enzymatically-active beta-II tryptase. The
 CC active site mutants of proteolytic tryptase provide a tool to investigate
 CC the structural and functional properties of the protease and its
 CC enzymatic activity, and for modelling studies. The enzymatically-active,
 CC recombinant proteolytic tryptase produced are useful as an antigen to
 CC generate anti-human tryptase antibodies and in drug screening for
 CC compounds which act as tryptase inhibitors, antagonists, agonists, etc.
 CC AAS20775-AAS20790 encode for recombinant human beta-II tryptase active
 CC site mutants
 XX
 SQ Sequence 735 BP; 139 A; 245 C; 231 G; 120 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.17e-119 Length: 735
 Score: 1374.00 Matches: 245
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.64% Indels: 0
 DB: 6 Gaps: 0

US-09-598-982-21 (1-249) x AAS20779 (1-735)

QY 5 IleValGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24

Db 1 ATCGTCGGGGTCCAGGAGGCCCCAGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 60
 QY 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
 Db 61 CACGGCCCATACTGGATGCACTTCTCGGGGGTCCCTCATCCACCCCAAGTGGGTGCTG 120
 QY 45 ThrAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 64
 Db 121 ACCGCGCGGGTGGCGTGGACCGGACGTCAGGATCTGGCCGCCCTCAGGGTGCAACTG 180
 QY 65 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuProValSerArgIleIleValHis 84
 Db 181 CGGAGCAGCAGCCTCTACTACGAGGACCACTGCTGCGGTGACGAGGATCATCTGTCAC 240
 QY 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluGluPro 104
 Db 241 CCACAGTTCTACACCGCCCGGATCGGAGCGGACATCGCCCTGCTGAGCTGGAGGAGCCG 300
 QY 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
 Db 301 GTGAAGGTCTCCAGCCACGTCACACGCTACCCCTGCCCTCAGAGACCTTCCCC 360
 QY 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
 Db 361 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGCACATATGATGAGCGCCTCCCA 420
 QY 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
 Db 421 CGGCCATTTCTCTGAAGCAGGTGAAGTCCCCATATGAAACACCATTTGTGACGCA 480
 QY 165 LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspAspMetLeu 184
 Db 481 AAATACCACTTGGCGCTACACGGGAGACGATCGCATCGCTCGGTGACGACATGCTG 540
 QY 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
 Db 541 TGTGTCGGGAAACACCGCGAGGACTCATGCCAGGGGACTCCCGAGGGGCCCTGCTGTGC 600
 QY 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224
 Db 601 AAGTGAATGGCAACCTGGCTGCGAGCGGGCGTGTGAGCTGGGGCGAGGGCTGTGCCAG 660
 QY 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTrpLeuAspTrpIleHisHisTyr 244
 Db 661 CCCAACCGGCTGGCATCTACACCCCGTGTACCTACTACTTGGACTGGATCCACCACTAT 720
 QY 245 ValProLysLysPro 249
 Db 721 GTCCCAAAAAGCCG 735

RESULT 12
 AAS20784
 ID AAS20784 standard; DNA; 771 BP.
 XX
 AC AAS20784;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE DNA encoding human beta-II tryptase active site mutant D91A #3.
 XX
 KW Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
 KW enzyme; mutant; ds.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200198470-A2.
 XX
 XX 27-DEC-2001.
 XX
 XX 20-JUN-2001; 2001WO-US019681.
 PF
 XX


```
QY 25 HisGlyProTyrTrpMetHisPheCysGlySerLeuIleHisProGlnTrpValLeu 44
Db 61 CACGCCCATCTGATGACCTTCTGGGGGGCTCCCTCATCCACCCCGAGTGGTGTCTG 120
QY 45 ThrAlaAlaAlaCysValGlyProAspValHisAspLeuAlaAlaLeuArgValGlnLeu 64
Db 121 ACCGACGCGACTCGGTGGGACCGGACGCTCAAGGATCTGGCGGCTCAGGGTGCAACTG 180
QY 65 ArgGluGlnHisLeuTyrTrpGlnAspGlnLeuProValSerArgIleValHis 84
Db 181 CGGAGACGACCTCTACTACGAGACGAGCTGCGGGTCTGAGGATCATCGTGAC 240
QY 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluGluPro 104
Db 241 CCACAGTCTACACCGCCCATCGGAGCGACATCGCCCTGCTGGAGCTGGAGAGCCG 300
QY 105 ValHisValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
Db 301 GTGAAGGTCTCCAGCCAGCTCCACACGGTCACTCCCTGCGCTCAGAGACCTTCCCC 360
QY 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
Db 361 CCGGGATGCGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 145 ProProPheProLeuLysGlnValHisValProIleMetGluAsnHisIleCysAspAla 164
Db 421 CCGCCATTCTCTGAAGCAGCTGAGGTCCCTCCCATATGGAACCATTTGTGACGCA 480
QY 165 LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspMetLeu 184
Db 481 AATATACCACTTGGCGCTACACGGAGACGACGTCGCTCGGTGAGGACATGCTG 540
QY 185 CysAlaGlyAsnThrArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
Db 541 TGTGCGGGAAACCCCGAGGAGCTCATGCGAGGGCGACTCCGAGGGCCCTCGTGTGC 600
QY 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224
Db 601 AAGGTGATGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTrpLeuAspTrpIleHisTyr 244
Db 661 CCCAACCGCGCTGCGATCATACCGCGTGTACCTACTACTGCTGCTGCTGCTGCTGCTGCT 720
QY 245 ValProLysLysPro 249
Db 721 GTCCCCAAAAGCCG 735
```

RESULT 15

AAS20766

ID AAS20766 standard; DNA; 735 BP.

XX AC AAS20766;

XX DT 09-APR-2002 (first entry)

XX DE DNA encoding recombinant human mature beta-II tryptase.

XX KW Human; proteolytic tryptase; protease; recombinant beta-II tryptase;

XX KW enzyme; gene; mutant; ds.

XX OS Homo sapiens.

XX OS Synthetic.

XX Key Location/Qualifiers

FH CDS 1..735

FT /tag= a

FT /partial

FT /product= "Recombinant mature beta-II tryptase"

FT /note= "This sequence lacks both start and stop codons"

XX PN

XX WO200198470-A2.

```
PD 27-DEC-2001.
XX 20-JUN-2001; 2001WO-US019681.
XX 21-JUN-2000; 2000US-00598982.
XX (PROM-) PROMEGA CORP.
XX Maffit M, Niles AL, Haak-Frendscho M;
XX WPI; 2002-114578/15.
DR P-ESDB; RAU12008.
XX DNA construct for producing enzymatically-inactive proteolytic tryptase,
XX comprises DNA sequence encoding proteolytic tryptase having an active
XX site mutation.
XX Disclosure; Page 78-79; 126pp; English.
XX The present invention relates to recombinant human proteolytic tryptases,
XX active site mutants of these tryptases and the methods for producing
XX these. The method involves the production of a DNA expression construct
XX comprising a promoter operably linked to a secretion signal sequence
XX which is operably linked to a DNA sequence encoding a proteolytic
XX tryptase with an active site mutation (the construct drives expression of
XX a mature proteolytic tryptase that lacks enzymatic activity due to the
XX active site mutation, in hosts transformed to contain the construct). The
XX method is useful for producing enzymatically-active beta-II tryptase. The
XX active site mutants of proteolytic tryptase provide a tool to investigate
XX the structural and functional properties of the protease and its
XX enzymatic activity, and for modelling studies. The enzymatically-active,
XX recombinant proteolytic tryptase produced are useful as an antigen to
XX generate anti-human tryptase antibodies and in drug screening for
XX compounds which act as tryptase inhibitors, antagonists, agonists, etc.
XX The present sequence encodes for recombinant human mature beta-II
XX tryptase
```

SQ Sequence 735 BP; 141 A; 245 C; 229 G; 120 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.27e-119 Length: 735

Score: 1368.00 Matches: 244

Percent Similarity: 99.59% Conservative: 0

Best Local Similarity: 99.59% Mismatches: 1

Query Match: 98.21% Indels: 0

DB: 6 Gaps: 0

US-09-598-982-21 (1-249) x AAS20766 (1-735)

QY 5 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24

Db 1 ATCTGGGGGTTCAGGAGGCCCCCAGAGAGAGTGGCCCTGGCAGGTGAGCTGAGAGTC 60

QY 25 HisGlyProTyrTrpMetHisPheCysGlySerLeuIleHisProGlnTrpValLeu 44

Db 61 CACGCCCATCTGATGACCTTCTGGGGGGTCTCCCTCATCCACCCCGAGTGGTGTG 120

QY 45 ThrAlaAlaAlaCysValGlyProAspValHisAspLeuAlaAlaLeuArgValGlnLeu 64

Db 121 ACCGACGCGACTCGGTGGGACCGGACGCTCAAGGATCTGGCGGCTCAGGGTGCAACTG 180

QY 65 ArgGluGlnHisLeuTyrTrpGlnAspGlnLeuProValSerArgIleValHis 84

Db 181 CGGAGACGACCTCTACTACGAGCCAGCTGCTGCGGTCAGCAGATCATCGTGAC 240

QY 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluPro 104

Db 241 CCACAGTCTACACCGCCCATCGGAGCGACATCGCCCTGCTGGAGCTGGAGAGCG 300

QY 105 ValHisValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124

Db 301 GTGAAGGTCTCCAGCCAGCTCCACACGGTCACTCCCTGCGCCCTCAGAGACCTTCCCC 360

```
QY 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
Db |||||
361 CCGGGATGCCGTCTGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCTCCCA 420
QY 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
Db |||||
421 CCGCCATTCTCTGAAGCAGGTGAAGTCCCCATAATGAAAAACCAATTTGTGACGCA 480
QY 165 LysTyrHisLeuGlyAlaTyrThrGlyAspValArgTleValArgAspAspMetLeu 184
Db |||||
481 AATACCACTTGGCGCTACACGGGAGACGCTCCGCATCGTCCGTGACGACATGCTG 540
QY 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
Db |||||
541 TGTGCCGGGAACACCCGGAGGACTCATGCCAGGGGACTCCGGAGGGCCCTGGTGTGC 600
QY 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224
Db |||||
601 AAGTGAATGGACCTGGCTGCAGCGGGGGTGGTCACTGGGGCGAGGGCTGTGCCAG 660
QY 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 244
Db |||||
661 CCCAACCGCGCTGGCACTACACCGGTGTCACTTGGACTGGATCCACCACTAT 720
QY 245 ValProLysLysPro 249
Db |||||
721 GTCCCCAAAAAGCG 735
```

Search completed: July 22, 2004, 16:02:43
Job time : 479 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 22, 2004, 17:23:03 ; Search time 520 Seconds
(without alignments)
2340.743 Million cell updates/sec

Title: US-09-598-982-21

Perfect score: 1393

Sequence: 1 LEKRIVGQAPRSKWPQV.....IYTRVYLLDTHHYVVKPK 249

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3216467 seqs, 2444149694 residues

Total number of hits satisfying chosen parameters: 6432934

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xip
-Q=/cgn2_1/USPTO.spool.p/US09598982/runat_20072004_064412_6622/app_query.fasta_1.391
-DB=Published Applications NA -QPM=fastacp -SUFFIX=rnpb -MINMATCH=0.1
-LOOCL=0 -LCOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Blosum62
-TRANS=human40.cdi -LIST=45 -DOCLAL=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09598982 @CNC 1.1 912 @runat_20072004_064412_6622
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -USPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-XGAPOP=6 -XGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
------------	-------	-------------	--------	----	-------------

RESULT 1
US-10-352-684A-47
; Sequence 47, Application US/10352684A
; Publication No. US20030215452A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; APPLICANT: Welch, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
; FILE REFERENCE: MPI02-019P1RNMNM
; CURRENT APPLICATION NUMBER: US/10/352,684A
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/364,476

1	1368	98.2	1143	16	US-10-352-684A-47	Sequence 47, Appl
2	1368	98.2	1143	17	US-10-287-226-93	Sequence 93, Appl
3	1363	97.8	828	17	US-10-287-226-91	Sequence 91, Appl
4	1344	96.5	1081	9	US-09-954-456-2126	Sequence 2126, Ap
5	1344	96.5	1081	10	US-09-960-706-680	Sequence 680, App
6	1344	96.5	1081	10	US-09-873-319-427	Sequence 427, App
7	1344	96.5	1081	10	US-09-873-367C-155	Sequence 155, App
8	1344	96.5	1081	10	US-09-873-367C-714	Sequence 714, Appl
9	1329	95.4	2662	17	US-10-275-505-27	Sequence 27, Appl
10	1323	95.0	828	17	US-10-287-226-89	Sequence 89, Appl
11	1312	94.2	858	17	US-10-287-226-87	Sequence 87, Appl
12	1274	91.5	1154	16	US-10-352-684A-45	Sequence 45, Appl
13	1274	91.5	1158	13	US-10-116-802-240	Sequence 240, App
14	1054	75.7	1187	17	US-10-275-505-22	Sequence 22, Appl
15	664.5	47.7	846	10	US-09-813-432-11	Sequence 11, Appl
16	664.5	47.7	846	13	US-10-246-583-11	Sequence 11, Appl
17	664.5	47.7	846	16	US-10-174-364-11	Sequence 11, Appl
18	664.5	47.7	846	17	US-10-689-832-11	Sequence 11, Appl
19	634	45.5	873	15	US-10-117-323-2	Sequence 2, Appl
20	605.5	43.5	1122	9	US-09-900-754-1	Sequence 1, Appl
21	599.5	43.0	948	13	US-10-150-813-15	Sequence 15, Appl
22	599.5	43.0	948	13	US-10-139-854-15	Sequence 15, Appl
23	599.5	43.0	948	15	US-10-131-409-15	Sequence 15, Appl
24	599.5	43.0	948	16	US-10-150-811-15	Sequence 15, Appl
25	584	41.9	978	15	US-10-311-955-1	Sequence 1, Appl
26	583.5	41.9	958	17	US-10-311-035-29	Sequence 29, Appl
27	569.5	40.9	867	9	US-09-888-615-56	Sequence 56, Appl
28	569.5	40.9	895	15	US-10-117-323-34	Sequence 34, Appl
29	569.5	40.9	1218	16	US-10-274-639-36	Sequence 36, Appl
30	569.5	40.9	1218	17	US-10-333-574-36	Sequence 36, Appl
31	568	40.8	858	13	US-10-150-813-21	Sequence 21, Appl
32	568	40.8	858	13	US-10-139-854-21	Sequence 21, Appl
33	568	40.8	858	15	US-10-131-409-21	Sequence 21, Appl
34	568	40.8	858	16	US-10-150-811-21	Sequence 21, Appl
35	563.5	40.5	780	15	US-10-266-035-3	Sequence 3, Appl
36	563.5	40.5	783	17	US-10-391-364-22	Sequence 22, Appl
37	563.5	40.5	980	15	US-10-266-035-1	Sequence 1, Appl
38	563.5	40.5	980	15	US-10-040-367-30	Sequence 30, Appl
39	563.5	40.5	980	17	US-10-391-364-20	Sequence 20, Appl
40	563.5	40.5	1110	14	US-10-040-655-1	Sequence 1, Appl
41	563.5	40.5	1110	14	US-10-041-006A-1	Sequence 1, Appl
42	563.5	40.5	1129	13	US-10-147-493-221	Sequence 221, App
43	563.5	40.5	1129	13	US-10-145-127-221	Sequence 221, App
44	563.5	40.5	1129	13	US-10-160-503-221	Sequence 221, App
45	563.5	40.5	1129	13	US-10-143-118-221	Sequence 221, App

```

; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 60/403,221
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(833)
US-10-352-684A-47

Alignment Scores:
Pred. No.: 2,3e-158 Length: 1143
Score: 1368.00 Matches: 244
Percent Similarity: 99.59% Conservative: 0
Best Local Similarity: 99.59% Mismatches: 1
Query Match: 98.21% Indels: 0
DB: 16 Gaps: 0

US-09-598-982-21 (1-249) x US-10-352-684A-47 (1-1143)

QY 5 IleValGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24
DB 96 ATCGTGGGGTTCAGAGGCCCCCAGAGCAAGTGGCCCTGGCAGGTGAGCTGAGAGTC 155
QY 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
DB 156 CACGCCCATCTAGTGTCACTTCTGCGGGGGCTCCCTCATCCACCCCGAGTGGGTGCTG 215
QY 45 ThrAlaAlaCysValGlyProAspValLysAspLeuAlaLeuArgValGlnLeu 64
DB 216 ACCGAGCGCACTGCTGGGACCGGACGTCAGGATCTGGCCGCTCAGGTGCACTG 275
QY 65 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 84
DB 276 CGGGAGCAGCACTTACTACAGGACCACTGCTGCTGGCCGCTCAGGATCATCTGTCAC 335
QY 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuLeuGluLeuPro 104
DB 336 CCACAGTTCTACACGCCCGCAGATCGAGCGACATCGCCCTGCTGGAGCTGAGAGCGG 395
QY 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
DB 396 GTGAAGGTCCTCAGCCGCTCACAGGTCACCTGCTGGCCGCTGCTGAGACCTTCCCTCC 455
QY 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
DB 456 CGGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 515
QY 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
DB 516 CGCCATTTCTCTCAAGCAGGTGAAGTCCCATTAATGGAACCAACATTTGTGACGCA 575
QY 165 LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspAspMetLeu 184
DB 576 AATATCCACCTTGGCGCTTACACGGGAGACGACGTCCTGCTGCTGCTGCTGCTGCTGCTG 635

```

185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
636 TGTGCGGGGAACACCCGAGGAGGACTCATGCGAGGGGCTCCGAGGGGCTGGTGTGC 695

205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224
696 AAGGTGAATGGCCTGGCTGCAGGGGGCGGTGTGCTAGCTGGGCGAGGGCTGTGCCAG 755

225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisTyr 244
756 CCNACCGGCTGGCATCATACCCGTTGCTACCTACTTGGACTGGATCCACCATAT 815

245 ValProLysLysPro 249
816 GTCCCAAAAAGCG 830

RESULT 2
US-10-287-226-93
; Sequence 93, Application US/10287226
; Publication No. US2004008675A1
; GENERAL INFORMATION:
; APPLICANT: Agee, Michele L.,
; APPLICANT: Alsbrook, John P.,
; APPLICANT: Berghs, Constance,
; APPLICANT: Boldog, Ference,
; APPLICANT: Burgess, Catherine E.,
; APPLICANT: Chant, John S.,
; APPLICANT: Chaudhuri, Amitabha,
; APPLICANT: DiPippo, Vincent A.,
; APPLICANT: Edinger, Shlomit R.,
; APPLICANT: Eisen, Andrew,
; APPLICANT: Ellerman, Karen,
; APPLICANT: Gangolli, Esha A.,
; APPLICANT: Gorman, Linda,
; APPLICANT: Gerlach, Valerie,
; APPLICANT: Ji, Weizhen,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Khramtsov, Nikolai,
; APPLICANT: Li, Li,
; APPLICANT: MacDougall, John R.,
; APPLICANT: Malvankar, Uriel M.,
; APPLICANT: Mezes, Peter S. E.,
; APPLICANT: Millet, Charles E.,
; APPLICANT: Millet, Isabelle,
; APPLICANT: Ooi, Chean Eng,
; APPLICANT: Ort, Tatiana,
; APPLICANT: Padigaru, Muralidhara,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rastelli, Luca,
; APPLICANT: Rieger, Daniel K.,
; APPLICANT: Rothenberg, Mark E.,
; APPLICANT: Shenoy, Suresh G.,
; APPLICANT: Spaderna, Steven K.,
; APPLICANT: Spytek, Kimberley A.,
; APPLICANT: Taupier, Jr., Raymond J.,
; APPLICANT: Vernet, Corine A.M.,
; APPLICANT: Zerhusen, Bryan D.,
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-480C
; CURRENT APPLICATION NUMBER: US/10/287,226
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: 60/334,421
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,392
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/360,148
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/364,000
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/404,821
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/334,526

;; PRIOR FILING DATE: 2001-11-30
;; PRIOR APPLICATION NUMBER: 60/354,409
;; PRIOR FILING DATE: 2002-02-04
;; PRIOR APPLICATION NUMBER: 60/364,227
;; PRIOR FILING DATE: 2002-03-13
;; PRIOR APPLICATION NUMBER: 60/334,027
;; PRIOR FILING DATE: 2001-11-28
;; PRIOR APPLICATION NUMBER: 60/331,641
;; PRIOR FILING DATE: 2001-11-20
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 673
;; SOFTWARE: CuraSeqlist version 0.1
;; SEQ ID NO 93
;; LENGTH: 1145
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (8)..(832)
US-10-287-226-93

Alignment Scores:
Pred. No.: 2,31e-158 Length: 1145
Score: 1368.00 Matches: 244
Percent Similarity: 99.59% Conservative: 0
Best Local Similarity: 99.59% Mismatches: 1
Query Match: 98.21% Indels: 0
DB: 17 Gaps: 0

US-09-598-982-21 (1-249) x US-10-287-226-93 (1-1145)

Qy 5 IleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24
Db 98 ATCGTTGGGGTTCAGAGAGCCGCCAGGAGCAAGTGGCCCTGGCAGGTGAGCTGAGATC 157
Qy 25 HisGlyProTyrTrpMetHisPheCysGlySerLeuIleHisProGlnTrpValLeu 44
Db 158 CACGCCCATCTACTGGATGCACTTCTGCGGGGCTCCCTCATCCACCCAGTGGGTGCTG 217
Qy 45 ThrAlaAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 64
Db 218 ACCGAGCGCACTGGGTGGGACCGGACGTCAGGATCTGGCGGCCCTCAGGGTGAACCTG 277
Qy 65 ArgGluGlnHisLeuTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 84
Db 278 CGGGAGCAGCACTTACTACAGACCACTGCTGCGGTGAGGATCATCTGTGAC 337
Qy 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluPro 104
Db 338 CCACAGTTCTACACGCCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCG 397
Qy 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
Db 398 GTGAAGGTCTCCAGCCAGTCACACGCTCACCGTCCCTGCCCCCTCAGAGACCTTCCCC 457
Qy 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
Db 458 CCGGGATGCCGTGCTGGGTCACTGGCTGGGCGCATGTGGCAATGATGAGCGCTCCCA 517
Qy 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
Db 518 CCGCCATTCTCTCAAGCAGGTGAAGTCCCAATAATGGAACCAACATTTGTGACGCA 577
Qy 165 LysTyrHisLeuGlyAlaTyrThrGlyAspAspValArgIleValArgAspMetLeu 184
Db 578 AATACCACTTGGCGCTTACACGGAGACGACGTCGCCATCTCGTCCGTGACGACATGCTG 637
Qy 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
Db 638 TGTGCGGGNACACCGGAGGACTCATGCCAGGGCGACTCCGGAGGGCCCTCGTGTGTC 697
Qy 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224

Db 698 AAGGTGAATGCACCTGGCTGCAGCGGGCGTGGTGCAGCTGGGCGAGGGCTGTGCCAG 757
Qy 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisTyr 244
Db 758 CCCAACCGGCTGGCATCTACACCGGTGTACCTACTTGGACTGGATCCACCACCTAT 817
Qy 245 ValProLysLysPro 249
Db 818 GTCCCCAAAGAGCG 832

RESULT 3

US-10-287-226-91
;; Sequence 91, Application US/10287226
;; Publication No. US20040086875A1
;; GENERAL INFORMATION:
;; APPLICANT: Agee, Michele L.,
;; APPLICANT: Alsbrook, John P.,
;; APPLICANT: Berghs, Constance,
;; APPLICANT: Boldog, Ference,
;; APPLICANT: Burgess, Catherine E.,
;; APPLICANT: Chant, John S.,
;; APPLICANT: Chaudhuri, Amitabha,
;; APPLICANT: DiPippo, Vincent A.,
;; APPLICANT: Edinger, Shlomit R.,
;; APPLICANT: Eisen, Andrew,
;; APPLICANT: Ellerman, Karen,
;; APPLICANT: Gangolli, Esha A.,
;; APPLICANT: Gorman, Linda,
;; APPLICANT: Gerlach, Valerie,
;; APPLICANT: Ji, Weizhen,
;; APPLICANT: Kekuda, Ramesh,
;; APPLICANT: Khramtsov, Nikolai,
;; APPLICANT: Li, Li,
;; APPLICANT: Malyankar, Uriel M.,
;; APPLICANT: MacDougall, John R.,
;; APPLICANT: Mezes, Peter S.,
;; APPLICANT: Miller, Charles E.,
;; APPLICANT: Millet, Isabelle,
;; APPLICANT: Ooi, Chean Eng,
;; APPLICANT: Ort, Tatiana,
;; APPLICANT: Padigaru, Muralidhara,
;; APPLICANT: Patturajan, Meera,
;; APPLICANT: Rastelli, Luca,
;; APPLICANT: Rieger, Daniel K.,
;; APPLICANT: Rothenberg, Mark E.,
;; APPLICANT: Shenoy, Suresh G.,
;; APPLICANT: Spaderna, Steven K.,
;; APPLICANT: Spytek, Kimberley A.,
;; APPLICANT: Taupier, Jr., Raymond J.,
;; APPLICANT: Vernet, Corine A.M.,
;; APPLICANT: Zethusen, Bryan D.,
;; APPLICANT: Zhong, Mei
;; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;; FILE REFERENCE: 21402-480C
;; CURRENT APPLICATION NUMBER: US/10/287,226
;; PRIOR FILING DATE: 2002-11-04
;; PRIOR APPLICATION NUMBER: 60/334,421
;; PRIOR FILING DATE: 2001-11-30
;; PRIOR APPLICATION NUMBER: 60/354,392
;; PRIOR FILING DATE: 2002-02-04
;; PRIOR APPLICATION NUMBER: 60/360,148
;; PRIOR FILING DATE: 2002-02-27
;; PRIOR APPLICATION NUMBER: 60/364,000
;; PRIOR FILING DATE: 2002-03-13
;; PRIOR APPLICATION NUMBER: 60/404,821
;; PRIOR FILING DATE: 2002-08-20
;; PRIOR APPLICATION NUMBER: 60/334,526
;; PRIOR FILING DATE: 2001-11-30
;; PRIOR APPLICATION NUMBER: 60/354,409
;; PRIOR FILING DATE: 2002-02-04
;; PRIOR APPLICATION NUMBER: 60/364,227
;; PRIOR FILING DATE: 2002-03-13
;; PRIOR APPLICATION NUMBER: 60/334,027

```

; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/331,641
; PRIOR FILING DATE: 2001-11-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 673
; SOFTWARE: CuraSeqlist version 0.1

```

105 ValLysValSerHisValHisThrValThrLeuProAlaSerGluThrPhePro 124
125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
145 ProProPheProLeuLysGlnValLysValProLleMetGluAsnHisIleCysAspAla 164
165 LysTrpHisLeuGlyAlaValThrGlyAspValArgIleValArgAspMetLeu 184
185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyProLeuValCys 204
205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224
225 ProAsnArgProGlyIleValThrArgValThrTrpLeuAspTrpIleHisTyr 244
245 ValProLysLysPro 249
788 GTCCCCAAAAAGCCG 802

RESULT 5

US-09-960-706-680
; Sequence 680, Application US/09960706
; Publication No. US20030134280A1
; GENERAL INFORMATION:
; APPLICANT: Mungler, William E.
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
; TITLE OF INVENTION: Gene Expression Profiles
; FILE REFERENCE: 44921-5029-01US
; CURRENT APPLICATION NUMBER: US/09/960,706
; PRIOR FILING DATE: 2001-09-24
; PRIOR FILING DATE: 60/223,323
; PRIOR FILING DATE: 2000-08-07
; PRIOR FILING DATE: 09/873,319
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 680
; LENGTH: 1081
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 M33493
US-09-960-706-680

Alignment Scores:
Pred. No.: 1.94e-155 Length: 1081
Score: 1344.00 Matches: 241
Percent Similarity: 98.37% Conservative: 0
Best Local Similarity: 98.37% Mismatches: 4
Query Match: 96.48% Indels: 0
DB: 10 Gaps: 0

US-09-598-982-21 (1-249) x US-09-960-706-680 (1-1081)

5 l1eValGlyGlnGluAlaProArgSerLysTrpTrpTrpGlnValSerLeuArgVal 24
68 ATCGTTGGGGTCAGAGAGCCCGCCAGGACCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTTC 127
25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44

128 CGCGACCATGACTGGATGTCACCTTCTGGGGGGGCTCCCTCATCCACCCCGAGTGGTGTCTG 187
45 ThrAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 64
188 ACCGACGCGCACTCGTGGGACCGGACGTCAGGATCTGGCGCCCTCAGGGTGAACCTG 247
65 ArgGluGlnHisLeuTyrTrpGlnAspGlnLeuProValSerArgIleIleValHis 84
248 CGGAGGAGGAGCACTCTACTACGAGGACGAGTGTCTGGCGGTGACAGGATCATCGTGAC 307
85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluPro 104
308 CCACAGTCTTACACCGCCAGATCGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGCG 367
105 ValLysValSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
368 GTGAAGGTCTCCAGCCACGTCACCGGTCACTGCGCCCTGCTGCTCAGAGACCTTCCCC 427
125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
428 CGGCGGATGCGGTGCTGCTGGTCACTGGCTGGGGCGATGTGGACATGATGAGGGCTCCCA 487
145 ProProPheProLeuLysGlnValLysValProLleMetGluAsnHisIleCysAspAla 164
488 CGGCAATTTCCCTCTGAAGCAGGTGAAGGTCCCATATATGAAAAACCATTTGTGACGCA 547
165 LysTrpHisLeuGlyAlaValThrGlyAspValArgIleValArgAspMetLeu 184
548 AATATACCACTTGGCGCTTACCGGGAGACACGCTCCGATCGTCCGTGAGACATGTGTG 607
185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyProLeuValCys 204
608 TGTCCGGGAACACCCGGAGGAGTCTATCCGAGGCGACTCCGGAGGGGCCCTGGTGTGC 667
205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224
668 AAGTGAATGCACTGGCTGCGAGCGGCGGTGTCAGCTGGGGCGAGGGGTGTGCCAG 727
225 ProAsnArgProGlyIleValThrArgValThrTrpLeuAspTrpIleHisTyr 244
728 CCCAACCGGCGCTGGCATCTACCCCGTGTCACTTACTTGGACTGGATCCACCAT 787
245 ValProLysLysPro 249
788 GTCCCCAAAAAGCCG 802

RESULT 6

US-09-873-319-427
; Sequence 427, Application US/09873319A
; Publication No. US20030134324A1
; GENERAL INFORMATION:
; APPLICANT: Mungler, William E.
; APPLICANT: Kulkarni, Prakash
; APPLICANT: Getzenberg, Robert H.
; APPLICANT: Waga, Iwao
; APPLICANT: Yamamoto, Jun
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic
; TITLE OF INVENTION: Hyperplasia Using Gene Expression Profiles
; FILE REFERENCE: 44921-5029-US
; CURRENT APPLICATION NUMBER: US/09/873,319A
; CURRENT FILING DATE: 2001-06-05
; EARLIER APPLICATION NUMBER: US 60/223,323
; EARLIER FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 755
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 427
; LENGTH: 1081
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134324A1 M33493
US-09-873-319-427

Alignment Scores:

Pred. No.: 1.94e-155 Length: 1081
 Score: 1344.00 Matches: 241
 Percent Similarity: 98.37% Conservative: 0
 Best Local Similarity: 98.37% Mismatches: 4
 Query Match: 96.48% Indels: 0
 DB: 10 Gaps: 0

US-09-598-982-21 (1-249) x US-09-873-319-427 (1-1081)

Qy 5 ILeValGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24
 Db 68 ATCGTTGGGGTCCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 127
 Qy 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuLeuHisProGlnTrpValLeu 44
 Db 128 CGCAGCAGTACTGGATGTCATTTCTGGGGGGCTCCCTCATCCACCCCGAGTGGGTGCTG 187
 Qy 45 ThrAlaAlaLaCysValGlyProAspValLysAspLeuAlaLeuArgValGlnLeu 64
 Db 188 ACCGAGCGCACTCGTGGGAGCGGAGCGTCAAGGATCTGGCGGCCCTCAGGGTCAACTG 247
 Qy 65 ArgGlnHisLeuTyrTrpGlnAspGlnLeuLeuProValSerArgIleValHis 84
 Db 248 CGGAGAGCAGCACCTCTACTACGAGGACGAGTGTCTGGGGTCCAGGAGTATCATGTGCAC 307
 Qy 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluGluPro 104
 Db 308 CCACAGTCTTACACCGCCCGAGATCGGAGCGGACATCGCCCTGTGGAGTGGAGAGCGG 367
 Qy 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
 Db 368 GTGAAGTCTCTCAGCAGCGTCCACACGCTCACCCCTGCCCTGCTCAGAGACCTTCCCC 427
 Qy 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValLysAspGlnLeuPro 144
 Db 428 CCGGGAGTGGCTGCTGGGTACCTGGCTGGGGCGATGTGGACATGATGAGCGCTCCCA 487
 Qy 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
 Db 488 CCGCAATTTCTCTGAAGCAGGTGAAGTCCCCCATATGGAAACCAATTTGTGAGCGCA 547
 Qy 165 LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspAspMetLeu 184
 Db 548 AAATACCACTTGGCGCTTACACGGGAGACGAGTCCGCTCGCATCTCGTGGAGCATGCTG 607
 Qy 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
 Db 608 TGTCCGGGAACACCCCGAGGAGCTCATGCGGGGAGCTCCGGAGGGCCCTGGTGTGC 667
 Qy 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224
 Db 668 AAGTGAATGGCACTGGCTGCAGCGGGCGTGTGTAGCTGGGGCGAGGGGTGTGGCCAG 727
 Qy 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTrpLeuAspTrpIleHisTyr 244
 Db 728 CCCAACCGGCTGGCATCTACACCCGTCACTTACTTGGACTGGATCCACCACTAT 787
 Qy 245 ValProLysPro 249
 Db 788 GTCCCCAAAAGCGG 802

RESULT 7

US-09-873-367C-155
 ; Sequence 155, Application US/09873367C
 ; Publication No. US20030165839A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Paul
 ; APPLICANT: Soppet, Daniel
 ; APPLICANT: Endress, Gregory
 ; APPLICANT: Augustus, Meena
 ; APPLICANT: Ebner, Reinhard
 ; APPLICANT: Carter, Kenneth

; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
 ; TITLE OF INVENTION: Signature Gene Sets
 ; FILE REFERENCE: 689290-64
 ; CURRENT APPLICATION NUMBER: US/09/873,367C
 ; CURRENT FILING DATE: 2003-04-29
 ; PRIOR APPLICATION NUMBER: U.S. 60/236,891
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: U.S. 60/236,842
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: U.S. 60/244,867
 ; PRIOR FILING DATE: 2000-11-01
 ; PRIOR APPLICATION NUMBER: U.S. 60/245,084
 ; PRIOR FILING DATE: 2000-11-01
 ; NUMBER OF SEQ ID NOS: 1067
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 155
 ; LENGTH: 1081
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-873-367C-155

Alignment Scores:

Pred. No.: 1.94e-155 Length: 1081
 Score: 1344.00 Matches: 241
 Percent Similarity: 98.37% Conservative: 0
 Best Local Similarity: 98.37% Mismatches: 4
 Query Match: 96.48% Indels: 0
 DB: 10 Gaps: 0

US-09-598-982-21 (1-249) x US-09-873-367C-155 (1-1081)

Qy 5 ILeValGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24
 Db 68 ATCGTTGGGGTCCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 127
 Qy 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuLeuHisProGlnTrpValLeu 44
 Db 128 CGCAGCAGTACTGGATGTCATTTCTGGGGGGCTCCCTCATCCACCCCGAGTGGGTGCTG 187
 Qy 45 ThrAlaAlaLaCysValGlyProAspValLysAspLeuAlaLeuArgValGlnLeu 64
 Db 188 ACCGAGCGCACTCGTGGGAGCGGAGCGTCAAGGATCTGGCGGCCCTCAGGGTCAACTG 247
 Qy 65 ArgGlnHisLeuTyrTrpGlnAspGlnLeuLeuProValSerArgIleValHis 84
 Db 248 CCGAGAGCAGCACCTCTACTACGAGGACCGAGTGTCTGGGGTCCAGGAGTATCATGTGCAC 307
 Qy 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluGluPro 104
 Db 308 CCACAGTCTTACACCGCCCGAGATCGGAGCGGACATCGCCCTGTGGAGTGGAGAGCGG 367
 Qy 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
 Db 368 GTGAAGTCTCTCAGCAGCGTCCACACGCTCACCCCTGCCCTGCTCAGAGACCTTCCCC 427
 Qy 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValLysAspGlnLeuPro 144
 Db 428 CCGGGAGTGGCTGCTGGGTACCTGGCTGGGGCGATGTGGACATGATGAGCGCTCCCA 487
 Qy 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
 Db 488 CCGCAATTTCTCTGAAGCAGGTGAAGTCCCCCATATGGAAACCAATTTGTGAGCGCA 547
 Qy 165 LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspAspMetLeu 184
 Db 548 AAATACCACTTGGCGCTTACACGGGAGACGAGTCCGCTCGCATCTCGTGGAGCATGCTG 607
 Qy 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
 Db 608 TGTCCGGGAACACCCCGAGGAGCTCATGCGGGGAGCTCCGGAGGGCCCTGGTGTGC 667
 Qy 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224

Db 668 AAGGTGAATGCACCTGCTGCAGCGGGCGTGTGCTAGCTGGGGGAGGGGTGTGCCCGAG 727
Qy 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 244
Db 728 CCCAACCGGCTGGCACTACACCGGTGTACCTACTACTTGGACTGGATCCACCACTAT 787
Qy 245 ValProLysLysPro 249
Db 788 GTCCCCAAAAGCGG 802

RESULT 8
US-09-873-367C-714
; Sequence 714, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; APPLICANT: Soppet, Daniel
; APPLICANT: Endress, Gregory
; APPLICANT: Augustus, Meena
; APPLICANT: Ebner, Reinhard
; APPLICANT: Carter, Kenneth
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-64
; CURRENT APPLICATION NUMBER: US/09/873,367C
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,891
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,842
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/244,867
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: U.S. 60/245,084
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 714
; LENGTH: 1081
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-367C-714

Alignment Scores:
Pred. No.: 1,94e-155 Length: 1081
Score: 1344.00 Matches: 241
Percent Similarity: 98.37% Conservative: 0
Best Local Similarity: 98.37% Mismatches: 4
Query Match: 96.48% Indels: 0
DB: 10 Gaps: 0

US-09-598-982-21 (1-249) x US-09-873-367C-714 (1-1081)

Qy 5 IleValGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24
Db 68 ATCTTGGGGTCCAGGAGGCCGCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTCAGAGTC 127
Qy 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
Db 128 CGCAGCCGATCTGATGATGACCTTCTCGCGGGGCTCCCTCATCCACCCAGTGGGTGCTG 187
Qy 45 ThrAlaAlaLacCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 64
Db 188 ACCGAGCGCACTGGTGGGACCGGACGCTCAAGATCTGGCGCCCTCAGGTCGCACTG 247
Qy 65 ArgGlnGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleValHis 84
Db 248 CGGAGCAGCACCTCTACTACGAGCAGCAGTGTCTGGCGGTGAGGATCATCTGTGCAC 307
Qy 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluPro 104
Db 308 CCACAGTTCTACACCGCCGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGCGG 367
Qy 105 VallysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124

Db 368 GTGAAGGTCTCCAGCCAGCTCCACCGGTACCTGCCCTGCCCTCAGAGACCTTCCCC 427
Qy 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAspGluArgLeuPro 144
Db 428 CCGGGATGCGGTGCTGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCTCCCA 487
Qy 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
Db 488 CGCCCAITTTCTCTGAAGCAGGTGAGGTGCCCATATGGAACCAATTTGTGACGCA 547
Qy 165 LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspMetLeu 184
Db 548 AATATACCACCTTGGCGCTACACGGGAGACGACCTCCGTCATCGTCGACGACATGCTG 607
Qy 185 CysAlaGlyAsnThrArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
Db 608 TGTCCGGGAACACCGGAGGAGTCTCATGCCAGGGCGACTCCGGAGGGCCCTGGTGTGC 667
Qy 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224
Db 668 AAGTGAATGACCTGGCTCGAGCGGGCGTGTGTCAGCTGGGGCGAGGGGTGTGCCAG 727
Qy 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 244
Db 728 CCCAACCGGCTGGCACTACACCGGTGTACCTACTACTTGGACTGGATCCACCACTAT 787
Qy 245 ValProLysLysPro 249
Db 788 GTCCCCAAAAGCGG 802

RESULT 9
US-10-275-505-27
; Sequence 27, Application US/10275505
; Publication No. US20040081961A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DELEGANE, Angelo M.; IAL, Preeti G.
; APPLICANT: HAPALIA, April J.A.; PATTERSON, Chandra
; APPLICANT: WALLIA, Narinder K.; KEARNEY, Liam
; APPLICANT: TRIBOULEY, Catherine M.; KHAN, Farrah A.
; APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Yalda; ELLIOTT, Vicki S.
; APPLICANT: NGUYEN, Darniel B.; GANDHI, Aneena R.
; APPLICANT: YANG, Junning; HERNANDEZ, Roberto
; APPLICANT: POLICKY, Jennifer L.; LU, Dying Aina M.
; APPLICANT: REDDY, Roopa M.; YUE, Henry
; APPLICANT: TANG, Y. Tom
; TITLE OF INVENTION: PROTEASES
; FILE REFERENCE: PI-0085 USN
; CURRENT APPLICATION NUMBER: US/10/275,505
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: PCT/US01/14651
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/209,402
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 60/207,477
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/205,803
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: 60/203,566
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 60/202,082
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PERL Program
; SEQ ID NO 27
; LENGTH: 2662
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7472460CB1

US-10-275-505-27

Alignment Scores:

Pred. No.: 4.65e-153 Length: 2662
 Score: 1329.00 Matches: 238
 Percent Similarity: 97.14% Conservatives: 0
 Best Local Similarity: 97.14% Mismatches: 7
 Query Match: 95.41% Indels: 0
 DB: 17 Gaps: 0

US-09-598-982-21 (1-249) x US-10-275-505-27 (1-2662)

Qy 5 IleValGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24
 Db 701 ATCGTTGGGGTCAAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCTGAGAGTC 760
 Qy 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuLeuHisProGlnTrpValLeu 44
 Db 761 CGGACCGATACCTGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCGAGTGGTCTG 820
 Qy 45 ThrAlaAlaCysValGlyProAspValLysAspLeuAlaLeuArgValGlnLeu 64
 Db 821 ACCGAGCGACTGCTGGGAGCGGAGCTCAAGATCTGCCGCCCTCAGGGTCAACTG 880
 Qy 65 ArgGluGlnHisLeuTyrTrpGlnAspGlnLeuLeuProValSerArgIleValHis 84
 Db 881 CGGAGCAGCACCTCTACTACAGGACAGCTGCTGCCGGTCAAGAGATCATCGTGCAC 940
 Qy 85 ProGlnPheTyrThrAlaGlnIleGlyValAspIleAlaLeuLeuGluPro 104
 Db 941 CCACAGTTCACACCGCCAGATCGGAGCGGACATCGCTGCTGGAGCTGGAGGACCG 1000
 Qy 105 ValLysValSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
 Db 1001 GTGAACGTCCTCCAGCACGCTCCACACGCTCACCTGCCCTGCCTCAGAGACTTCCCC 1060
 Qy 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
 Db 1061 CCGGGATGCGTGGTCTGCTGGTCTGCTGGTGGGCGATGTGACATGTATGAGCGCTCCCA 1120
 Qy 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
 Db 1121 CCGCATTTCTCTGAAGCATGTGAAGTCCCCATAATGAAACCAATTTGAGCGCA 1180
 Qy 165 LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspMetLeu 184
 Db 1181 AATACCACTTGGCGCTTACACGGAGACGCTCCGATCGTCCGTGACGATGCTG 1240
 Qy 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
 Db 1241 TGTGCGGGAAACCCCGAGGGAUTCATGCGAGGCGACTCCGAGGGCGCCCTGGTGTGC 1300
 Qy 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGln 224
 Db 1301 AAGTGATGACCTTGGCTGCGAGCGGGGTGTGATGAGTGGGAGGGCTGTGCCAG 1360
 Qy 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTrpLeuAspTrpIleHisTyr 244
 Db 1361 CCCAACCGGCTGGCATCTACACCGTGTCACTTACTTGTGACTGGATCCACCACTAT 1420
 Qy 245 ValProLysLysPro 249
 Db 1421 GTCCCCAAAAGCGG 1435

RESULT 10

US-10-287-226-89

; Sequence 89, Application US/10287226

; Publication No. US20040086875A1

; GENERAL INFORMATION:

; APPLICANT: Agee, Michele L.,

; APPLICANT: Alsobrook, John P.,

; APPLICANT: Berghs, Constance,

; APPLICANT: Boldog, Ference,

; APPLICANT: Burgess, Catherine E.,
 ; APPLICANT: Chant, John S.,
 ; APPLICANT: Chaudhuri, Amitabha,
 ; APPLICANT: Dipippo, Vincent A.,
 ; APPLICANT: Edinger, Shlomit R.,
 ; APPLICANT: Eisen, Andrew,
 ; APPLICANT: Ellerman, Karen,
 ; APPLICANT: Gangolli, Esha A.,
 ; APPLICANT: Gorman, Linda,
 ; APPLICANT: Gerlach, Valerie,
 ; APPLICANT: Ji, Weizhen,
 ; APPLICANT: Kekuda, Ramesh,
 ; APPLICANT: Khramtsov, Nikolai,
 ; APPLICANT: Li, Li,
 ; APPLICANT: Malyankar, Uriel M.,
 ; APPLICANT: MacDougall, John M.,
 ; APPLICANT: Mezes, Peter S.,
 ; APPLICANT: Miller, Charles E.,
 ; APPLICANT: Millet, Isabelle,
 ; APPLICANT: Ooi, Chean Eng,
 ; APPLICANT: Ort, Tatiana,
 ; APPLICANT: Padigaru, Muralidhara,
 ; APPLICANT: Patturajan, Meera,
 ; APPLICANT: Rastelli, Luca,
 ; APPLICANT: Rieger, Daniel K.,
 ; APPLICANT: Rothenberg, Mark E.,
 ; APPLICANT: Shenov, Suresh G.,
 ; APPLICANT: Spaderna, Steven K.,
 ; APPLICANT: Spytek, Kimberley A.,
 ; APPLICANT: Taupier, Jr., Raymond J.,
 ; APPLICANT: Vernet, Corine A.M.,
 ; APPLICANT: Zerhusen, Bryan D.,
 ; APPLICANT: Zhong, Mei
 ; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 21402-480C
 ; CURRENT APPLICATION NUMBER: US/10/287,226
 ; CURRENT FILING DATE: 2002-11-04
 ; PRIOR APPLICATION NUMBER: 60/334,421
 ; PRIOR FILING DATE: 2001-11-30
 ; PRIOR APPLICATION NUMBER: 60/354,392
 ; PRIOR FILING DATE: 2002-02-04
 ; PRIOR APPLICATION NUMBER: 60/360,148
 ; PRIOR FILING DATE: 2002-02-27
 ; PRIOR APPLICATION NUMBER: 60/364,000
 ; PRIOR FILING DATE: 2002-03-13
 ; PRIOR APPLICATION NUMBER: 60/404,821
 ; PRIOR FILING DATE: 2002-08-20
 ; PRIOR APPLICATION NUMBER: 60/334,526
 ; PRIOR FILING DATE: 2001-11-30
 ; PRIOR APPLICATION NUMBER: 60/354,409
 ; PRIOR FILING DATE: 2002-02-04
 ; PRIOR APPLICATION NUMBER: 60/364,227
 ; PRIOR FILING DATE: 2002-03-13
 ; PRIOR APPLICATION NUMBER: 60/334,027
 ; PRIOR FILING DATE: 2001-11-28
 ; PRIOR APPLICATION NUMBER: 60/331,641
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 673
 ; SOFTWARE: CuraseqList version 0.1
 ; SEQ ID NO 89
 ; LENGTH: 828
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(825)
 ; US-10-287-226-89

Alignment Scores:

Pred. No.: 5.21e-153

Score: 1323.00

Percent Similarity: 97.14%

Length: 828

Matches: 234

Conservative: 4


```
Best Local Similarity: 95.51% Mismatches: 7
Query Match: 94.97% Indels: 0
DB: 17 Gaps: 0

US-09-598-982-21 (1-249) x US-10-287-226-89 (1-828)

QY 5 lleValGlyGlyGlnGluAlaProArgSerLysTrpTrpGlnValSerLeuArgVal 24
DB 91 ATTGTGGGGGACAGAGGCCCCAGGAGCAAGTGGCCCTGCAGGTGAGCTGAGAGTC 150
QY 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
DB 151 CGCGCCCATATCTGATGACATCTTCGCGGGGCTCCCTCATCCACCCCGAGTGGGTGTTA 210
QY 45 ThrAlaAlaAlaCysValGlyProAspValLysAspValLysAlaAlaValGlnLeu 64
DB 211 ACCCGGGGCACTGGTGAACCGGACATCAAGGATCTGGCCGCTCAGGGTGAACATG 270
QY 65 ArgGluGlnHisLeuTyrTrpGlnAspGlnLeuProValSerArgIleIleValHis 84
DB 271 CGGAGGACGACCTCTACTACAGGACGAGCTGCTGCCGTCAGCAGGATCATCTGTGCAC 330
QY 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluPro 104
DB 331 CCACAGTTCTATCATCATCCAGACCGGGGCGGACATCGCCCTCTGAGCTGGAGGAGGCC 390
QY 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
DB 391 GTGAACATCTCCAGCACCATCCACAGCTGACGCTGCCCTGCTCGAGAGACCTTCCCC 450
QY 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
DB 451 CGGGGATGCGTGTGGTCTACTGGTCTGCTGGGCGGAGCTGGCAATAATAGAGCGCTCCCA 510
QY 145 PropProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
DB 511 CGCGCATTTCTCTGAACAGGTGAAGTCCCAATAATGAAACACACATTTGTGACGCA 570
QY 165 LysTyrHisLeuGlyValatThrGlyAspValArgIleValArgAspMetLeu 184
DB 571 AAATACCACTTGGCGCTTACAGGGAGACGACGCTCGCATCTCGTGACGACATGCTG 630
QY 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
DB 631 TGTGCGGGAAACACCGGAGGACTCATGCCAGGCGACTCCGAGGCGCCCTGCTGTGTC 690
QY 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlnGlyCysAlaGln 224
DB 691 AAGGTGAATGACCATCTGCTGCGAGCGGCGTGGTCAAGTGGGGGAGGGCTGTGCCAG 750
QY 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisTyr 244
DB 751 CCCAACCGGCTGGCATCTACACCGGTGTCACCTACTTGGACTGGATCCACCATAT 810
QY 245 ValProLysLysPro 249
DB 811 GTCCCCAAAAGCGG 825

RESULT 11
US-10-287-226-87
; Sequence 87, Application US/10287226
; Publication No. US20040086875A1
; GENERAL INFORMATION:
; APPLICANT: Agee, Michele L.,
; APPLICANT: Alsobrook, John P.,
; APPLICANT: Berghs, Constance,
; APPLICANT: Boldog, Ference,
; APPLICANT: Burgess, Catherine E.,
; APPLICANT: Chant, John S.,
; APPLICANT: Chaudhuri, Amitabha,
; APPLICANT: DiPippo, Vincent A.,
; APPLICANT: Edinger, Shalomit R.,
; APPLICANT: Eisen, Andrew,
```

```
; APPLICANT: Ellerman, Karen,
; APPLICANT: Gangolli, Esha A.,
; APPLICANT: Gorman, Linda,
; APPLICANT: Gerlach, Valerie,
; APPLICANT: Ji, Weizhen,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Khrantsov, Nikolai,
; APPLICANT: Li, Li,
; APPLICANT: Malyankar, Uriel M.,
; APPLICANT: MacDougall, John R.,
; APPLICANT: Mezes, Peter S.,
; APPLICANT: Miller, Charles E.,
; APPLICANT: Millet, Isabelle,
; APPLICANT: Ooi, Chean Eng,
; APPLICANT: Ort, Tatiana,
; APPLICANT: Padigaru, Muralidhara,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Pastelli, Luca,
; APPLICANT: Rieger, Daniel K.,
; APPLICANT: Rothenberg, Mark E.,
; APPLICANT: Shenoy, Suresh G.,
; APPLICANT: Spaderina, Steven K.,
; APPLICANT: Spytek, Kimberley A.,
; APPLICANT: Taupier, Jr., Raymond J.,
; APPLICANT: Vernet, Corine A.M.,
; APPLICANT: Zerhusen, Bryan D.,
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-480C
; CURRENT APPLICATION NUMBER: US/10/287,226
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: 60/334,421
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,392
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/360,148
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/364,000
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/404,821
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/334,526
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,409
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/364,227
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/334,027
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/331,641
; PRIOR FILING DATE: 2001-11-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 673
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 87
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (8)..(844)
US-10-287-226-87

Alignment Scores:
Pred. No.: 1.24e-151 Length: 858
Score: 1312.00 Matches: 238
Percent Similarity: 96.75% Conservative: 0
Best Local Similarity: 96.75% Mismatches: 2
Query Match: 94.19% Indels: 6
DB: 17 Gaps: 2

US-09-598-982-21 (1-249) x US-10-287-226-87 (1-858)
```

```

Qy 5 IleValGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24
Db 122 ATCGTCGGGGTTCAGGAGGCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCTGAGAGTC 181
Qy 25 HisGlyProTyrTrpMetHisPheCysGlySerLeuLeuHisProGlnTrpValLeu 44
Db 182 CACGGCCCATCTGATGATGCACTTCTGGGGGGCTCCCTCATCCACCCCGAGTGGGTGCTG 241
Qy 45 ThrAlaAlaCysValGlyProAspValLysAspLeuAlaLeuArgValGlnLeu 64
Db 242 ACCGAGCGCACTCGTGGGAGCGGAGCTCAAGATCTGGCCGCCCTCAGGTGCAACTG 301
Qy 65 ArgGluGlnHisLeuTyrTrpGlnAspGlnLeuProValSerArgIleValHis 84
Db 302 CGGGAGCAGCACCTCTACTACAGACACAGCTGCTGGCGGTGACAGGATCATGTCAC 361
Qy 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluGluPro 104
Db 362 CCACAGTTCATACCGGCCAGATCGGAGCGGACATCGCTGCTGGAGCTGGAGAGCG 421
Qy 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
Db 422 GTGAACTCTCCAGCCACGTCACACGCTGACCTGCCCCCTGCTCAGAGACCTTCCCC 481
Qy 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
Db 482 CCGGGGATGCGTCTGGTCACTGGCTGGTGGGGCGATGTG-----CTCCCA 526
Qy 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
Db 527 CCGGCATTCTCTGAAAGAGGTGAAGTCCCCATAATGGAAGAACCAATTGTGAGCGCA 586
Qy 165 LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspMetLeu 184
Db 587 AAATACACCTTGGGCTTACACGGAGACAGCTCCGATCGTCGTCGAGCATGCTG 646
Qy 185 CysAlaGlyAsnThrArgArgAspSerCys---GlnGlyAspSerGlyGlyProLeuVal 203
Db 647 TGTCCGGGAACACCCGGAGGAGCTCATGTCAGCAGGCGGAGCTCCGGAGGGCCCTGTGTG 706
Qy 204 CysLysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAla 223
Db 707 TGCAAGGTGAATGGCACTGCTGTCAGCGGGCGGTGTCAGCTGGGGCGAGGGCTGTGCC 766
Qy 224 GlnProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHis 243
Db 767 CAGCCCAACCGCCCTGGCATCTACACCGTGTACCTACTACTTGGACTGGATCCACCCAC 826
Qy 244 TyrValProLysLysPro 249
Db 827 TATGTCCCAAAAGCGC 844

RESULT 12
US-10-352-684A-45
; Sequence 45, Application US/10352684A
; Publication No. US20030215452A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; APPLICANT: Welch, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 146, 199, 12303, 13906,
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
; FILE REFERENCE: MPI02-019PIRNONMIM
; CURRENT APPLICATION NUMBER: US/10/352,684A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258

```

```

; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/364,476
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18) ... (845)
US-10-352-684A-45

Alignment Scores:
Pred. No.: 8,93e-147 Length: 1154
Score: 1274.00 Matches: 226
Percent Similarity: 94.69% Conservative: 6
Best Local Similarity: 92.24% Mismatches: 13
Query Match: 91.46% Indels: 0
DB: 16 Gaps: 0

US-09-598-982-21 (1-249) x US-10-352-684A-45 (1-1154)
Qy 5 IleValGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24
Db 108 ATCGTCGGGGTTCAGGAGGCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCTGAGAGTC 167
Qy 25 HisGlyProTyrTrpMetHisPheCysGlySerLeuLeuHisProGlnTrpValLeu 44
Db 168 CGCAGCCGATCTGATGATGCACTTCTGGGGGGCTCCCTCATCCACCCCGAGTGGGTGCTG 227
Qy 45 ThrAlaAlaCysValGlyProAspValLysAspLeuAlaLeuArgValGlnLeu 64
Db 228 ACCGCGGCGCACTCGCTGGGAGCGGAGCTCAAGGATCTGGCCACCCCTCAGGGTGCACCTG 287
Qy 65 ArgGluGlnHisLeuTyrTrpGlnAspGlnLeuProValSerArgIleValHis 84
Db 288 CCGGAGCAGCACCTCTACTACAGGACGAGCTGCTGGCAGTCAGCAGGATCATGTCGAC 347
Qy 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluGluPro 104
Db 348 CCACAGTTCATCATCCAGACTGGAGCGGATATCGCCCTGCTGGAGCTGGAGAGGCC 407
Qy 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
Db 408 GTGAACATCTCCAGCGCGCTCCACAGGTCATGCTGCCCTGCTCGAGACCTTCCCTCC 467
Qy 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
Db 468 CCGGGAGTGGCTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCCCTCCCA 527
Qy 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
Db 528 CCGCCATTCCCTCGAGCAGGTGAAGTCCCTCCCAATATGGAAGAACCAATTGTGAGCGCA 587
Qy 165 LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspMetLeu 184

```


Alignment Scores:

Pred. No.: 1.19e-119 Length: 1187
 Score: 1054.00 Matches: 186
 Percent Similarity: 83.54% Conservative: 17
 Best Local Similarity: 76.54% Mismatches: 40
 Query Match: 75.66% Indels: 0
 DB: 17 Gaps: 0

US-09-598-982-21 (1-249) x US-10-275-505-22 (1-1187)

QY 5 IleValGlyGlnGluAlaProArgSerIysTrpProTrpGlnValSerLeuArgVal 24
 Db 263 ATTGTGGGGGACAGGAGGACATGCGGGAACAAAGTGGCCCTGCAGGTCGCTGCTGCC 322
 QY 25 HisGlyProTyrTrpMetHisPheCysGlySerLeuIleHisProGlnTrpValLeu 44
 Db 323 AATGACACCTACTGATGTCATTTCTGGGTGGCTCCCTCATCCACCCACAGTGGTGGTC 382
 QY 45 ThrAlaAlaCysValGlyProAspValIysAspLeuAlaAlaLeuArgValGlnLeu 64
 Db 383 ACTGGGCACACTGTGTGGGACCGGATGTTCTGACCCCAACAAAGTTCAGAGTACAGCTC 442
 QY 65 ArgGlnGlnHisLeuTyrTrpGlnAspGlnLeuProValSerArgIleIleValHis 84
 Db 443 CGTAAGCAGTACCTCTATTACCATGACACCATGATGACTGTGACCCAGATCATCACAC 502
 QY 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluPro 104
 Db 503 CCGGACTTCTACATCGTCCAGGATGGGCGACATTCGCCCTGCTGAACCTCACAAACCT 562
 QY 105 ValIysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
 Db 563 GTGAACATTTCTGACTATGTCACCCCTGTCCCTGCTGCTGCTGCTGCTGCTGCTGCT 622
 QY 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
 Db 623 TCAGGAACGTTGTCTGGGTGACAGGCTGGGGTAACATCGACAATGTTGTAACCTGCCG 682
 QY 145 ProProPheProLeuLysGlnValIysValProIleMetGluAsnHisIleCysAspAla 164
 Db 683 CCACCAITTCCTTTGAAGGAGGTCAAGTTCCTATATAGAAACCCACTTTGTGACTTG 742
 QY 165 LysTrpHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspAspMetLeu 184
 Db 743 AAGTATCACAAAGGTCTCATCACAGGTGACAATCTCCACATTTCCGAGATGACATGCTG 802
 QY 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
 Db 803 TGTGCTGGGAATGAGGACATGACTCTCTCCAGGGGACCTCCGAGGACCTCTGCTGCTGC 862
 QY 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGlyGlyCysAlaGln 224
 Db 863 AAGGTAGAAGACACTGGCTGTCAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 922
 QY 225 ProAsnArgProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisHisTyr 244
 Db 923 CCCAACAGGCTGSCATCTACACCCGGGTCACTATTACTTGGACTGGATCCACCACTAT 982
 QY 245 ValProLys 247
 Db 983 GTCCCCCAAG 991

RESULT 15

US-09-813-432-11
 ; Sequence 11, Application US/09813432
 ; Publication No. US2003014848A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Taupier Jr., Raymond J
 ; APPLICANT: Majmuder, Kamud
 ; APPLICANT: Spaderna, Steven K
 ; APPLICANT: Smithson, Glenda
 ; APPLICANT: Mezes, Peter S

; APPLICANT: Vernet, Corine A. M.
 ; TITLE OF INVENTION: No. US2003014848A1el Polypeptides and Amino Acids Encoding Same
 ; FILE REFERENCE: 15966-729
 ; CURRENT APPLICATION NUMBER: US/09/813,432
 ; CURRENT FILING DATE: 2001-03-20
 ; PRIOR APPLICATION NUMBER: 60/190,835
 ; PRIOR FILING DATE: 2000-03-20
 ; PRIOR APPLICATION NUMBER: 60/190,768
 ; PRIOR FILING DATE: 2000-03-20
 ; PRIOR APPLICATION NUMBER: 60/190,972
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: 60/191,199
 ; PRIOR FILING DATE: 2000-03-22
 ; PRIOR APPLICATION NUMBER: 60/191,947
 ; PRIOR FILING DATE: 2000-03-24
 ; PRIOR APPLICATION NUMBER: 60/192,665
 ; PRIOR FILING DATE: 2000-03-28
 ; PRIOR APPLICATION NUMBER: 60/192,657
 ; PRIOR FILING DATE: 2000-03-28
 ; PRIOR APPLICATION NUMBER: 60/192,984
 ; PRIOR FILING DATE: 2000-03-28
 ; PRIOR APPLICATION NUMBER: 60/192,664
 ; PRIOR FILING DATE: 2000-03-28
 ; PRIOR APPLICATION NUMBER: 60/192,836
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: 60/193,843
 ; PRIOR FILING DATE: 2000-03-31
 ; NUMBER OF SEQ ID NOS: 78
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 11
 ; LENGTH: 846
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-813-432-11

Alignment Scores:

Pred. No.: 7.46e-72 Length: 846
 Score: 664.50 Matches: 129
 Percent Similarity: 65.06% Conservative: 33
 Best Local Similarity: 51.81% Mismatches: 82
 Query Match: 47.70% Indels: 5
 DB: 10 Gaps: 3

US-09-598-982-21 (1-249) x US-09-813-432-11 (1-846)

QY 5 IleValGlyGlnGluAlaProArgSerIysTrpProTrpGlnValSerLeuArgVal 24
 Db 96 ATTGTGGGGGACAGGATGCCCCCGGGAAGTGGCGGTGGCAGGTGAGGCTGAGGTC 155
 QY 25 -----HisGlyProTyrTrpMetHisPheCysGlySerLeuIleHisProGln 41
 Db 156 TACAGCTACCACTGGGCTCTCTGGGCGCACATCTGTGGGGGCTCCCTCATCCACCCCGAG 215
 QY 42 TrpValLeuThrAlaAlaCysValGlyProAspValIysAspLeuAlaLeuArg 61
 Db 216 TGGGTGTGATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 275
 QY 62 ValGlnLeuArgGluGlnHisLeuTyrTrpGlnAspGlnLeuProValSerArgIle 81
 Db 276 ATCCACGCTGGGACGTGATCTACGGGGGCGGGGCTGTGTAACGTACGACCGGATC 335
 QY 82 IleValHisProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeu 101
 Db 336 ATGCTCCACCCCAACTATGTCACCTGGGGGCTGGGTGCGGATGTGGCCCTGCTCCAGCTG 395
 QY 102 GluGluProValIysValSerSerHisValHisThrValThrLeuProProAlaSerGlu 121
 Db 396 GTGAGCCCCATGATCGGAGCGGCTAATGTAGGACGCTCAAGCTCTCCCGGCTCGCTG 455
 QY 122 ThrPheProGlyMetProCysTrpValThrGlyTyrGlyAspValAspAsnAspGlu 141
 Db 456 GAGCTCACCCCGAAGGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 515

Search completed: July 22, 2004, 19:33:58
Job time : 526 secs

This Page Blank (uspio)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 22, 2004, 14:36:26 ; Search time 83 Seconds
(without alignments)
946.555 Million cell updates/sec

Title: US-09-598-982-21

Perfect score: 1393

Sequence: 1 LEKRIVGQAPRSPKQV.....IYRTVYLDWIHHVVKPK 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mbc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rhodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1342	96.3	275	4 Q96RZ6	Q96RZ6 homo sapien
2	1286	92.3	275	4 Q86TMB	Q86TMB homo sapien
3	1286	92.3	276	4 Q86UAS	Q86UAS homo sapien
4	1032.5	78.4	275	6 Q7YS62	Q7YS62 equus caball
5	1051	75.4	271	6 Q8HYJ2	Q8HYJ2 bos taurus
6	1046	75.1	273	11 Q921N4	Q921N4 mus musculus
7	1022	73.4	233	4 Q96RZ7	Q96RZ7 homo sapien
8	1019	73.2	273	6 Q9XSM1	Q9XSM1 ovis aries
9	1005	72.1	237	6 Q29464	Q29464 bos taurus
10	678	48.7	318	11 Q80UR4	Q80UR4 mus musculus
11	651	46.7	277	6 Q8SQ44	Q8SQ44 mus musculus
12	640	45.9	279	11 Q9NWS4	Q9NWS4 mus musculus
13	596.5	42.8	328	11 Q8BJR6	Q8BJR6 mus musculus
14	589.5	42.3	321	4 Q96RZ8	Q96RZ8 homo sapien
15	587.5	42.2	277	11 Q80NM7	Q80NM7 mus musculus
16	568	40.8	274	11 Q924N9	Q924N9 mus musculus

17	564.5	40.5	311	11 Q80XZ3	Q80XZ3 rattus norv
18	549.5	39.4	320	13 Q7TOX2	Q7TOX2 xenopus lae
19	543	39.0	389	13 Q9PVX7	Q9PVX7 xenopus lae
20	538.5	38.7	327	4 Q8N171	Q8N171 homo sapien
21	537	38.5	331	11 Q8R1A6	Q8R1A6 mus musculus
22	537	38.5	331	11 Q80X17	Q80X17 mus musculus
23	536.5	38.5	284	4 Q8NF86	Q8NF86 homo sapien
24	536.5	38.5	310	11 Q81XC4	Q81XC4 mus musculus
25	534.5	38.4	317	13 Q9DGR3	Q9DGR3 xenopus lae
26	531.5	38.2	310	11 Q9QY29	Q9QY29 mus musculus
27	530	38.0	339	11 Q99L44	Q99L44 mus musculus
28	521.5	37.4	340	11 Q8BJV6	Q8BJV6 mus musculus
29	494	35.5	328	11 Q80Z40	Q80Z40 rattus norv
30	492.5	35.4	297	11 Q88781	Q88781 rattus norv
31	492	35.3	453	11 Q812A6	Q812A6 mus musculus
32	488	35.0	371	11 Q8CJ16	Q8CJ16 rattus norv
33	488	35.0	445	11 Q8CJ17	Q8CJ17 rattus norv
34	481	34.5	455	11 Q8CDR0	Q8CDR0 mus musculus
35	479	34.4	471	11 Q8CF80	Q8CF80 mus musculus
36	478.5	34.4	307	11 Q7TML0	Q7TML0 mus musculus
37	476	34.2	336	11 Q80YD8	Q80YD8 mus musculus
38	473	34.0	558	4 Q86YM4	Q86YM4 homo sapien
39	472	33.9	329	13 Q42272	Q42272 xenopus lae
40	469.5	33.7	335	11 Q8VIF2	Q8VIF2 mus musculus
41	469	33.7	624	6 Q95ME7	Q95ME7 oryctolagus
42	468	33.6	537	4 Q9BYE1	Q9BYE1 homo sapien
43	468	33.6	581	4 Q9BYE2	Q9BYE2 homo sapien
44	463.5	33.3	624	11 Q91Y47	Q91Y47 mus musculus
45	460.5	33.1	624	11 Q9DAT3	Q9DAT3 mus musculus

ALIGNMENTS

RESULT 1

Q96RZ6	PRELIMINARY;	PRT;	275 AA.
AC Q96RZ6;			
DT 01-DEC-2001 (TRENBLrel. 19, Created)			
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)			
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)			
DE Trypsinase I.			
GN TRYPTASEC.			
OS Homo sapiens (Human)			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=21096910; PubMed=11157797;			
RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,			
RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,			
RA Higgs D.R.;			
RT "Sequence, structure and pathology of the fully annotated terminal 2			
RT Mb of the short arm of human chromosome 16.";			
RL Hum. Mol. Genet. 10:339-352(2001).			
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.			
DR EMBL; AB006466; AAK61271.1; -.			
DR HSSP; P00761; IAN1.			
DR GO; GO:0004263; F:chymotrypsin activity; IEA.			
DR GO; GO:0008233; F:peptidase activity; IEA.			
DR GO; GO:0004295; F:trypsin activity; IEA.			
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.			
DR InterPro; IPR009003; Cys_Ser trypsin.			
DR InterPro; IPR001254; Peptidase S1.			
DR Pfam; PF00089; trypsin; 1			
DR PRINTS; PF00722; CHYMOTRYPSIN.			
DR SMART; SM00020; Tryp_Spc; 1.			
DR PROSITE; PS02040; TRYPSIN_DOM; 1.			
DR PROSITE; PS00134; TRYPSIN_HIS; 1.			
DR PROSITE; PS00135; TRYPSIN_SER; 1.			
KW Hydrolase; Protease; Serine protease.			

SQ SEQUENCE 275 AA; 30601 MW; 2F4AAAAB7DDE483E CRC64;

Query Match 96.3%; Score 1342; DB 4; Length 275;
 Best Local Similarity 98.0%; Pred. No. 2.4e-123;
 Matches 240; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 IVGGQAPRSKWPQVSLRVHGPVWVHFCGSLIHPQWVLTAAACVGPDKDLAALRVQL 64
 DB 31 IVGGQAPRSKWPQVSLRVHGPVWVHFCGSLIHPQWVLTAAACVGPDKDLAALRVQL 90

QY 65 REQHLYYQDQLLPVSRRIIVHPQFYTAQIGADIALLELEPVPKVS SHVHTVTLPPASETFP 124
 DB 91 REQHLYYQDQLLPVSRRIIVHPQFYTAQIGADIALLELEPVPKVS SHVHTVTLPPASETFP 150

QY 125 PGMPCWVTGMDVNDRLPPFPKQVKVPIIMENHICDAKYHLGAYTGDDVRLVRDML 184
 DB 151 PGMPCWVTGMDVNDRLPPFPKQVKVPIIMENHICDAKYHLGAYTGDDVRLVRDML 210

QY 185 CAGNTRDSCQDGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYIYLDWIHY 244
 DB 211 CAGNTRDSCQDGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYIYLDWIHY 270

QY 245 VPKKP 249
 DB 271 VPKKP 275

RESULT 2

Q86TM8 PRELIMINARY; PRT; 275 AA.

AC Q86TM8
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to trypsin, alpha.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RA EMBL; BC028059; AAH28059.1; -
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR009003; Cys Ser trypsin.
 DR InterPro; IPR001254; Peptidase S1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00134; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 SQ SEQUENCE 275 AA; 30713 MW; 189C3BBBCB473A3 CRC64;

Query Match 92.3%; Score 1286; DB 4; Length 275;
 Best Local Similarity 93.5%; Pred. No. 7.4e-118;
 Matches 229; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 5 IVGGQAPRSKWPQVSLRVHGPVWVHFCGSLIHPQWVLTAAACVGPDKDLAALRVQL 64
 DB 31 IVGGQAPRSKWPQVSLRVHGPVWVHFCGSLIHPQWVLTAAACVGPDKDLAALRVQL 90

QY 65 REQHLYYQDQLLPVSRRIIVHPQFYTAQIGADIALLELEPVPKVS SHVHTVTLPPASETFP 124
 DB 91 REQHLYYQDQLLPVSRRIIVHPQFYTAQIGADIALLELEPVPKVS SHVHTVTLPPASETFP 150

QY 125 PGMPCWVTGMDVNDRLPPFPKQVKVPIIMENHICDAKYHLGAYTGDDVRLVRDML 184
 DB 151 PGMPCWVTGMDVNDRLPPFPKQVKVPIIMENHICDAKYHLGAYTGDDVRLVRDML 210

QY 185 CAGNTRDSCQDGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYIYLDWIHY 244
 DB 211 CAGNTRDSCQDGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYIYLDWIHY 270

QY 245 VPKKP 249
 DB 271 VPKKP 275

RESULT 2

Q86TM8 PRELIMINARY; PRT; 275 AA.

AC Q86TM8
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to trypsin, alpha.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, Lung, and Testis;
 RA Strausberg R.;
 RA EMBL; BC028059; AAH28059.1; -
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR009003; Cys Ser trypsin.
 DR InterPro; IPR001254; Peptidase S1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00134; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 SQ SEQUENCE 275 AA; 30713 MW; 189C3BBBCB473A3 CRC64;

Query Match 92.3%; Score 1286; DB 4; Length 275;
 Best Local Similarity 93.5%; Pred. No. 7.4e-118;
 Matches 229; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 5 IVGGQAPRSKWPQVSLRVHGPVWVHFCGSLIHPQWVLTAAACVGPDKDLAALRVQL 64
 DB 31 IVGGQAPRSKWPQVSLRVHGPVWVHFCGSLIHPQWVLTAAACVGPDKDLAALRVQL 90

QY 65 REQHLYYQDQLLPVSRRIIVHPQFYTAQIGADIALLELEPVPKVS SHVHTVTLPPASETFP 124
 DB 91 REQHLYYQDQLLPVSRRIIVHPQFYTAQIGADIALLELEPVPKVS SHVHTVTLPPASETFP 150

QY 125 PGMPCWVTGMDVNDRLPPFPKQVKVPIIMENHICDAKYHLGAYTGDDVRLVRDML 184
 DB 151 PGMPCWVTGMDVNDRLPPFPKQVKVPIIMENHICDAKYHLGAYTGDDVRLVRDML 210

QY 185 CAGNTRDSCQDGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYIYLDWIHY 244
 DB 211 CAGNTRDSCQDGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYIYLDWIHY 270

QY 245 VPKKP 249
 DB 271 VPKKP 275

RESULT 2

Q86TM8 PRELIMINARY; PRT; 276 AA.

AC Q86TM8
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to trypsin, alpha (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RA EMBL; BC051852; AAH51852.1; -
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR009003; Cys Ser trypsin.
 DR InterPro; IPR001254; Peptidase S1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 FT NON_TER
 SQ SEQUENCE 276 AA; 30869 MW; 8CDC5BA037955F9C CRC64;

Query Match 92.3%; Score 1286; DB 4; Length 276;
 Best Local Similarity 93.5%; Pred. No. 7.4e-118;
 Matches 229; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 5 IVGGQAPRSKWPQVSLRVHGPVWVHFCGSLIHPQWVLTAAACVGPDKDLAALRVQL 64

DB 151 PGMPCWVTGMDVNDRLPPFPKQVKVPIIMENHICDAKYHLGAYTGDDVRLVRDML 210

QY 185 CAGNTRDSCQDGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYIYLDWIHY 244
 DB 211 CAGNTRDSCQDGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVYIYLDWIHY 270

QY 245 VPKKP 249
 DB 271 VPKKP 275

RESULT 3

Q86TM8 PRELIMINARY; PRT; 276 AA.

AC Q86TM8
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to trypsin, alpha (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RA EMBL; BC051852; AAH51852.1; -
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR009003; Cys Ser trypsin.
 DR InterPro; IPR001254; Peptidase S1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 FT NON_TER
 SQ SEQUENCE 276 AA; 30869 MW; 8CDC5BA037955F9C CRC64;

Query Match 92.3%; Score 1286; DB 4; Length 276;
 Best Local Similarity 93.5%; Pred. No. 7.4e-118;
 Matches 229; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 5 IVGGQAPRSKWPQVSLRVHGPVWVHFCGSLIHPQWVLTAAACVGPDKDLAALRVQL 64


```

Db 32 IVGGQAPRSKWPQVSLRVDRYWMHFCGSLIHPQWLTAAHCLGPDVKDLATLRVOL 91
QY 65 REQHLHYQDQLLPVSRRIIVHPQFYTAQIAGDIALLELEPEPVKVS HVHTVTLPPASETFP 124
Db 92 REQHLHYQDQLLPVSRRIIVHPQFYIQTGADIALLELEPEPVNISSRVHTVMLPPASETFP 151
QY 125 PGMPCWVTGWGVDNDELRPLPPFPPLKQVKVPIEMENHICDAKYHLGAYTGDDVRIVRDDML 184
Db 152 PGMPCWVTGWGVDNDELRPLPPFPPLKQVKVPIEMENHICDAKYHLGAYTGDDVRIVRDDML 211
QY 185 CAGNTRRDS CGDGGPLVCKVNGTWLQAGVVSWMGEGCAQPNRPPIYTRVTVYLDWIHY 244
Db 212 CAGNTRRDS CGDGGPLVCKVNGTWLQAGVVSWMGEGCAQPNRPPIYTRVTVYLDWIHY 271
QY 245 VPKKP 249
Db 272 VPKKP 276

```

RESULT 4

```

Q7YS62
ID Q7YS62 PRELIMINARY; PRT; 275 AA.
AC Q7YS62;
DT 01-OCT-2003 (TremBLrel. 25, Created)
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
DE Trypsinase (EC 3.4.21.59).
GN MTCL.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Dacre K.J.; McAleese S.; Pemberton A.; McGorun B.C.;
RT "cDNA sequence of two equine mast cell proteases and the differential
RT expression of trypsinase and equine mast cell protease-1 in equine
RT tissues."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Dacre K.J.;
RT "The role of mast cells and mast cell proteases in equine heaves.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ515902; CAD56807.1; -.
KW Hydrolase.
SQ SEQUENCE 275 AA; 30476 MW; 718F57A4DBEE21ED CRC64;

```

```

Query Match 78.4%; Score 1092.5; DB 6; Length 275;
Best Local Similarity 77.8%; Pred. No. 7, 1e-99;
Matches 193; Conservative 19; Mismatches 35; Indels 1; Gaps 1;

QY 1 LEKR-IVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWLTAAACVGPDKDLAA 59
Db 26 LEREGIVGGQASGSKWPQVSLRKNTEYKXHFHFCGSLIHPQWLTAAHCVGPDIEDFRD 85
QY 60 LRVLREQHLYQDQLLPVSRRIIVHPQFYTAQIAGDIALLELEPEPVKVS HVHTVTLPPA 119
Db 86 IRVLREQHLYQDQLLPVSRRIIVHPQFYIQTGADIALLELEPEPVNISSRVHTVMLPPA 145
QY 120 SETPPGMPGCVWVTGWGVDNDELRPLPPFPPLKQVKVPIEMENHICDAKYHLGAYTGDDVRI 179
Db 146 SETPPGPGTGWGVDNDELRPLPPFPPLKQVKVPIEMENHICDAKYHLGAYTGDDVRI 205
QY 180 RDDLMLCAGNTRRDS CGDGGPLVCKVNGTWLQAGVVSWMGEGCAQPNRPPIYTRVTVYLD 239
Db 206 QADMLCAGNRRHDS CGDGGPLVCKVNGTWLQAGVVSWMGEGCAQPNRPPIYTRVTVYLD 265
QY 240 WIHYVVK 247
Db 266 WIQYVVK 273

```

```

RESULT 5
QBHYJ2
ID QBHYJ2 PRELIMINARY; PRT; 271 AA.
AC QBHYJ2;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Trypsinase.
GN BLT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Gumbacurta A.; Fiorucci L.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF515641; AAN77096.1; -.
DR FIR; S24190; S24190.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF00089; trypsin; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
SQ SEQUENCE 271 AA; 29902 MW; 1B68B5A188A80CFA CRC64;

Query Match 75.4%; Score 1051; DB 6; Length 271;
Best Local Similarity 75.9%; Pred. No. 8, 2e-95;
Matches 186; Conservative 22; Mismatches 3; Indels 0; Gaps 0;

QY 5 IVGGQAPRSKWPQVSLRVHGPYWMHFCGSLIHPQWLTAAACVGPDKDLALRVOL 64
Db 27 IVGGQAPGSRPQVSLRVSRVRRHHCGLIHPQWLTAAHCVGPEVHGSPYRVOL 86
QY 65 REQHLHYQDQLLPVSRRIIVHPQFYTAQIAGDIALLELEPEPVKVS HVHTVTLPPASETFP 124
Db 87 REQHLHYQDQLLPVSRRIIVHPQFYIQTGADIALLELEPEPVNISSRVHTVMLPPASETFP 146
QY 125 PGMPCWVTGWGVDNDELRPLPPFPPLKQVKVPIEMENHICDAKYHLGAYTGDDVRIVRDDML 184
Db 147 PGTQCWVTGWGVDNDELRPLPPFPPLKQVKVPIEMENHICDAKYHLGAYTGDDVRIVRDDML 206
QY 185 CAGNTRRDS CGDGGPLVCKVNGTWLQAGVVSWMGEGCAQPNRPPIYTRVTVYLDWIHY 244
Db 207 CAGSDGRDSCGDGGPLVCKVNGTWLQAGVVSWMGEGCAQPNRPPIYTRVTVYLDWIHY 266
QY 245 VPKKP 249
Db 267 VPQGP 271

RESULT 6
Q921N4
ID Q921N4 PRELIMINARY; PRT; 273 AA.
AC Q921N4;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Mast cell protease 7.
GN MCP7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; BC011328; AAHL1328.1; -.
DR HSP; P00761; IAN1.
DR MGD; MGI:96943; Mcpt7.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 273 AA; 30332 MW; 5141746514035BE CRC64;

Query Match 75.1%; Score 1046; DB 11; Length 273;
Best Local Similarity 76.1%; Pred. No. 2.6e-94;
Matches 185; Conservative 17; Mismatches 41; Indels 0; Gaps 0;

Qy 5 IVGGQAPRSKWPQVSLRVHGPYMHFCGSLIHPQWLTAAACVGPVDVKDLAALRVOL 64
Db 29 IVGGQAHGKWPQVSLRVHGPYMHFCGSLIHPQWLTAAHCVGPVDVADPKVRVOL 88

Qy 65 REQLHYQDQLPVSRILVHPQFYTAQIGADIALLELEPVPKSSHVHTVTLPPASETFP 124
Db 89 RKQLYVYHDLMTYSQITHPDFIVQDGDADIALKLTPVNI SDYVHPVPLPASETFP 148

Qy 125 PGMPCWVTGWDVNDRLPPFPKQVKVPIEMNHICDAKYHLGAYTGDDVIRVDDML 184
Db 149 SGTLCWVTGNGINDGNVNLPPFPKQVKVPIEMNHICDLKYLITGDNVHIVRDDML 208

Qy 185 CAGNTRDSCGSDGGGLVCKVNGTWTQAGVVSNGEGCAQPNRGIYTRVYILDWHY 244
Db 209 CAGNEGHSQSDGGGLVCKVETWTQAGVVSNGEGCAQPNRGIYTRVYILDWHY 268

Qy 245 VPK 247
Db 269 VPK 271

RESULT 7
Q96RZ7 PRELIMINARY; PRT; 233 AA.
AC Q96RZ7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mast cell tryptase beta III.
GN TRYPTASEB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21096910; PubMed=11157797;
RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA Higgs D.R.;
RT "Sequence, structure and pathology of the fully annotated terminal 2
RT Mb of the short arm of human chromosome 16.";
RL Hum. Mol. Genet. 10:339-352(2001).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AE006466; AAK61270.1; -.
DR HSP; P00761; IAN1.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.

DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 233 AA; 25874 MW; 246A96C71B2CE6D0 CRC64;

Query Match 73.4%; Score 1022; DB 4; Length 233;
Best Local Similarity 97.4%; Pred. No. 4.8e-92;
Matches 186; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 IVGGQAPRSKWPQVSLRVHGPYMHFCGSLIHPQWLTAAACVGPVDVKDLAALRVOL 64
Db 31 IVGGQAPRSKWPQVSLRVHGPYMHFCGSLIHPQWLTAAHCVGPVDVADPKVRVOL 90

Qy 65 REQLHYQDQLPVSRILVHPQFYTAQIGADIALLELEPVPKSSHVHTVTLPPASETFP 124
Db 91 REQLHYQDQLPVSRILVHPQFYTAQIGADIALLELEPVPKSSHVHTVTLPPASETFP 150

Qy 125 PGMPCWVTGWDVNDRLPPFPKQVKVPIEMNHICDAKYHLGAYTGDDVIRVDDML 184
Db 151 PGMPCWVTGWDVNDRLPPFPKQVKVPIEMNHICDAKYHLGAYTGDDVIRVDDML 210

Qy 185 CAGNTRDSCQ 195
Db 211 CAGNTRDSCQ 221

RESULT 8
Q9XSM1 PRELIMINARY; PRT; 273 AA.
AC Q9XSM1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tryptase (EC 3.4.21.59).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Bone marrow;
RX MEDLINE=20308142; PubMed=10848900;
RA Pemberton A.D., McAliese S.M., Huntley J.F., Collie D.D.S.,
RA Scudamore C.L., McEuen A.R., Walls A.F., Miller H.R.P.;
RT "cDNA sequence of two sheep mast cell tryptases and the differential
RT expression of tryptase and sheep mast cell proteinase-1 in lung,
RT dermis and gastrointestinal tract.";
RL Clin. Exp. Allergy 30:818-883(2000).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; Y18223; CAB41988.1; -.
DR HSP; P20231; IAO1.
DR MEROPS; S01.118; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.

```

DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Protease; Serine protease.
 FT CHAIN 29 273 TRYPTASE.
 SQ SEQUENCE 273 AA; 30156 MW; 88A19DC779053898 CRC64;

Query Match 73.2%; Score 1019; DB 6; Length 273;
 Best Local Similarity 71.8%; Pred. No. 1.1e-91;
 Matches 176; Conservative 29; Mismatches 40; Indels 0; Gaps 0;

QY 5 IVGQEAPEAKSPWQVSLRVHGFYMMHFCGSLIHPQWVLTAAACVGPDKLAALRVQL 64
 Db 29 IIGKEAPGSRPWQVSLRVHGFYMMHFCGSLIHPQWVLTAAACVGPDKLAALRVQL 88

QY 65 RQHLHYQDLPLVSRILVHGFYTAQIGADIALLEPEPVKSVSHVHTVTLPPASETFP 124
 Db 89 RQHLHYQDLPLVSRILVHGFYTAQIGADIALLEPEPVKSVSHVHTVTLPPASETFP 148

QY 125 PGMPQWVTGWDVNDERLPPFPPLKQVPIVMEHICDAKYLHGYTGDVRIVRDDML 184
 Db 149 PGQCVWVTGWDVNDERLPPFPPLKQVPIVMEHICDAKYLHGYTGDVRIVRDDML 208

QY 185 CAGNTRRDSQGDGGLVCKVNGTGLQAGVSWGEGCAQPNRPGIYTRVYLYDWHY 244
 Db 209 CAGDGRDSCQGDGGLVCKVNGTGLQAGVSWGEGCAQPNRPGIYTRVYLYDWHY 268

QY 245 VPKKP 249
 Db 269 VPQEP 273

RESULT 9
 Q29464 PRELIMINARY; PRT; 237 AA.
 ID Q29464
 AC Q29464
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Trypsin (EC 3.4.21.59) (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver capsule;
 RX MEDLINE=96203914; PubMed=8620861;
 RA Pallaro M., Gambacorta A., Fiorucci L., Mignogna G., Barra D.,
 RA Ascoli F.;
 RT "CDNA cloning and primary structure of trypsin from bovine mast cells
 and evidence of the expression of bovine pancreatic trypsin inhibitor
 mRNA in the same cells."
 RL Eur. J. Biochem. 237:100-105(1996).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL; X94982; CAA64438.1; --
 DR PIR; S68702; S68702.
 DR HSSP; P20231; IAOL.
 DR MEROPS; S01.118; --
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0030019; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR Hydrolase; Protease; Serine protease.
 FT NON_TER 1 1

SQ SEQUENCE 237 AA; 26550 MW; EA537A75294EFFBA CRC64;
 Query Match 72.1%; Score 1005; DB 6; Length 237;
 Best Local Similarity 75.4%; Pred. No. 2.3e-90;
 Matches 178; Conservative 21; Mismatches 37; Indels 0; Gaps 0;

QY 14 SKWPQVSLRVHGFYMMHFCGSLIHPQWVLTAAACVGPDKLAALRVQLRQHLHYQD 73
 Db 2 SQMPQVSLRVHGFYMMHFCGSLIHPQWVLTAAACVGPDKLAALRVQLRQHLHYQD 61

QY 74 QLLPVSRILVHGFYTAQIGADIALLEPEPVKSVSHVHTVTLPPASETFP 133
 Db 62 QLLPVSRILVHGFYTAQIGADIALLEPEPVKSVSHVHTVTLPPASETFP 121

QY 134 WGDVNDERLPPFPPLKQVPIVMEHICDAKYLHGYTGDVRIVRDDMLCAGNTRRDS 193
 Db 122 WGVNONGRLPPFPPLKQVPIVMEHICDAKYLHGYTGDVRIVRDDMLCAGNTRRDS 181

QY 194 CQDSDGGLVCKVNGTGLQAGVSWGEGCAQPNRPGIYTRVYLYDWHYVPKKP 249
 Db 182 CQDSDGGLVCKVNGTGLQAGVSWGEGCAQPNRPGIYTRVYLYDWHYVPKKP 237

RESULT 10
 Q80UR4 PRELIMINARY; PRT; 318 AA.
 ID Q80UR4
 AC Q80UR4
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mast cell protease-11.
 GN MCP11.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Bone-marrow;
 RA Wong G.W., Yasuda S., Li L., Stevens R.L.;
 RT "Cloning and characterization of mouse mast cell protease-11 (mMCP-11)."
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY261775; AAP21675.1; --
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR Protease.
 SQ SEQUENCE 318 AA; 35037 MW; 6F69B6653FF54FEA CRC64;

Query Match 48.7%; Score 678; DB 11; Length 318;
 Best Local Similarity 52.4%; Pred. No. 3.9e-58;
 Matches 130; Conservative 37; Mismatches 75; Indels 6; Gaps 2;

QY 5 IVGQEAPEAKSPWQVSLRVHGFYMMHFCGSLIHPQWVLTAAACVGPDKLAALRVQL 61
 Db 35 IVGQEAPEAKSPWQVSLRVHGFYMMHFCGSLIHPQWVLTAAACVGPDKLAALRVQL 94

QY 62 VOLRQHLHYQDLPLVSRILVHGFYTAQIGADIALLEPEPVKSVSHVHTVTLPP 118
 Db 95 VOLRQHLHYQDLPLVSRILVHGFYTAQIGADIALLEPEPVKSVSHVHTVTLPP 154

QY 119 ASETFPFGMPFQWVTGWDVNDERLPPFPPLKQVPIVMEHICDAKYLHGYTGDVRI 178
 Db 119 ASETFPFGMPFQWVTGWDVNDERLPPFPPLKQVPIVMEHICDAKYLHGYTGDVRI 178

```

Db 155 ASLRSSKTKCWAGVGVNIENWMLPPPHYHLREVAIVPIVENNDCEQKYQTNSSSDSTTRI 214
QY 179 VRDMLCAGNTRRDSQSGGGLVCKVNGTQWLGAGVSWGEGCAQPNRPGIYTRYYL 238
Db 215 IKDDMLCAGKEGRDCKAGSGGLVCRWNCWVQGVVSWGICGGLPDPFGVITRVMSYV 274
QY 239 DWIHHYVP 246
Db 275 SWIKCYVP 282

RESULT 11
Q8SQ44 PRELIMINARY; PRT; 277 AA.
AC Q8SQ44;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tryptase precursor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Sato M., Yoshida S., Iida K., Tomozawa T., Kido H., Yamashita M.;
RT "A Novel Influenza A Virus Activating Enzyme from Porcine Lungs:
RT Purification and Characterization.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB080655; BAB8761.1; -.
DR HSSP; P00761; IAMI.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Protease; Serine protease; Signal.
FT SIGNAL 1 30
FT CHAIN 31 277 TRYPTASE.
SQ SEQUENCE 277 AA; 30407 MW; 35FC8B569C0ED4C5 CRC64;

Query Match 46.7%; Score 651; DB 6; Length 277;
Best Local Similarity 50.6%; Pred. No. 1.5e-55;
Matches 126; Conservative 39; Mismatches 76; Indels 8; Gaps 3;

QY 5 IVGGOEAPRSKWPQVSL---RVHCPYMHFGGSLIHPQWLTAAACVGDVVDKDLAALR 61
Db 31 IVGHDVSTKYPQVQVSLRSYRVKLGWVHGHGSLVHPQWLTAAHCVDSHNLKPQDVR 90
QY 62 VQLREQLHYQDQLLPVSRRIIVHPOFY-TAQIGADIALLEELPEPVKSSHVHTVTLPPAS 120
Db 91 VQVQLKLYDGDQLTKVQIIRHPKYLGFAGKGADIALQLLEAPLTLSARVNVGTPSAT 150
QY 121 ETFPPGMECWTVGWGDVNDERLPPFPPLKQVYPMENHICDAKYHLGAVTGDDVRIVR 180
Db 151 LKVPKGRKRCVTVGWNIRKHLNLSLPPYHLQVEVEPIVANKVCKHYR---TGPNKPIK 206
QY 181 DDMLCAGNTRRDSQSGGGLVCKVNGTQWLGAGVSWGEGCAQPNRPGIYTRYIYLDW 240
Db 207 ADMLCAGSKGLDSCQSGGGLVCKVNGTQWLGAGVSWGEGCAQPNRPGIYTRYIYLDW 240
QY 241 IHHYVPKPK 249
Db 267 IYQVPRSP 275

```

```

RESULT 12
Q99MS4 PRELIMINARY; PRT; 279 AA.
AC Q99MS4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Implantation serine proteinase 2.
DE ISP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21361749; PubMed=11467974;
RA O'Sullivan C.M., Liu S.Y., Rancourt S.L., Rancourt D.E.;
RT "Regulation of the trypsin-related proteinase ISP2 by progesterone in
RT endometrial gland epithelium during implantation in mice.";
RL Reproduction 122:235-244 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/c; TISSUE=Uterus;
RA Shen Q.-X., Wang J., Huang Z.-P.;
RT "Identification of endometrial factors involved in mouse embryo
RT implantation.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AF305425; AAK15264.2; -.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.315; -.
DR MGD; MGI:2149952; Isp2.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 279 AA; 30986 MW; 81C43A59935244D7 CRC64;

Query Match 45.9%; Score 640; DB 11; Length 279;
Best Local Similarity 49.8%; Pred. No. 1.8e-54;
Matches 120; Conservative 36; Mismatches 81; Indels 4; Gaps 2;

QY 5 IVGGOEAPRSKWPQVSLRVHGPY---WMHFGGSLIHPQWLTAAACVGDVVDKDLAALR 61
Db 31 IVGHSAPQGRKWPQVSLRIYRYTAFVWVHNGGSLIHPQWLTAAHCIREDADPSVR 90
QY 62 VQLREQLHYQDQLLPVSRRIIVHPOFYTAQIGADIALLEELPEPVKSSHVHTVTLPPASE 121
Db 91 IRVGEAVLYGKELLSVSRVIIHPDFVHAGLGSVALIQLAVSVQSPFNVPKLPSESL 150
QY 122 TFPFGMPQWTVGWGDVNDERLPPFPPLKQVYPMENHICDAKYHLGA-YTGDDVRIVR 180
Db 151 EVTKKDVCTVWGAVSTHRLPPYRLQVQVKIIDNSLCEEMVHNATRNHQKUIL 210
QY 181 DDMLCAGNTRRDSQSGGGLVCKVNGTQWLGAGVSWGEGCAQPNRPGIYTRYIYLDW 240
Db 211 KDMLCAGNQGDSCVGDGGLVCKVNGTQWLTGVWSWGICALDFDFGVARVQSFLPW 270
QY 241 I 241

```

```
Db 271 I 271
RESULT 13
Q8BJR6 PRELIMINARY; PRT; 328 AA.
AC Q8BJR6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to MARAPIN precursor (Channel-activating protease 2-like
DE protein) (Pancrasin).
GN MPN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
EX MEDLINE=22345683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129SvEvTac;
RA Brathwaite M., Waeltz P., Schlessinger D., Nagaraja R.;
RA Bhagwandin V.J., Hau L.W., Mallen-St Clair J., Wolters P.J.,
RA Caughey G.H.;
RA "Structure and activity of human pancreasin, a novel tryptic serine
RT peptidase expressed primarily by the pancreas.";
RL J. Biol. Chem. 274:3363-3371 (2003).
DR EMBL; AK080281; BAC37864.1; -
DR EMBL; AY162410; AAO17162.1; -
DR EMBL; AF542056; AAO27572.1; -
DR MGD; MGI:2450123; Mpn.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYSPIN_DOM; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Protease.
SQ SEQUENCE 328 AA; 35789 MW; DC0B20F1AB3EB840 CRC64;
Query Match 42.8%; Score 596.5; DB 11; Length 328;
Best Local Similarity 45.1%; Pred No. 4e-50;
Matches 114; Conservative 48; Mismatches 74; Indels 17; Gaps 5;
QY 4 RIVGQEA PRSKWPQVSLRVHG PVMHFCGSLHPQWLTAACVGDVXD----- 56
Db 37 RVVGGNALEGEWPQVSLRNG---IHFCGSLIAPTWLTAACFS-NTSDISIYQVL 92
QY 57 LAALRVLRQEHLYQDQLLPVSRILVHPQFYTAIGADIALLEBPVKVSHVTVTL 116
Db 93 LGALKIQPGPHALY-----VPVKQKSNPQYQGMASADVALVELQGPVTFNTYILPVCL 148
117 PPASETPPGMPCWVTGWGDVDNDRLPPLPKQVKVPIIMENHICDAKYHLGAYTGDDV 176
149 PDPSVIFESGMNCWVTGWGSESDQRLNPNRVLKLAVPIIDTPKCNLLYNKVDSDQL 208
177 RIVRDDMLCAG--NTRRDSQCGSGPLVCKVNGTGLQGVVSWGEGCAQPNRPGIYTRV 234
209 KTIKDDMLCAGFAEGKKDACKGDSGGPLVCLVDQSVQAGVISWGEGCARRNRPGVYIRV 268
235 TYILDWIIHHYVPK 247
269 TSHKWHQIIE 281
RESULT 14
Q96RZ8 PRELIMINARY; PRT; 321 AA.
AC Q96RZ8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE HS transmembrane tryptase, gene name TMT, AF175522.1.
DE TRPA.
GN TRPA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21096910; PubMed=11157797;
RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA Higgs D.R.;
RA "Sequence, structure and pathology of the fully annotated terminal 2
RT Mb of the short arm of human chromosome 16.";
RL Hum. Mol. Genet. 10:339-352 (2001).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AE006466; AAK61269.1; -
DR HSSP; P00761; 1ANL.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYSPIN_DOM; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
KW Hydrolase; Protease; Serine protease; Transmembrane.
SQ SEQUENCE 321 AA; 33829 MW; PFF5089EDC4FC73D CRC64;
Query Match 42.3%; Score 589.5; DB 4; Length 321;
Best Local Similarity 48.4%; Pred No. 1.9e-49;
Matches 118; Conservative 33; Mismatches 80; Indels 13; Gaps 6;
QY 4 RIVGQEA PRSKWPQVSLRVHG PVMHFCGSLHPQWLTAACVGDVXDLAALRVQ 63
Db 37 RIVGHAAPAGAWPQVSLRLRR---VHVCGLSLSPQWLTAACFSGSLNS-SDYQVH 92
QY 64 LREQHLYYQDQLLPVSRILVHPQFYTAIG--ADIALLEBPVKVSHVHTVTLPPASE 121
Db 93 LGELBITLSPHFSTVRQIILHSS-PSGQFGTGDIALVELSVPTLSSRIPLVCLPEASD 151
122 TFPMPGMCWVTGWGDVDNDRLPPLPKQVKVPIIMENHICDAKYHLGAYTGDDVIRVD 181
152 DFCFQIRCWVTGWGTYRGEPLPPYSIREVKVSVVDTETCRD-----YFGGSGSILQP 206
182 DMLCAGNTRRDSQCGSGPLVCKVNGTGLQGVVSWGEGCAQPNRPGIYTRVTVLDM 241
Db 207 DMLCARGF-GDACQDSDSGPLVQVNGAWVQAGIVSWGEGCGRPNRPGYTRVPAYNWI 265
```

Search completed: July 22, 2004, 15:25:07
Job time : 85 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 22, 2004, 15:33:07 ; Search time 3069 Seconds
(without alignments)
2422.836 Million cell updates/sec

Title: US-09-598-982-21
Perfect score: 1393
Sequence: 1 LEXRIVGQAEPRSKWPMQV.....IYTRVYYLDWIHHVVKP 249

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+pn.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09598982/runat_20072004_064410_6500/app_query.fasta_1.391
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09598982@cgn_1_1_6425/runat_20072004_064410_6500 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hcc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hcc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_nam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1263	90.7	1030	12	BM919268 AGENCOURT
2	1109.5	79.6	904	13	BQ720404 AGENCOURT
3	1062	76.2	589	13	BU071733 im33a09.y
4	1060	76.1	619	14	CD671851 im33a09.y
5	1024	73.5	1000	12	BI413250 602986390
6	1023	73.4	930	14	CB203717 AGENCOURT
7	972	69.8	635	14	CD671891 fg08b10.y
8	966	69.3	642	14	CD672689 fg15a06.y
9	960	68.9	722	13	BX091892 BX091892
10	945.5	67.9	811	12	BG697540 602660760
11	915	65.7	502	13	BQ082929 K-RST0144
12	905	65.0	581	13	BU787772 1034c08.y
13	891	64.0	736	12	BG542089 602571309
14	855	61.4	929	14	CF583026 AGENCOURT
15	845.5	60.7	806	14	CF553058 AGENCOURT
16	832	59.7	917	13	BQ721078 AGENCOURT
17	800	57.4	686	13	BU073263 im33a09.x
18	800	57.4	859	14	CF583025 AGENCOURT
19	789	56.6	639	9	AA131142 z131b01.r
20	785	56.4	678	12	BG483591 602503309
21	773	55.5	671	14	CB840425 M15E-0715
22	715	51.3	474	10	AW823937 uf61e03.y
23	690	49.5	558	12	BI790801 id09c06.y
24	681	48.9	512	10	BF724180 bx01h02.y
25	680	48.8	699	14	CA438721 UI-H-DT1-
26	678	48.7	1219	11	AK081986 Mus muscu
27	672	48.2	690	14	CA439686 UI-H-DT1-
28	662	47.5	688	12	BQ003361 UI-H-E11-
29	657	47.2	693	12	BM991728 UI-H-DT1-
30	654	46.9	692	12	BM989945 UI-H-D10-
31	653	46.9	1928	11	AK040500 Mus muscu
32	644	46.2	371	10	BF359130 QV3-ET006
33	638	45.8	682	14	CA425354 UI-H-DT0-
34	629.5	45.2	676	12	BG964077 602828831
35	624	44.8	376	10	BF850308 CM3-EN007
36	623	44.7	660	14	CB589106 AGENCOURT
37	622	44.7	620	9	AA049080 mj50f09.r
38	618	44.4	411	10	BE862270 UI-M-BH0-
39	599	43.0	525	12	BI775716 468400 MA
40	598	42.9	545	12	BI681216 460544 MA
41	596.5	42.8	1150	11	AK080281 Mus muscu
42	592.5	42.5	730	29	CC546157 CH240_429
43	584	41.9	581	14	CA867461 1r28f02.y
44	566	40.6	538	10	BE751979 204246 MA
45	560	40.2	569	12	BI287271 UI-R-CW0s

ALIGNMENTS

RESULT 1
BM919268
LOCUS BM919268 1030 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT_6715837 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5748499
5', mRNA sequence.
ACCESSION BM919268
VERSION BM919268.1 GI:19369647
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1030)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LHAM12776 row: f column: 20
 High quality sequence stop: 719.

FEATURES

Location/Qualifiers
 1. 1030
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5748499"
 /lab_host="DH10B"
 /clone.lib="NIH_MGC 120"

/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPOK6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 4.9e-117 Length: 1030
 Score: 1263.00 Matches: 228
 Percent Similarity: 93.93% Conservative: 4
 Best Local Similarity: 92.31% Mismatches: 13
 Query Match: 90.67% Indels: 2
 DB: 12 Gaps: 0

US-09-598-982-21 (1-249) x BM919268 (1-1030)

Qy 5 IleValGlyGlnGluAlaProArgSerIysTrpProTrpGlnValSerLeuArgVal 24
 Db 123 ATCTGCGGGGTACAGGAGGCCCCCAGGAGCAAGTGGCTGGCAGGTGAGCTGAGAGTC 182
 Qy 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
 Db 183 CGGACCGGATGAGTGGATGCACTTCTGTGGGGGCTCCCTCATCCACCCGAGTGGGTGCTG 242
 Qy 45 ThrAlaAlaAlaCysValGlyProAspValIysAspLeuAlaAlaLeuArgValGlnLeu 64
 Db 243 ACCGGCGGCACTGCTGGGACCGGACGTCAGAGATCTGGCCACCTTCAGGTGCACTG 302
 Qy 65 ArgGlnGlnHisLeuTyrTrpGlnAspGlnLeuLeuProValSerArgIleValHis 84
 Db 303 CGGAGAGCAGCACCTCTACTACAGGACGAGTGTGGCGGTGAGGATCATCGTGAC 362
 Qy 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuGluLeuGluPro 104
 Db 363 CCACAGTTCATCATCACCAGCTGGAGCGGATATCGCCCTGTGGAGCTGGAGAGCCC 422
 Qy 105 ValIysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
 Db 423 GTGAACATCTCCACCGCGTCACACGCTCATGTGCCCTGTCTGGAGACTTCCCT 482
 Qy 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
 Db 483 CCGGGGATGCGTCTGGGTACGTGCTGGGGCGATGTGACAAATGATGAGCCCTCCCA 542
 Qy 145 ProProPheProLeuLysGlnValIysValProIleMetGluAsnHisIleCysAspAla 164

Db 543 CCGCATTTCCCTGAAAGCAGGTGAAGTCCCAATAATGAAAAACCACTTTGTGACGCA 602
 Qy 165 LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspMetLeu 184
 Db 603 AAATACCACCTTGGCGCTTACACGGAGAGACATCCGCATCATCCGAGGACATGCTG 662
 Qy 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
 Db 663 TGTCCCGGGAACCCCGAGGACTCATGCCAGGCGGACTCTGGAGGGCCCTTGTGTGC 722
 Qy 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrpGly--GluGlyCysAlaG 224
 Db 723 AAGGTGAATGGCACTGGCTACAGCGGGGTGTGTGAGTGGGACGAGGGGCTGTGCC 782
 Qy 224 lnProAsnArgProGlyLysTyrThrArgValThrTyrLeuAspTrpIleHisIst 244
 Db 783 AGCCCAACCGCGCTGGCATCTACACCGGTGTCCTACTTGGACTGGATCACCACCT 842
 Qy 244 YrValProLysLysPro 249
 Db 843 ATGTCCCAAAAAGCG 859

RESULT 2

BQ720404

LOCUS

DEFINITION

AGENCOURT 8477973 Lupski sympathetic_trunk Homo sapiens cDNA clone

IMAGE:6196776 5', mRNA sequence.

ACCESSION

BQ720404

VERSION

BQ720404.1 GI:21859301

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 904)

AUTHORS

NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LHAM13605 row: m column: 01

High quality sequence stop: 587.

Location/Qualifiers

1. 904

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6196776"

/sex="male"

/tissue type="sympathetic trunk"

/dev stage="adult, 16 yr"

/lab_host="DH10B"

/clone.lib="Lupski sympathetic trunk"

/note="vector: pCMV-SPOK6 (Life Technologies); Site 1:

NotI; Site 2: SalI; cDNA made by oligo-dr priming.

Directionally cloned using the following adaptors:

5'-TCGACCCACCGCTCCG-3' and

5'-GACTAGTCTTAGATCGGAGCGGCCCT(15)-3'. Size selected >

1 kb for average insert length 1.9 kb. This is a primary

library, non-amplified. Library constructed by Life

Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor

College of Medicine); available through Life

Technologies."

ORIGIN

Alignment Scores:


```

Pred. No.: 1.39e-101 Length: 904
Score: 1109.50 Matches: 207
Percent Similarity: 88.24% Conservative: 3
Best Local Similarity: 86.97% Mismatches: 17
Query Match: 79.65% Indels: 11
DB: 13 Gaps: 1

US-09-598-982-21 (1-249) x BQ720404 (1-904)

Qy 5 lIeValGlyGlnGluAlaProArgSerIysTrpProTrpGlnValSerLeuArgVal 24
Db 100 ATCGTTGGGGTGTGAGAGGCCCGCCAGGAGCAAGTGGCCCTGCGAGGTGAGCTGAGAGTC 159
Qy 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
Db 160 CGCAGCCATGACTGGATGCACTTCTGGGGGGCTCCCTCATCCACCCCGAGTGGGTGCTG 219
Qy 45 ThrAlaAlaCysValGlyProAspValIysAspLeuAlaLeuArgValGlnLeu 64
Db 220 ACCGAGCGCACTGGTGGGACCG-----GTGCAACTG 252
Qy 65 ArgGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 84
Db 253 CGGAGCAGCACCTCTACTACGAGCAGCAGCTGCTGCCGGTGCAGCAGGATCATCTGCAC 312
Qy 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluPro 104
Db 313 CCACAGTTCTACACGCCCCAGATGGAGCGACATCGCCCTGTGGAGCTGGAGAGCGG 372
Qy 105 ValIysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
Db 373 GTGAACGTCTCCAGCCACGTCCACAGGTCAACCTGCCCTGCCCTCAGAGACCTTCCCC 432
Qy 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
Db 433 CCGGGAGTCCCGTGTGGGTCACTGGCTGGGGCGATGTGGCAATGATGAGCGCTCCCA 492
Qy 145 ProProPheProLeuIysGlnValIysValProIleMetGluAsnHisIleCysAspAla 164
Db 493 CCGGCATTTCTCTGAGCAGGTGAGTCCCATATGGAACCAACCATTTGTGACGCA 552
Qy 165 LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspMetLeu 184
Db 553 AAATACCACTTGGCGCTACACGGAGACGACGTCCGATCGTCCGTGACGACATGCTG 612
Qy 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
Db 613 TGTCCGGGAACACCCGAGGAGTCTATCCGAGGCGACTCCGAGGGCCCTCGTGGGC 672
Qy 205 LysValAsnGlyThrTrpLeuGlnAlaGlyVal-ValSerTrpGlyGluGlyCysAlaG1 224
Db 673 AACCGAATGGCCCTGGCTGGCAGCGGGCTGGGTCACTGGGGCGAGGGCTGGGCCG 732
Qy 224 nProAsnArgProGlyIleTyrThr-ArgValThrTyrTyrLeuAspTrp 240
Db 733 GCCCAACCGGGGGCTTCTACACCCCGGCCCTCTCCTCTGCGAATGG 782

```

```

RESULT 3
BU071733
LOCUS
DEFINITION
  BU071733.1 589 bp mRNA linear EST 27-AUG-2002
  im33a09.y1 Human insulinoma Homo sapiens cDNA clone IMAGE:6036761
  5' similar to SW:TRYB_HUMAN P20231 BETA-TRYPTASE PRECURSOR ; mRNA
  sequence.
ACCESSION
  BU071733
VERSION
  BU071733.1 GI:22512922
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 589)
  Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
  Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,

```

```

TITLE
JOURNAL
COMMENT
Hallier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: im33a09.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 433.
FEATURES
    source
    1..589
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:6036761"
    /tissue_type="insulinoma"
    /lab_host="DH10B (phage-resistant)"
    /clone_lib="Human insulinoma"
    /note="Organ: pancreas; Vector: pBluescript SK-; Site 1:
    XhoI; Site 2: EcoRI; Constructed with lambda ZapII system
    (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
    pBluescript SK- by Dr. H. Inoue following the Washington
    University protocol
    (http://genome.wustl.edu/est/lambda_protocol.shtml).
    Please contact Hiroshi Inoue, MD/PhD for further
    information on this library (Metabolism Division, Permutt
    Laboratory, Washington University School of Medicine, Box
    8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
    is a Washington University Pancreas EST project library."
ORIGIN
Alignment Scores:
Pred. No.: 4.62e-97 Length: 589
Score: 1062.00 Matches: 192
Percent Similarity: 99.48% Conservative: 0
Best Local Similarity: 99.48% Mismatches: 1
Query Match: 76.24% Indels: 0
DB: 13 Gaps: 0

US-09-598-982-21 (1-249) x BU071733 (1-589)

```

```

Qy 53 AspValIysAspLeuAlaLeuArgValGlnLeuArgGluHisLeuTyrGln 72
Db 10 GACGTCAAGGATCTGGCGCCCTCAGGGTGCACCTGGGGAGCAGCACCTCTACTACCAG 69
Qy 73 AspGlnLeuLeuProValSerArgIleIleValHisProGlnPheTyrThrAlaGlnIle 92
Db 70 GACCAGCTGTCTGCCGGTGCAGCAGGATCATCTGCACCCACACAGTTCTACACCGCCAGATC 129
Qy 93 GlValAlaAspIleAlaLeuLeuGluLeuGluProValIysValSerSerHisValHis 112
Db 130 GGAGCGGACATCGCCCTGTCTGGAGCTGGAGGCGGGTGAACGTCCTCAGCACCGTCCAC 189
Qy 113 ThrValThrLeuProProAlaSerGluThrPheProProGlyMetProCysTrpValThr 132
Db 190 ACGGTACCCCTGCCCTTCAGACCTTCCCCCGGGGATGCCGTGTGGGTACT 249
Qy 133 GlyTrpGlyAspValAspAsnAspGluArgLeuProProPheProLeuIysGlnVal 152
Db 250 GGCTGGGGCGATGTGGACAATGATGAGCGGCTCCCGCCATTTCTCTCTGAAGCAGGTG 309

```

153 LysValProIleMetGluAenHisIleCysAspAlaLysTyrHisLeuGlyAlaTyrThr 172
 310 AAGTCCCAATATGGAACACCACTTTGTGACCAAAATACCACTTGGCGCTACAG 369

173 GlyAspValAlaArgIleValArgAspMetLeuCysAlaGlyAenThrArgArgAsp 192
 370 GGAGACACATCGCATCGTCCGTGAGACATGCTGTGCGGGAACACCGGAGGAC 429

193 SerCysGlnGlyAspSerGlyGlyProLeuValCysLysValLanGlyThrTrpLeuGln 212
 430 TCATGCCAGGGGACTCCGAGGGCCCTGTGTGCAAGGTGAATGCACCTGCTGCAG 489

213 AlaGlyValValSerTrpGlyGluGlyCysAlaGlnProAsnArgProGlyIleTyrThr 232
 490 GCGGGCGTGTGTCAGTGGGCGAGGGTGTGCCAGCCCAACCGGCTGCATCTACACC 549

233 ArgValThrTyrTyrLeuAspTrpIleHisHisTyrVal 245
 550 CGTGTCACTACTACTTGGACTGGATCCACCACTATATGC 588

RESULT 4
 CD671851 619 bp mRNA linear EST 24-JUN-2003
 LOCUS
 DEFINITION fg07g11.y1 Human Iris cDNA (Normalized): fg Homo sapiens cDNA clone fg07g11.5', mRNA sequence.

ACCESSION
 VERSION CD671851
 KEYWORDS CD671851.1 GI:32173582
 SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE
 Eukaryota; Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 619)

AUTHORS Wistow G., Bernstein, S.L., Ray, S., Wyatt, M.K., Behal, A.,

Touhman, J.W., Bouffard, G., Smith, D. and Peterson, K.
 Expressed sequence tag analysis of adult human iris for the NEIBank Project: steroid-response factors and similarities with retinal pigment epithelium

JOURNAL Mol. Vis. 8 (4), 185-195 (2002)

MEDLINE 22103462

PUBMED 12107412

COMMENT Contact: Wistow G
 Section on Molecular Structure and Function
 National Eye Institute
 6/331, NIH, Bethesda, MD 20892-2740, USA
 Tel: 301 402 3452
 Fax: 301 495 0078
 Email: graeme@helix.nih.gov

Plate: 07 row: 9 column: 11

Seq primer: M13Rpl reverse primer (ABI).

Location/Qualifiers

1..619

FEATURES

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="fg07g11"

/tissue_type="Iris"

/dev_stage="Adult"

/lab_host="EMDH10B"

/clone_lib="Human Iris cDNA (Normalized): fg"

/notes="Organ: Eye; Vector: pCMVSPORT6; A human iris library (bx) was normalized by self-subtraction. One portion of double stranded plasmid DNA representing the library was linearized by NotI. This NotI digested library was used as a template for biotinylated RNA synthesis using SP6 RNA polymerase. Another portion of the double stranded plasmid library was converted to single-stranded circles in vitro using Gene II and Exonuclease III (Life Technologies). Single-stranded DNA (1 mg) was hybridized (Cot 500) with 41 mg of Bio-RNA and vector blocking oligonucleotides. The hybridized Bio-RNA/ss-circles were removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural

ORIGIN Sequencing Center (NISC) "

Alignment Scores: 7.95e-97 Length: 619

Pred. No.: 1060.00 Matches: 190

Score: 94.15% Conservative: 3

Best Local Similarity: 92.68% Mismatches: 12

Query Match: 76.09% Indels: 0

DB: 14 Gaps: 0

US-09-598-982-21 (1-249) x CD671851 (1-619)

Qy 8 GlyGlnGluAlaProArgSerLysTrpTrpGlnValSerLeuArgValHisGlyPro 27

Db 3 GGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 62

Qy 28 TyrTrpMetHisPheCysGlySerLeuIleHisProGlnTrpValLeuThrAlaAla 47

Db 63 TACTGGATGCACTTCTGTGGGGGCTCCCTCATCCACCCCGAGTGGTGGTGGTGG 122

Qy 48 AlaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeuArgGln 67

Db 123 CACTGCTGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 182

Qy 68 HisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHisProGlnPhe 87

Db 183 CACCTCTACTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 242

Qy 88 TyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluProValLysVal 107

Db 243 TACATCATCCAGACTGGAGCGGATATCCGCTGCTGGAGCTGGAGGAGCGCGTGAACATC 302

Qy 108 SerSerHisValHisThrValThrLeuProProAlaSerGluThrPheProGlyMet 127

Db 303 TCCAGCGCGCTCCACAGGTCATGTCGCCCTGCTCGGAGACCTTCCCGCCCGGGATG 362

Qy 128 ProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuProProPhe 147

Db 363 CCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 422

Qy 148 ProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAlaLysTyrHis 167

Db 423 CCGCTGAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 482

Qy 168 LeuGlyAlaTyrThrGlyAspValArgIleValArgAspMetLeuCysAlaGly 187

Db 483 CTTGGCCCTTACACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 542

Qy 188 AsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCysLysValAsn 207

Db 543 AACACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 602

Qy 208 GlyThrTrpLeuGln 212

Db 603 GGCACCTGGCTACAG 617

RESULT 5

BI413250 1000 bp mRNA linear EST 14-AUG-2001

LOCUS 602986390F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5142478 5',

DEFINITION mRNA sequence.

ACCESSION BI413250

VERSION BI413250.1

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1000)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: InCyt Genomics, Inc.
 Clone distribution: NCI-CCGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 High quality sequence start: 32
 High quality sequence stop: 849.

FEATURES

source

1..1000
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="Czech II"
 /db_xref="taxon:10090"
 /clone="IMAGE:5142478"
 /tissue_type="pooled lung tumors"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NCI CGAP Lu33"
 /note="Organ: lung; Vector: pT73D-Pac (Pharmacina) with a modified polylinker; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer [5', TGTTACCAATCGAAGTGGGAGCGCCCTGTGTTTTTTTTTTT 3']
 Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacina), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:
 Pred. No.: 7,38e-93 Length: 1000
 Score: 1024.00 Matches: 188
 Percent Similarity: 84.15% Conservative: 19
 Best Local Similarity: 76.42% Mismatches: 35
 Query Match: 73.51% Indels: 4
 DB: 12 Gaps: 0

US-09-598-982-21 (1-249) x BT413250 (1-1000)

QY 5 lleValGlyGlnGluAlaProArgSerLysTrpTrpGlnValSerLeuArgVal 24
 DB 75 ATCGTGGGAGCATGAGGCTTCTGAGAGTAAGTGGCCCTGGCAGGTGAGCTT 134
 QY 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
 DB 135 AAATTAACACTGGATATTTCTGGGAGGCTTCTCATCCACCCACAGTGGGTGCTC 194
 QY 45 ThrAlaAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 64
 DB 195 ACTGGGCACACTGTGTGGACCGGCACATCAAAAGCCACAGCTCTTCGGGTGCAGCTT 254
 QY 65 ArgGluGlnHisLeuTyrTrpGlnAspGlnLeuLeuProValSerArgIleIleValHis 84
 DB 255 COTGAGCAGTATCTACTATATGGGACCAAGCTCTCTTTTGAACCGGATCGTGGTGCAC 314
 QY 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluPro 104
 DB 315 CCCCACTATTACAGCCCGGGTGGGAGAGCTTCTGCTGAGCTTGAAGTCCCT 374
 QY 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
 DB 375 GTGAATGTCTCCACCATATCCACCCCATATCCCTGCCCCCTGCCTCGGAGACCTTCCCC 434
 QY 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144
 DB 435 CCTGGGACATCGTGTGGGTGACAGGCTGGGGCGACATTGATAATACGAGGCTCTCCCA 494

QY 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
 DB 495 CCTCTTATCTCTGAAGCAAGTGAAGTTCCTTCCATTGTGGAACAGCTGTGTGACCGG 554
 QY 165 Lys-TyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspAspMetIle 184
 DB 555 AAGTAACACACTGGCTCTACAGGGAGATGATTTTCCCATTTGTCCATGATGGCATGCT 614
 QY 184 uCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyProLeuValCy 204
 DB 615 GTGTGCTGGAATACCAAGAGAGACTCTCTGCAGGGCGATTACAGGGGGCCACTGGTCTG 674
 QY 204 sLysValAsnGlyThrTrpLeuGlnAlaGlyValValSer-TrpGlyGluGlyCysAlaG 224
 DB 675 CAAAGTGAAGGTACCTGGCTGCAGGCAGAGTGGTCACTGGGTGAGGGTGGCGCAC 734
 QY 224 ln-ProAsnArgProGlyIleTyrThrArgValThr-TyrTyrLeuAspTrpIleHisHi 243
 DB 735 AGCCCAACAAAGCTGGCATCTACACCGGTGACCATACTACTTAGACTGGATCCAGC 794
 QY 243 sTyrValPro 246
 DB 795 TTATGTCCCT 804

CB203717 930 bp mRNA linear EST 05-FEB-2003
 AGENCOURT_11288628 NIH_MGC_135 Mus musculus cDNA clone
 IMAGE:30142408 5', mRNA sequence.
 CB203717
 CB203717.1 GI:28240351
 EST
 Mus musculus (house mouse)
 Mus musculus
 ORGANISM
 REFERENCE
 1 (bases 1 to 930)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 AUTHORS
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL
 Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. David Rowe
 cDNA Library Preparation: Invitrogen Corp
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDAM0051 row: j column: 17
 High quality sequence stop: 681.
 Location/Qualifiers
 1..930
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:30142408"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_135"
 /note="Vector: pCMVSPORT6.1; Site 1: EcoRV; Site 2: NotI; Normalized full-length enriched library from pooled mouse embryonic limb, maxilla and mandible, day 12.5, 13.5, 14.5, and 15.5 (size selected for the 0.5-1 kb fragments) Cloned directionally, priming method: Oligo-dT. cDNA enrichment: >1k bp, Average insert size 1.6k bp.
 Normalization (Cot value): 7.5 kb. Priming sequence: 5'-GACTAGTCTTAGATCGAGCGGCCCTT3' Tissue contributed by, David Rowe. Library constructed by ResGen, Invitrogen Corp."

FEATURES
 source
 1..930
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:30142408"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_135"
 /note="Vector: pCMVSPORT6.1; Site 1: EcoRV; Site 2: NotI; Normalized full-length enriched library from pooled mouse embryonic limb, maxilla and mandible, day 12.5, 13.5, 14.5, and 15.5 (size selected for the 0.5-1 kb fragments) Cloned directionally, priming method: Oligo-dT. cDNA enrichment: >1k bp, Average insert size 1.6k bp.
 Normalization (Cot value): 7.5 kb. Priming sequence: 5'-GACTAGTCTTAGATCGAGCGGCCCTT3' Tissue contributed by, David Rowe. Library constructed by ResGen, Invitrogen Corp."

ORIGIN
 Alignment Scores:
 Pred. No.: 8.33e-93 Length: 930

Score: 1023.00 Matches: 188
 Percent Similarity: 83.81% Conservativity: 19
 Best Local Similarity: 76.11% Mismatches: 36
 Query Match: 73.44% Indels: 4
 DB: 14 Gaps: 0

US-09-598-982-21 (1-249) x CB203717 (1-930)

Qy 5 ILeValGlyGlnGlnAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24
 Db 42 ATCGTGGGAGACATGAGCTTCTGAGAGTAAGTGGCCCTGGCAGGTGAGCTGAGATT 101
 Qy 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
 Db 102 AAATTAACACTACTGGATACATTCTTCGCGAGGCTCTCTCATCCACCCACAGTGGGTGCTC 161
 Qy 45 ThrAlaAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 64
 Db 162 ACTCGGGCACACTGTGTGGGACCGCACATCAAAAGCCACAGCTTCTCCGGTGGAGCTT 221
 Qy 65 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 84
 Db 222 CGTGAGCAGTATCTACTATGAGGACAGCTCTCTTTGAACCGGATCTGGTGCAC 281
 Qy 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluGluPro 104
 Db 282 CCCCACTATTACAGCGCGGAGGTGGGCGACAGCTTGCCTCTGTGGAGCTTGAGTCCCT 341
 Qy 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
 Db 342 GTGAATGTCTCCACCATATCCACCCATATTCCTTGCCTGCCCCCTGGAGACCTTCCCC 401
 Qy 125 ProGlyMetProCysTrpValThrGlyTyrpGlyAspValAspAsnAspGluArgLeuPro 144
 Db 402 CCTGGGACATCGTCTGGTGACAGGCTGGGGGACATTGATATGACGACCTCTCCCA 461
 Qy 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAla 164
 Db 462 CCTCCTTATCTCTGAAGCAAGTGAAGGTTCCCATTTGGAAAACAGCCTGTGTGACCGG 521
 Qy 165 LysTyrHisLeuGlyAlaTyrThrGlyAspValArgIleValArgAspMetLeu 184
 Db 522 AAGTACCACACTGGCCTCTACCGGGAGATGATTTTCCCATTTGCATGATGGGATGCTG 581
 Qy 185 CysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCys 204
 Db 582 TGTCTGGAATAACACAGAGAGACTCTCTCCAGGGGATTCAGGGGGCCACTGTGTCTGC 641
 Qy 205 LysValAsnGlyThrTrpLeuGlnAlaGlyValValSerTrp-GlyGluGlyCysAlaG 224
 Db 642 AAAGTGAAGGTACCTGGCTGCGAGCGAGGTGTGTGAGTGGNGTGAGGGCTGCGCACA 701
 Qy 224 nProAsnArgProGlyIleTyrThrArg-ValThr-TyrTyrLeuAspTrpIleHis-Hi 243
 Db 702 GCCCAACAGCTGGCATCTACACCGGGGTGACATNACTTAGACTGATCCACNG 761
 Qy 243 sTyrValProLys 247
 Db 762 CTATGTCCTGAA 774

RESULT 7

CD671891 635 bp mRNA linear EST 24-JUN-2003
 LOCUS fg08b10.y2 Human Iris cDNA (Normalized): fg Homo sapiens cDNA clone
 DEFINITION fg08b10 5', mRNA sequence.

ACCESSION CD671891

VERSION CD671891.1 GI:32173622

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 635)

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Wistow, G., Bernstein, S.L., Ray, S., Wyatt, M.K., Behal, A.,
 Touchman, J.W., Bouffard, G., Smith, D., and Peterson, K.
 Expressed sequence tag analysis of adult human iris for the NEIBank
 Project: steroid-response factors and similarities with retinal
 pigment epithelium
 Mol. Vis. 8 (4), 185-195 (2002)
 22103462
 12107412
 Contact: Wistow G
 Section on Molecular Structure and Function
 National Eye Institute
 6/331, NIH, Bethesda, MD 20892-2740, USA
 Tel: 301 402 3452
 Fax: 301 496 0078
 Email: graeme@helix.nih.gov
 Plate: 08 row: b column: 10
 Seq primer: M13RP1 reverse primer (ABI).
 Location/Qualifiers
 1..635
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="fg08b10"
 /tissue_type="Iris"
 /dev_stage="Adult"
 /lab_host="EMDH108"
 /clone_lib="Human Iris cDNA (Normalized): fg"
 /note="Organ: Eye; Vector: pCMVSPORT6; A human iris
 library (bx) was normalized by self-subtraction. One
 portion of double stranded plasmid DNA representing the
 library was linearized by NotI. This NotI digested library
 was used as a template for biotinylated RNA synthesis
 using SP6 RNA polymerase. Another portion of the double
 stranded plasmid library was converted to single-stranded
 circles in vitro using Gene II and Exonuclease III (Life
 Technologies). Single-stranded DNA (1 mg) was hybridized
 (Cot 500) with 41 mg of Bio-RNA and vector blocking
 oligonucleotides. The hybridized Bio-RNA/ss-circles were
 removed by streptavidin:phenol extraction. EST analysis
 was performed on the library at the NIH Intramural
 Sequencing Center (NISC)."

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.: 6,71e-88 Length: 635
 Score: 972.00 Matches: 176
 Percent Similarity: 98.32% Conservativity: 0
 Best Local Similarity: 98.32% Mismatches: 3
 Query Match: 69.78% Indels: 0
 DB: 14 Gaps: 0

US-09-598-982-21 (1-249) x CD671891 (1-635)

Qy 5 ILeValGlyGlnGlnAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24
 Db 97 ATCGTGGGGGTGAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCTGAGAGTC 156
 Qy 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
 Db 157 CATGGCCCATCTGATGTCACCTTCTGCGGGGGCTCCCTCATCCACCCCGAGTGGGTGCTG 216
 Qy 45 ThrAlaAlaAlaCysValGlyProAspValLysAspLeuAlaAlaLeuArgValGlnLeu 64
 Db 217 CTGCGACGCGACCTGCTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCACCTG 276
 Qy 65 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 84
 Db 277 CGGAGAGCAGCACCTCTACTACAGGACCACTGCTGCCGGTGCAGCAGGATCATCTGCAC 336
 Qy 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluGluPro 104
 Db 337 CCCAGTCTTACACCGCCGAGATCGGACCGGACATCGCCCTGTGGAGCTGGAGGACCG 396

QY 105 VallysValSerSerHisValHisThrValThrLeuProAlaSerGluThrPhePro 124
 Db 397 GTGAAGTCTCCAGCACGTCACACGGTCACTCCCTGCCCTCGCTCAGAGACCTTCCCC 456
 QY 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAsnAspGluArgLeuPro 144
 Db 457 CCGGGGATGCCGTGGTCTACTGCTGGGGCGATGTGGCAATGATGAGCGCTCCCA 516
 QY 145 ProProPheProLeuGlyGlnValValProIleMetGluAsnHisGlyCysAspAla 164
 Db 517 CGCCCATTTCTCTGAAGCAGGTGAAGTCCCAATATGGAACACACATTTGTACGCA 576
 QY 165 LysTyHisLeuGlyAlaValThrGlyAspValArgIleValArgAspMet 183
 Db 577 AATATCCACCTTGGCGCTTACACGGGAGACGCTCGCATGCTCGTGACGACATG 633

RESULT 8

CD672689 642 bp mRNA linear EST 24-JUN-2003
 LOCUS fg15a06.y2 Human Iris cDNA (Normalized): fg Homo sapiens cDNA clone
 DEFINITION fg15a06 5', mRNA sequence.

ACCESSION CD672689
 VERSION CD672689.1 GI:32174420

KEYWORDS

SOURCE EST.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 642)

Wistow,G., Bernstein,S.L., Ray,S., Wyatt,M.K., Behal,A.,

Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.

Expressed sequence tag analysis of adult human iris for the NEIBank

Project: steroid-response factors and similarities with retinal

pigment epithelium

Mol. Vis. 8 (4), 185-195 (2002)

22103462

12107412

Contact: Wistow G

Section on Molecular Structure and Function

National Eye Institute

6/331, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452

Fax: 301 496 0078

Email: graeme@helix.nih.gov

Plate: 15 row: a column: 06

Seq primer: M13RPL reverse primer (ABI).

Location/Qualifiers

1. .642

FEATURES

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="fg15a06"

/tissue_type="iris"

/dev_stage="Adult"

/lab_host="EMD10B"

/clone_lib="Human Iris cDNA (Normalized): fg"

/note="Organ: Eye; Vector: pCMVSPORT6; A human iris

library (bx) was normalized by self-subtraction. One

portion of double stranded plasmid DNA representing the

library was linearized by NotI. This NotI digested library

was used as a template for biotinylated RNA synthesis

using SP6 RNA polymerase. Another portion of the double

stranded plasmid library was converted to single-stranded

circles in vitro using Gene II and Exonuclease III (Life

Technologies). Single-stranded DNA (1 mg) was hybridized

(Cot 500) with 41 mg of Bio-RNA and vector blocking

oligonucleotides. The hybridized Bio-RNA/ss-circles were

removed by streptavidin:phenol extraction. EST analysis

was performed on the library at the NIH Intramural

Sequencing Center (NISC)."

Pred. No.: 2,77e-87 Length: 642
 Score: 966.00 Matches: 176
 Percent Similarity: 96.70% Conservatives: 0
 Best Local Similarity: 96.70% Mismatches: 6
 Query Match: 69.35% Indels: 0
 DB: 14 Gaps: 0

US-09-598-982-21 (1-249) x CD672689 (1-642)

QY 5 lleValGlyGlyGlnGluAlaProArgSerLysTrpProTrpGlnValSerLeuArgVal 24
 Db 96 ATCGTTGGGGGTGAG 155
 QY 25 HisGlyProTyTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
 Db 156 CGCGACCGATCTGGATGACTTCTGCGGGGGCTCCCTCATCCACCCAGTGGGTGTG 215
 QY 45 ThrAlaAlaAlaCysValGlyProAspValLysValLysValLysValLysValLys 64
 Db 216 ACCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 275
 QY 65 ArgGluGlnHisLeuTyTrpGlnAspGlnLeuLeuProValSerArgIleIleValHis 84
 Db 276 CGGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 335
 QY 85 ProGlnPheTyThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluPro 104
 Db 336 CCACAGTCTTACACCGCCAGATCGAGCGGACATCGCCCTCTGAGCTGGAGGAGCG 395
 QY 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
 Db 396 GTGAAGTCTCCAGCACGTCACACGGTGGCGCTGCCCTCGCTCAGAGACCTTCCCC 455
 QY 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAsnAspGluArgLeuPro 144
 Db 456 CCGGGGATGCCGTGGTCTACTGCTGGGGCGATGTGGCAATGATGAGCGCTCCCA 515
 QY 145 ProProPheProLeuLysGlnValLysValProIleMetGluAsnHisGlyCysAspAla 164
 Db 516 CGCCCATTTCTCTGAAGCAGGTGAAGTCCCAATATGGAACACACATTTGTACGCA 575
 QY 165 LysTyHisLeuGlyAlaValThrGlyAspValArgIleValArgAspMetLeu 184
 Db 576 AATATCCACCTTGGCGCTTACACGGGAGACGCTCGCATGCTCGTGACGACATGCTG 635
 QY 185 CysAla 186
 Db 636 TGTGCC 641

RESULT 9

LOCUS BX091892

DEFINITION

BX091892 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
 IMAGE:110380, mRNA sequence.

ACCESSION BX091892

VERSION BX091892.1 GI:27822632

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 722)

Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,

Radelof,J., Schneider,D. and Korn,B.

Human Unigeneset - RZPD3

Unpublished (2003)

Contact: Ina Rofes

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPD; IMAGE:110380

RZPDLIB; I.M.A.G.E. cDNA Clone Collection;

Human Unigeneset - RZPD3 (RZPDLIB No.972)

http://www.rzpd.de/CloneCards/cgi-

ORIGIN

Alignment Scores:

105 ValysValSerSerHisValHisThrValThrLeuProAlaSerGluThrPhePro 124
 400 GTGAAGGTCTCAGCCAGCTCACACGGTACCTGCGCCCTGCTCAGACCTTCCCC 459
 125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAsp----- 140
 460 CCGGGATGCGGTGCTGGGTCACTGGCTGGGCGATGTGGCAATGATGGTGGGTCTGGG 519
 140 ----- 140
 520 GACAGTGGAGGTGGGCCAGGCTCTTAGCCACAGCCAGCCCTGGGCTCCCTCTGGGCT 579
 141 -----GluArgLeuPro----- 144
 580 CCAGTGGGGGTGGCCGGCCCTCCTGAGGCTGACCTCTTCCCACTGACGAGCGTCTC 639
 145 Pro-ProPheProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAl 164
 640 CCACGCAATTCCTCTGAAGCAGGTGAAGTCCCATATGGAACACCAATTTGTGACGG 699
 164 alystYrHis-LeuGlyAlaThrThrGlyAspValArgIleValArgAspAsp-Met 183
 700 CAAGATACACCTTGGGCGCTACACGGAGACGACGTCGCATCGTCCGTGACGAACATG 759
 184 LeuCysAlaGlyAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyPro 201
 760 CTGTGTGGGNAACCCG---GAGGACTCATGCCAGGGCGACTCCGGAGGGCCC 810

RESULT 11

BQ082929
 LOCUS K-EST0144841 S14K402 Homo sapiens cDNA clone S14K402-59-B11 5',
 DEFINITION mRNA sequence.

ACCESSION BQ082929

VERSION BQ082929.1 GI:19941018

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 502)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

Kim,Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 59 row: B column: 11

High quality sequence stop: 502.

Location/Qualifiers

FEATURES

source

1..502

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S14K402-59-B11"

/cell_line="K402"

/lab_host="Top10F"

/clone_lib="S14K402"

/note="Organ: Stomach; Vector: pTZ19RPL; Site 1: EcoRI;
 Site 2: NotI; The poly (A) + RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was

adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F, by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

Alignment Scores: 2.75e-82 Length: 502
 Pred. No.: 915.00 Matches: 166
 Score: 915.00
 Percent Similarity: 99.40% Conservative: 0
 Best Local Similarity: 99.40% Mismatches: 1
 Query Match: 65.69% Indels: 0
 DB: 13 Gaps: 0
 US-09-598-982-21 (1-249) x BQ082929 (1-502)
 QY 28 TyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeuThrAlaAla 47
 Db 2 TACTGGATGCACCTTCTGCGGGGGCTCCCTCATCCACCCCTAGTGGTGTCTGACCCAGCG 61
 QY 48 AlaCysValGlyProAspValLysAspLeuAlaLeuArgValGlnLeuArgGluGln 67
 Db 62 CACTGCGTGGGACCGGACGTCAGGATCTGGCGGCTCAGGGTCAACTGCGGGAGCAG 121
 QY 68 HisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHisProGlnPhe 87
 Db 122 CACCTCTACTACCGAGCAGCTGCTGCGGGTCAAGGATCATCGTGCACCCACGATTC 181
 QY 88 TyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluProValLysVal 107
 Db 182 TACACCGCCCGATCGGAGCGGACATCCCTTCCTGGAGCTGGAGAGCCGGTGAAGTTC 241
 QY 108 SerSerHisValHisThrValThrLeuProAlaSerGluThrPheProGlyMet 127
 Db 242 TCCACCCAGCTCCACACGTCACCTGCCCTGCTCAGAGACCTTCCCCCGGGGATG 301
 QY 128 ProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuProProPhe 147
 Db 302 CGGTCTGGTCACTGGTGGGGCGATGTGGACATATGATGAGCGCTCCACCGCATTT 361
 QY 148 ProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAlaLysTyrHis 167
 Db 362 CCTCTGAAGCAGGTGAAGTCCCCATATGAAAACCACTTTGTGACGCAAAATACCAC 421
 QY 168 LeuGlyAlaTyrThrGlyAspValArgIleValArgAspMetLeuCysAlaGly 187
 Db 422 CTTGGCGCTACACGGGAGACGCTCCGCTCGTCCGTCGACGACATGCTGTGTCGGCG 481
 QY 188 AsnThrArgArgAspSerCys 194
 Db 482 AACACCGGAGGACTCATGC 502

RESULT 12

BQ082929

LOCUS

DEFINITION

5', similar to SW:TRYB_HUMAN P20231 BETA-TRYPTASE PRECURSOR ;, mRNA

sequence.

ACCESSION BQ082929

VERSION BQ082929.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 502)

AUTHORS

Mellon,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,

Lemishka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S.,

Hillier,L., Marra,M., Page,D., Wylie,T., Martin,J., Blustain,A.,

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y., and Bowers, Y.

TITLE JOURNAL COMMENT

Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: i034c08.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. J. Ferrer In vivo mass-excised to

pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington

University Genome Sequencing Center For information on obtaining a

clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)

Seq primer: -408P from Gibco

High quality sequence stop: 427.

FEATURES source

1. .581

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:612824"

/tissue_type="insulinoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="Human insulinoma"

/note="Organ: pancreas; Vector: pBluescript SK-; Site: 1:

XhoI; Site 2: EcoRI; Constructed with lambda ZAPII system

(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to

pBluescript SK- by Dr. H. Inoue following the Washington

University protocol

(http://genome.wustl.edu/est/lambda_protocol.shtml).

Please contact Hiroshi Inoue, MD/PhD for further

information on this library (Metabolism Division, Permutt

Laboratory, Washington University School of Medicine, Box

8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this

is a Washington University Pancreas EST project library."

ORIGIN

Alignment Scores:

Pred. No.: 3.55e-81 Length: 581
Score: 905.00 Matches: 163
Percent Similarity: 98.79% Conservative: 0
Best Local Similarity: 98.79% Mismatches: 2
Query Match: 64.97% Indels: 0
DB: 13 Gaps: 0

US-09-598-982-21 (1-249) x BU787772 (1-581)

Qy 5 IleValGlyGlyGlnGluAlaProArgSerIlystrpProTrpGlnValSerLeuArgVal 24
Db 86 ATCGTCGGGGGTACAGGAGGCCCCAGAGCAAGTGGCCCTGGCAGGTGAGCTCAGAGTC 145
Qy 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValIleu 44
Db 146 CACGGCCCATCTAGATGCACTTCTGGGGGGCTCCCTCATCCACCCCGAGTGGTGTG 205
Qy 45 ThrAlaAlaLaCysValGlyProAspValIlystrpValIleAlaLeuArgValGlnIleu 64
Db 206 ACCGACGGCACTCGTGGGACCGAGCGTCAAGATCTGGCCGCCCTCAGGTCGCACTG 265
Qy 65 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 84
Db 266 CGGAGCAGCAGCACTCTACTACAGACAGCTGTGGCGGTGCACGAGATCATCTGCAC 325
Qy 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuPro 104
Db 326 CCACAGTTCACCGCCCGCATCGAGCGGACATCGCCCTGCTGGAGCTGGAGGCGG 385
Qy 105 ValIysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124

Db 386 GTGAACGCTCTCCAGCCACGTCACACGCTGACCCCTGCCCTCAGACACCTTCCCC 445
Qy 125 ProGlyMetProCysTrpValThrClyTrpGlyAspValAspAsnAspGluArgLeuPro 144
Db 446 CCGGGGATGCGGTGCTGGGTCACTGGCTGGGGCGATGGACATGATGAGCGCTCCCA 505
Qy 145 ProProPheProLeuLysGlnValIysValProIleMetGluAsnHisIleCysAspAla 164
Db 506 CCGCCATTCTCTGAGACAGGTGAGGTCCCCATAATGGAACCAACCATTTGTGACGCA 565
Qy 165 LysTyrHisLeuGly 169
Db 566 AATACCACCTTGGC 580

RESULT 13

BG542089

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BG542089 736 bp mRNA linear EST 03-APR-2001
602571309F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4695458 5',
mRNA sequence.

BG542089.1 GI:13534322

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgs.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Cloned through the I.M.A.G.E. Consortium/LLNL at:

Plate: LICM1521 row: b column: 03

High quality sequence stop: 725.

Location/Qualifiers

1. .736

FEATURES

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4695458"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC_77"

/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:

SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and

3' adaptors were used in cloning as follows: 5' adaptor

sequence: 5'-CAGCGCATATGGCC-3' and 3' adaptor sequence:

5'-ATTCTAGCCGCGGCGGCGGCGCATG-dt(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.9

kb (range 0.5-4.0 kb). 12/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 1.34e-79 Length: 736
Score: 891.00 Matches: 190
Percent Similarity: 90.52% Conservative: 1
Best Local Similarity: 90.05% Mismatches: 11
Query Match: 63.96% Indels: 11
DB: 12 Gaps: 1

US-09-598-982-21 (1-249) x BG542089 (1-736)

Qy 5 IleValGlyGlyGlnGluAlaProArgSerIlystrpProTrpGlnValSerLeuArgVal 24


```

115 ATCTGTGGGGTTCAGGAGGCCCCAGGAGCAAGTGGCCCTGCGAGTGTGAGCTGAGAGTC 174
QY 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
Db 175 CACGGCCCATCTGATGACATCTTCGGGGGGCTCCCTCATCCACCCCGAGTGGTGTCTG 234
QY 45 ThrAlaAlaCysValGlyProAspValGlyValGlyValGlyValGlyValGlyValGly 64
Db 235 ACCGAGCGCATCGGTGGGACCGGACCTCAAGATCTGGCCGCTCAGGGTGCACATG 294
QY 65 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 84
Db 295 CGGAGCAGCACCTCTACTACGAGACCACTGCTGCCGGTCAGCAGGATCATCGTGCAC 354
QY 85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluPro 104
Db 355 CCACAGTTCTACACCGCCGACATGGAGCGGACATCGCCCTGCTGGAGTGGAGGAGCG 414
QY 105 ValLysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124
Db 415 GTGAAGTCTCCAGCCAGTCCACAGGTCACCTGCCCTGCTCGAGACCTTCCCC 474
QY 125 Pro-GlyMetProCysTrpValThrGlyTrpGlyAspValAsp-AsnAspGluArgLeuP 144
Db 475 CCGGGGATGCGTGTGGTCACTGGCTGGGGCGATGTGGACCAATGATGAGCGCT-C 533
QY 144 roProProPheProLeuLysGlnVal-LysValProIleMetGluAsnHisIleCysAsp 163
Db 534 CACGGCATTCCTTCTGAAGCAGGTGAAGGTGCCCATTAATGGAACCAACATTTGTGAC 593
QY 164 AlalysTyrHisLeuGlyAla-TyrThrGlyAspAsp-ValArgIle-----ValArgA 181
Db 594 GCAAAATAACACCTTGGGGCTTACACGGGAGACGAAGTCCGCAATTCGTCCGTTGAACG 653
QY 181 spAspMetLeuCyAlaGlyAsnThrArgArgAspSerCysGlnGly-AspSer-GlyGI 200
Db 654 ACAT-TGCTGTGTGCCGGGAACACCGGAGGACTCATGCCGGCGGACTCCGGGAGG 712
QY 200 yProLeuValCysLysVal 206
Db 713 GCCCTGTGTGCAAGGTG 731

RESULT 14
CF583026/c
LOCUS
DEFINITION AGENCOURT_8786077_updated NIH_MGC_137 Mus musculus cDNA clone
IMAGE:6432257 3', mRNA sequence.
ACCESSION CF583026
VERSION CF583026.1 GI:35196288
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 929)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: CGAPs-remail.nih.gov
Tissue Procurement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000)
cDNA Library Preparation: Catherine Lee, Endocrine Pancreas
Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBD24 row: h column: 06

```

```

FEATURES
    High quality sequence stop: 546.
    Location/Qualifiers
        1..929
            /organism="Mus musculus"
            /mol_type="mRNA"
            /db_xref="taxon:10090"
            /clone="IMAGE:6432257"
            /lab_host="DH10B"
            /clone_lib="NIH_MGC_137"
            /note="Organ: pancreas; Vector: pSPORT1; Site 1: SalI;
            Site 2: NotI; Library consists of a pool of clones
            rearranged from the following libraries: Melton normalized
            mixed mouse pancreas 1 N1-MMS1, Amplified Melton mouse
            islets 1 MSL-A, and Kaestner ng3 wt. Clones rearranged in
            the laboratory of K. Kaestner (University of
            Pennsylvania). Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.:      8,49e-76      Length:      929
Score:          855.00      Matches:    161
Percent Similarity: 81.00%      Conservative: 18
Best Local Similarity: 72.85%      Mismatches: 35
Query Match:      61.38%      Indels:      8
DB:              14          Gaps:        3
US-09-598-982-21 (1-249) x CF583026 (1-929)
QY 32 PheCysGlyGlySerLeuIleHisProGlnTrpValLeuThrAlaAlaCys----- 49
Db 927 TTCTGCCGAGGG---TTTTTTCATCCACC---CCCAAGGGGGTGTCTCANTGGGGCAC 874
QY 50 -----ValGlyProAspValLysAspLeuAlaLeu-ArgValGlnLeuArgGluGI 67
Db 873 ACTGGTGGGACCCGACATCAAAAGACCCACAGCTCTTCCGGGTGCGAGCTTCGTGAGCA 814
QY 67 nHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHisProGlnPh 87
Db 813 GTATCTATATATGGGACCAAGCT-CTCTTTTGAACCGGATCGTGGTGCACCCCACTA 755
QY 87 eTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluProValLysVa 107
Db 754 TTACAGCGCCGAGGGTGGGGCAGACGTTGGCTTCTGCGAGCTTGAGGTCCCTGTGAATGT 695
QY 107 lSerSerHisValHisThrValThrLeuProProAlaSerGluThrPheProGlyMe 127
Db 694 CTCACCCCATATCACCCCATATCCCTGCCCTGCTCGAGACCTTCCCCCTGGGAC 635
QY 127 tProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuProProPh 147
Db 634 ATCGTGTGGTGCAGCGCTGGGGCGACATTGATAATGACGAGCTCTCCACCTCTTA 575
QY 147 eProLeuLysGlnValLysValProIleMetGluAsnHisIleCysAspAlaLysTyrHi 167
Db 574 TCCTCTGAAGCAAGTGAAGGTTCCTCAATTGTGAAAACACAGCTGTGTGACCGAGTACCA 515
QY 167 sLeuGlyAlaTyrThrGlyAspValArgIleValArgAspAspMetLeuCysAlaGI 187
Db 514 CACTGGGCTCTACACGGGAGATGATTTTCCCATTTGTCATGTCATGTCATGTCGTGG 455
QY 187 yAsnThrArgArgAspSerCysGlnGlyAspSerGlyGlyProLeuValCysLysValAs 207
Db 454 AAATACAGGAGACATCTCTCCAGGGCGATTGAGGGGGGCACCTGGTCTCTCAAGTGAA 395
QY 207 nGlyThrTrpLeuGlnAlaGlyValValSerTrpGlyGluGlyCysAlaGlnProAsnAr 227
Db 394 GGGTACCTGGCTGCAGGCAGGAGTGGTCAGCTGGGGTGAGGGCTGCGCACAGCCCAACA 335
QY 227 gProGlyIleTyrThrArgValThrTyrTyrLeuAspTrpIleHisTyrValProLy 247
Db 334 GCCTGGCATCTACACCGGGGTGACATACTACTTAGACTGGATCCACCGCTATGCTCTGA 275
QY 247 s 247

```

```

Db          274 G 274
RESULT 15
CF553058
LOCUS
DEFINITION CF553058 806 bp mRNA linear EST 22-SEP-2003
AGENCOURT_15594982 NIH MGC 183 Homo sapiens cDNA clone
IMAGE:30529468 5', mRNA sequence.
ACCESSION CF553058
VERSION CF553058.1 GI:34889892
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 806)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cagabs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM617 row: b column: 05
High quality sequence start: 18
High quality sequence stop: 611.
FEATURES
Location/Qualifiers
1..806
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30529468"
/lab_host="DH10B-Tona (T1 and T5 phage resistant)"
/clone_lib="NIH_MGC_183"
/note="Organ: Pooled muscle (cardiac and skeletal);
vector: pCMV-SPORT6.1; Site 1: EcoRV (destroyed); Site 2:
NotI; Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.7. Library was constructed by Invitrogen."
ORIGIN
Alignment Scores:
Pred. No.: 6.24e-75 Length: 806
Score: 845.50 Matches: 159
Percent Similarity: 89.01% Conservative: 3
Best Local Similarity: 87.36% Mismatches: 17
Query Match: 60.70% Indels: 3
DB: 14 Gaps: 1

US-09-598-982-21 (1-249) x CF553058 (1-806)

Qy 5 IleValGlyGlyGlnGluAlaProArgSerIysTrpProTrpGlnValSerLeuArgVal 24
Db 248 ATCGTCGGGGGTACGAGAGGCCGCCAGGAGAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 307
Qy 25 HisGlyProTyrTrpMetHisPheCysGlyGlySerLeuIleHisProGlnTrpValLeu 44
Db 308 CGCAGCCGATACGTGATGCATCTCTGTGGGGGCTCCCTCATCCACCCCGAGTGGGTGCTG 367
Qy 45 ThrAlaAlaCysValGlyProAspValIysAspLeuAlaLeuArgValGlnLeu 64
Db 368 ACCGCGCGGCACTGCCTGGGACCGGACGTCGAAGGATCTGGCCACCTCTCAGGGTGCAACTG 427
Qy 65 ArgGluGlnHisLeuTyrTyrGlnAspGlnLeuLeuProValSerArgIleIleValHis 84

```

428 CGGGAGCAGCACCTCTACTACAGGACCACTGCTGCCGGTCCAGCAGGATCATCGTGCAC 487

85 ProGlnPheTyrThrAlaGlnIleGlyAlaAspIleAlaLeuLeuGluLeuGluPro 104

488 CCACAGTTCTACATCATCCAGACTGGAGCGGATATCGCCCTGCTGGAGCTGGAGGAGCCC 547

105 ValIysValSerSerHisValHisThrValThrLeuProProAlaSerGluThrPhePro 124

548 GTGAACATCTCCAGCCGCGTCCACAGGTCTATGCTGCCCTGCTCGGAGACCTTCCCC 607

125 ProGlyMetProCysTrpValThrGlyTrpGlyAspValAspAsnAspGluArgLeuPro 144

608 CCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCCCTCCCA 667

145 ProProPheProLeuIysGlnValIysValProIleMetGluAsnHisIleCysAspAla 164

668 CCGCCATTTCCTTGAAGCAGGTGAAGTCCCATATATGGAACCAACATTTGTGACGCA 727

165 LysTyrHisLeuGly--AlaTyrThrGlyAspAsp---ValArgIleValArgAspAspM 183

728 AAATACCACTTGGGGCGCCCTACACGGGAGACGAACGTCGGGCATCATCCCGTGACGACA 787

183 et 183

788 TG 789

Search completed: July 22, 2004, 18:14:21

Job time : 3075 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 22, 2004, 10:05:00 ; Search time 5131 Seconds
(without alignments)
6512.859 Million cell updates/sec

Title: US-09-598-982-20

Perfect score: 771

Sequence: 1 gggccctcgagaaagaat.....cgtgaagcgccgcgctgt 771

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.on.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.or.*

22: em.ov.*

23: em.pat.*

24: em.ph.*

25: em.pl.*

26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg.hum.*

31: em.htg.inv.*

32: em.htg.other.*

33: em.htg.mus.*

34: em.htg.pln.*

35: em.htg.rod.*

36: em.htg.mam.*

37: em.htg.vrt.*

38: em.sy.*

39: em.htgo.hum.*

40: em.htgo.mus.*

41: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	771	100.0	771	6	AX347853	Sequence
2	769.4	99.8	771	6	AX347869	Sequence
3	764.6	99.2	771	6	AR165112	Sequence
4	764.6	99.2	771	6	AX347841	Sequence
5	764.6	99.2	771	6	BD211490	Enzymatic
6	763	99.0	771	6	AX347838	Sequence
7	761.4	98.8	771	6	AX347855	Sequence
8	759.8	98.5	771	6	AX347871	Sequence
9	755	97.9	771	6	AX347857	Sequence
10	755	97.9	771	6	AX347859	Sequence
11	753.4	97.7	771	6	AX347873	Sequence
12	753.4	97.7	771	6	AX347875	Sequence
13	735	95.3	735	6	AX347861	Sequence
14	733.4	95.1	735	6	AX347877	Sequence
15	731	94.8	1128	6	AR080461	Sequence
16	731	94.8	1128	9	HUMTRY2A	Human trypt
17	731	94.8	1137	6	AR080460	Sequence
18	731	94.8	1137	9	HUMTRY1A	Human trypt
19	731	94.8	1143	9	HUMTRYYP	Human beta-
20	731	94.8	1145	9	S55551	Sequence
21	731	94.8	1194	9	BC029356	Homo sapi
22	731	94.8	1235	9	BC038416	Homo sapi
23	728.6	94.5	735	6	AR165109	Sequence
24	728.6	94.5	735	6	AX347843	Sequence
25	728.6	94.5	735	6	BD211487	Enzymatic
26	727	94.3	735	6	AX347834	Sequence
27	726.2	94.2	1081	6	AR080462	Sequence
28	726.2	94.2	1081	6	AX329646	Sequence
29	726.2	94.2	1081	6	AX330205	Sequence
30	726.2	94.2	1081	6	AX334644	Sequence
31	726.2	94.2	1081	6	AX375047	Sequence
32	726.2	94.2	1081	9	HUMTRY3A	Human trypt
33	725.4	94.1	735	6	AX347863	Sequence
34	723.8	93.9	735	6	AX347879	Sequence
35	719	93.3	735	6	AX347865	Sequence
36	719	93.3	735	6	AX347867	Sequence
37	719	93.3	1221	6	AX014344	Sequence
38	719	93.3	1221	6	BD222223	Human nuc
39	718.2	93.2	2662	6	AX338508	Sequence
40	717.4	93.0	735	6	AX347881	Sequence
41	717.4	93.0	735	6	AX347883	Sequence
42	692.6	89.8	884	9	AF206665	Homo sapi
43	692.6	89.8	1206	9	BC028059	Homo sapi
44	692.6	89.8	1207	9	BC051852	Homo sapi
45	686.2	89.0	1154	6	AR080459	Sequence

ALIGNMENTS

RESULT 1
AX347853
LOCUS AX347853 771 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 20 from Patent WO0198470.
ACCESSION AX347853
VERSION AX347853.1 GI:18495660
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Maffit, M., Niles, A.L. and Haak-Frendscho, M.
TITLE Recombinant proteolytic tryptases, active site mutants thereof, and methods of making same

Pred. No. is the number of results predicted by chance to have a

```
JOURNAL Patent: WO 0198470-A 20 27-DEC-2001;
FEATURES PROMEGA CORPORATION (US)
source Location/Qualifiers
1. .771
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
<1_..756
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD22420.1"
/db_xref="GI:18495661"
/db_xref="RENTREMBL:CAD22420"
/translations="GPLEKRVGGQAPRSKWPQVSLRVHGPVWVHFGGSLIHPQWL
VLTAAACVGPDKDLAALRVOLREOHLVYQDQLLPVSRILVHPQVYTAQIGADIALLE
LESPVKVSSHVHTVLPASSETFPFPCWVTGWDVNDERLPPFPPLKQVPMENH
NHICDAKHILGAYTGDDVRIVRDMLCAGNTRRDSQCGSDGGLPVCKVNGTWLQAGVV
SWEGGCAQPNRPFGIYTRVYTLWDIHHVYPKKP"
ORIGIN
Query Match 100.0%; Score 771; DB 6; Length 771;
Best Local Similarity 100.0%; Pred. No. 2.3e-117; Indels 0; Gaps 0;
Matches 771; Conservative 0; Mismatches 0;
Qy 1 GGGCCCTCGAGAAAGAATCGTCGGGGGTGAGAGGCCCGCCAGAGCAAGTGCCCTGG 60
Db 1 GGGCCCTCGAGAAAGAATCGTCGGGGGTGAGAGGCCCGCCAGAGCAAGTGCCCTGG 60
Qy 61 CAGGTGAGCTGAGAGTCCAGGCCCATCTGGATGCACTTCTCGGGGGGTCTCCTCATC 120
Db 61 CAGGTGAGCTGAGAGTCCAGGCCCATCTGGATGCACTTCTCGGGGGGTCTCCTCATC 120
Qy 121 CACCCCGAGTGGGTGTCAGCCGCGCGTGTGGAGCGGACGTCAGAGATCTGGCC 180
Db 121 CACCCCGAGTGGGTGTCAGCCGCGCGTGTGGAGCGGACGTCAGAGATCTGGCC 180
Qy 181 GCCCTCAGAGTCCAGTCCAGCGCGGTGCGTGGAGCGGACGTCAGAGATCTGGCC 240
Db 181 GCCCTCAGAGTCCAGTCCAGCGCGGTGCGTGGAGCGGACGTCAGAGATCTGGCC 240
Qy 241 AGCAGGATCATCTGTCACCCACAGTTCACACCCCGAGATCGGAGCGGACATCGCCCTG 300
Db 241 AGCAGGATCATCTGTCACCCACAGTTCACACCCCGAGATCGGAGCGGACATCGCCCTG 300
Qy 301 CTGAGCTGAGGAGCGCGGTGAAGTCTCCAGCCACGTCACACGCTCACCTGCCCT 360
Db 301 CTGAGCTGAGGAGCGCGGTGAAGTCTCCAGCCACGTCACACGCTCACCTGCCCT 360
Qy 361 GCCTCAGAGACCTTCCCGCGGGGATCGCGTGTGGGTCACTGGCTGGGGCGATGTGAC 420
Db 361 GCCTCAGAGACCTTCCCGCGGGGATCGCGTGTGGGTCACTGGCTGGGGCGATGTGAC 420
Qy 421 AATGATGAGCCCTCCCGCGGGGATCGCGTGTGGGTCACTGGCTGGGGCGATGTGAC 480
Db 421 AATGATGAGCCCTCCCGCGGGGATCGCGTGTGGGTCACTGGCTGGGGCGATGTGAC 480
Qy 481 AACCACATTTGTGACGAAATACACCTTGGCGCTACACGGAGACGAGTCCGATC 540
Db 481 AACCACATTTGTGACGAAATACACCTTGGCGCTACACGGAGACGAGTCCGATC 540
Qy 541 GTCCGTGACGATCTGTCGCGGAAACACCGGAGGACTCATGCGAGGCGATCTC 600
Db 541 GTCCGTGACGATCTGTCGCGGAAACACCGGAGGACTCATGCGAGGCGATCTC 600
Qy 601 GGAGGGCCCTGTTGTCAGGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 660
Db 601 GGAGGGCCCTGTTGTCAGGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 660
Qy 661 GGCGAGGCTGTGCGGCGGAAACCGGCTGTGATCAACCGCTGTCACTACTTGT 720
Db 661 GGCGAGGCTGTGCGGCGGAAACCGGCTGTGATCAACCGCTGTCACTACTTGT 720
Qy 721 GACTGGATCCACCATATGTCCCGGAAAGCGGTGAAGCGCGCGCGTGT 771
Db 721 GACTGGATCCACCATATGTCCCGGAAAGCGGTGAAGCGCGCGCGTGT 771
```

```
Db 721 GACTGGATCCACCATATGTCCCGGAAAGCGGTGAAGCGCGCGCGTGT 771
RESULT 2
AX347869
LOCUS AX347869
DEFINITION Sequence 36 from Patent WO0198470.
ACCESSION AX347869
VERSION AX347869.1 GI:18495676
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1
AUTHORS Maffei, M., Niles, A.L. and Haak-Frendscho, M.
TITLE Recombinant proteolytic tryptases, active site mutants thereof, and
METHODS of making same
JOURNAL Patent: WO 0198470-A 36 27-DEC-2001;
PROMEGA CORPORATION (US)
FEATURES
source Location/Qualifiers
1. .771
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
<7_..756
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD22428.1"
/db_xref="GI:18495677"
/db_xref="RENTREMBL:CAD22428"
/translations="LEKRVGGQAPRSKWPQVSLRVHGPVWVHFGGSLIHPQWL
TABACVGPDKDLAALRVOLREOHLVYQDQLLPVSRILVHPQVYTAQIGADIALLE
EPNVSSHVHTVLPASSETFPFPCWVTGWDVNDERLPPFPPLKQVPMENH
ICDAKHILGAYTGDDVRIVRDMLCAGNTRRDSQCGSDGGLPVCKVNGTWLQAGVVSW
EGGCAQPNRPFGIYTRVYTLWDIHHVYPKKP"
ORIGIN
Query Match 99.8%; Score 769.4; DB 6; Length 771;
Best Local Similarity 99.9%; Pred. No. 4.2e-117; Indels 0; Gaps 0;
Matches 770; Conservative 0; Mismatches 1;
Qy 1 GGGCCCTCGAGAAAGAATCGTCGGGGGTGAGAGGCCCGCCAGAGCAAGTGCCCTGG 60
Db 1 GGGCCCTCGAGAAAGAATCGTCGGGGGTGAGAGGCCCGCCAGAGCAAGTGCCCTGG 60
Qy 61 CAGGTGAGCTGAGAGTCCAGGCCCATCTGGATGCACTTCTCGGGGGGTCTCCTCATC 120
Db 61 CAGGTGAGCTGAGAGTCCAGGCCCATCTGGATGCACTTCTCGGGGGGTCTCCTCATC 120
Qy 121 CACCCCGAGTGGGTGTCAGCCGCGCGTGTGGAGCGGACGTCAGAGATCTGGCC 180
Db 121 CACCCCGAGTGGGTGTCAGCCGCGCGTGTGGAGCGGACGTCAGAGATCTGGCC 180
Qy 181 GCCCTCAGAGTCCAGTCCAGCGCGGTGCGTGGAGCGGACGTCAGAGATCTGGCC 240
Db 181 GCCCTCAGAGTCCAGTCCAGCGCGGTGCGTGGAGCGGACGTCAGAGATCTGGCC 240
Qy 241 AGCAGGATCATCTGTCACCCACAGTTCACACCCCGAGATCGGAGCGGACATCGCCCTG 300
Db 241 AGCAGGATCATCTGTCACCCACAGTTCACACCCCGAGATCGGAGCGGACATCGCCCTG 300
Qy 301 CTGAGCTGAGGAGCGCGGTGAAGTCTCCAGCCACGTCACACGCTCACCTGCCCT 360
Db 301 CTGAGCTGAGGAGCGCGGTGAAGTCTCCAGCCACGTCACACGCTCACCTGCCCT 360
Qy 361 GCCTCAGAGACCTTCCCGCGGGGATCGCGTGTGGGTCACTGGCTGGGGCGATGTGAC 420
Db 361 GCCTCAGAGACCTTCCCGCGGGGATCGCGTGTGGGTCACTGGCTGGGGCGATGTGAC 420
Qy 421 AATGATGAGCCCTCCCGCGGGGATCGCGTGTGGGTCACTGGCTGGGGCGATGTGAC 480
Db 421 AATGATGAGCCCTCCCGCGGGGATCGCGTGTGGGTCACTGGCTGGGGCGATGTGAC 480
```

```
Db 421 AATGATGAGCGCTCCACCGCCATTTCCTCTGAAGCAGGTGAAGTCCCCCAATATGAA 480
Qy 481 AACCACATTTGTGACGCAAAATACACCTTGCGCCCTACACGGAGAGAGTCCGCGATC 540
Db 481 AACCACATTTGTGACGCAAAATACACCTTGCGCCCTACACGGAGAGAGTCCGCGATC 540
Qy 541 GTCCGTGACGACATGCTGTGTGCGCGGAACACCGGAGGAGTCAATGCGAGGGGCACTCC 600
Db 541 GTCCGTGACGACATGCTGTGTGCGCGGAACACCGGAGGAGTCAATGCGAGGGGCACTCC 600
Qy 601 GGAGGGCCCTGTGTGTCGAAGTGAATGGCACTCTGCGTGCAGGGCGGTGTCAGCTGG 660
Db 601 GGAGGGCCCTGTGTGTCGAAGTGAATGGCACTCTGCGTGCAGGGCGGTGTCAGCTGG 660
Qy 661 GGCGAGGCTGTGCCAGCCCAACCGGCTGGCATCTACACCGTGTCACTACTACTTG 720
Db 661 GGCGAGGCTGTGCCAGCCCAACCGGCTGGCATCTACACCGTGTCACTACTACTTG 720
Qy 721 GACTGGATCCACCTATGTCCCAAAAGCCGTGAAGCGGCCGCCGCTCGT 771
Db 721 GACTGGATCCACCTATGTCCCAAAAGCCGTGAAGCGGCCGCCGCTCGT 771

RESULT 3
AR165112
LOCUS AR165112 771 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 4 from patent US 6274366.
ACCESSION AR165112
VERSION AR165112.1 GI:16238527
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1. (bases 1 to 771)
  Maffitt,M.A., Niles,A.L. and Haak-Frendscho,M.
  Enzymatically-active recombinant human .beta.-tryptase and method
  of making same
  JOURNAL Patent: US 6274366-A 4 14-AUG-2001;
  FEATURES Location/Qualifiers
    source 1..771
      /organism="unknown"
      /mol_type="unassigned DNA"

ORIGIN
  Query Match 99.2%; Score 764.6; DB 6; Length 771;
  Best Local Similarity 99.5%; Pred. No. 2.6e-116;
  Matches 767; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGCCCCCTCGAGAAAAGAAATCGTCGGGGGTGAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
Db 1 GGGCCCCCTCGAGAAAAGAAATCGTCGGGGGTGAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
Qy 61 CAGGTGAGCTGAGAGTCCAGGCCCATCTGGATGCACTTCTGCGGGGGTCCCTCATC 120
Db 61 CAGGTGAGCTGAGAGTCCAGGCCCATCTGGATGCACTTCTGCGGGGGTCCCTCATC 120
Qy 121 CACCCCAAGTGGTCTCACCGCGCGCGTGGCGGACCGAGCTCAAGATCTGGCC 180
Db 121 CACCCCAAGTGGTCTCACCGCGAGCACTGCGTGGGACCGAGCTCAAGATCTGGCC 180
Qy 181 GCCCTCAGGTCGCACTCGGGGAGCAGCACCTCTACTACGAGGACCACTGCTGCGCGTC 240
Db 181 GCCCTCAGGTCGCACTCGGGGAGCAGCACCTCTACTACGAGGACCACTGCTGCGCGTC 240
Qy 241 AGCAGGATCTGTCACCCACAGTTCACCGGCCAGATCGGAGCGGACATCGCCCTG 300
Db 241 AGCAGGATCTGTCACCCACAGTTCACACCGCCAGATCGGAGCGGACATCGCCCTG 300
Qy 301 CTGAGCTGGAGGAGCGGTGAAGTCTCCAGCCAGCTCCACAGTTCACCTGCCCCCT 360
Db 301 CTGAGCTGGAGGAGCGGTGAAGTCTCTCAGCCAGCTCCACAGTTCACCTGCCCCCT 360
Qy 361 GCCTCAGAGACCTTCCCCCGGGGATGCGCTGCTGGTCACTGGTGGGCGGATGTGAC 420
```

```
Db 361 GCCTCAGAGACCTTCCCGCGGATGCGGTGCTGGGTCACTGCTGGGCGGATGTGGAC 420
Qy 421 AATGATGAGCGCTCCACCGCCATTTCCTCTGAAGCAGGTGAAGTCCCCCAATATGAA 480
Db 421 AATGATGAGCGCTCCACCGCCATTTCCTCTGAAGCAGGTGAAGTCCCCCAATATGAA 480
Qy 481 AACCACATTTGTGACGCAAAATACACCTTGCGCCCTACACGGAGAGAGTCCGCGATC 540
Db 481 AACCACATTTGTGACGCAAAATACACCTTGCGCCCTACACGGAGAGAGTCCGCGATC 540
Qy 541 GTCCGTGACGACATGCTGTGTGCGCGGAACACCGGAGGAGTCAATGCGAGGGGCACTCC 600
Db 541 GTCCGTGACGACATGCTGTGTGCGCGGAACACCGGAGGAGTCAATGCGAGGGGCACTCC 600
Qy 601 GGAGGGCCCTGTGTGTCGAAGTGAATGGCACTCTGCGTGCAGGGCGGTGTCAGCTGG 660
Db 601 GGAGGGCCCTGTGTGTCGAAGTGAATGGCACTCTGCGTGCAGGGCGGTGTCAGCTGG 660
Qy 661 GGCGAGGCTGTGCCAGCCCAACCGGCTGGCATCTACACCGTGTCACTACTACTTG 720
Db 661 GGCGAGGCTGTGCCAGCCCAACCGGCTGGCATCTACACCGTGTCACTACTACTTG 720
Qy 721 GACTGGATCCACCTATGTCCCAAAAGCCGTGAAGCGGCCGCCGCTCGT 771
Db 721 GACTGGATCCACCTATGTCCCAAAAGCCGTGAAGCGGCCGCCGCTCGT 771

RESULT 4
AX347841
LOCUS AX347841 771 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 8 from Patent WO0198470.
ACCESSION AX347841
VERSION AX347841.1 GI:18495648
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1. Maffitt,M., Niles,A.L. and Haak-Frendscho,M.
  Recombinant proteolytic tryptases, active site mutants thereof, and
  methods of making same
  JOURNAL Patent: WO 0198470-A 8 27-DEC-2001;
  FEATURES Location/Qualifiers
    source 1..771
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"
      <7..756
      /note="unnamed protein product"
      /codon_start=1
      /protein_id="CAD22418.1"
      /db_xref="GI:18495648"
      /translation="LEKRIVGQEPASRKPQWLSLRVHGPWMHFGGSLIHPQWL
      TAAHCVPDVKDLAALRVQLRECHLYYQDQLLPVSRILIVHPQFYAQIGADIALLELE
      EPKVSQSHVTVLPASSETFPFGMPCWVTGWGDVNDNDRLPFPPLKQKVPIMENH
      ICDAKYHLGAYTGDDVRIDMLCAGNTRDRSCQSDSGGSLVCKVNGTWLQAGVYSW
      GEGCAQPNRPGIYTRVTVYLDWIHHYVKKP"

ORIGIN
  Query Match 99.2%; Score 764.6; DB 6; Length 771;
  Best Local Similarity 99.5%; Pred. No. 2.6e-116;
  Matches 767; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGGCCCCCTCGAGAAAAGAAATCGTCGGGGGTGAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
Db 1 GGGCCCCCTCGAGAAAAGAAATCGTCGGGGGTGAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
Qy 61 CAGGTGAGCTGAGAGTCCAGGCCCATCTGGATGCACTTCTGCGGGGGTCCCTCATC 120
Db 61 CAGGTGAGCTGAGAGTCCAGGCCCATCTGGATGCACTTCTGCGGGGGTCCCTCATC 120
Qy 121 CACCCCAAGTGGTCTCACCGCGCGCGTGGCGGACCGAGCTCAAGATCTGGCC 180
Db 121 CACCCCAAGTGGTCTCACCGCGAGCACTGCGTGGGACCGAGCTCAAGATCTGGCC 180
Qy 181 GCCCTCAGGTCGCACTCGGGGAGCAGCACCTCTACTACGAGGACCACTGCTGCGCGTC 240
Db 181 GCCCTCAGGTCGCACTCGGGGAGCAGCACCTCTACTACGAGGACCACTGCTGCGCGTC 240
Qy 241 AGCAGGATCTGTCACCCACAGTTCACCGGCCAGATCGGAGCGGACATCGCCCTG 300
Db 241 AGCAGGATCTGTCACCCACAGTTCACACCGCCAGATCGGAGCGGACATCGCCCTG 300
Qy 301 CTGAGCTGGAGGAGCGGTGAAGTCTCCAGCCAGCTCCACAGTTCACCTGCCCCCT 360
Db 301 CTGAGCTGGAGGAGCGGTGAAGTCTCTCAGCCAGCTCCACAGTTCACCTGCCCCCT 360
Qy 361 GCCTCAGAGACCTTCCCCCGGGGATGCGCTGCTGGTCACTGGTGGGCGGATGTGAC 420
```

Db 61 CAGGTGAGCTGAGAGTCCAGGCGCCATATGAGTCACTTCTCGGGGGCTCCCTCATC 120
 Qy 121 CACCCCGAGTGGGTCTGACCGCGCGCGTGGACCGGACGTCAGGATCTGGCC 180
 Db 121 CACCCCGAGTGGGTCTGACCGCGCGCGTGGACCGGACGTCAGGATCTGGCC 180
 Qy 181 GCCCTCAGGTGCACTGCGGAGCAGCAGCTTCTACTACAGGACCGAGTCTGCCGTC 240
 Db 181 GCCCTCAGGTGCACTGCGGAGCAGCAGCTTCTACTACAGGACCGAGTCTGCCGTC 240
 Qy 241 AGCAGGATCATCTGTCACCCACAGTCTTACACCCCGCAGATCGGAGCGGACATGCCCTG 300
 Db 241 AGCAGGATCATCTGTCACCCACAGTCTTACACCCCGCAGATCGGAGCGGACATGCCCTG 300
 Qy 301 CTGAGGTGAGGAGCGCGTGAAGTCTCCAGGCGCCTACACGCTCACCGTCCGCCCT 360
 Db 301 CTGAGGTGAGGAGCGCGTGAAGTCTCCAGGCGCCTACACGCTCACCGTCCGCCCT 360
 Qy 361 GCCTCAGAGACCTTCCCGCGGAGTCCCGTCTGGGTCACTGGCTGGGGCGATGTGGAC 420
 Db 361 GCCTCAGAGACCTTCCCGCGGAGTCCCGTCTGGGTCACTGGCTGGGGCGATGTGGAC 420
 Qy 421 AATGATGAGCGCTCCCGCGGAGTCCCGTCTGGGTCACTGGCTGGGGCGATGTGGAC 480
 Db 421 AATGATGAGCGCTCCCGCGGAGTCCCGTCTGGGTCACTGGCTGGGGCGATGTGGAC 480
 Qy 481 AACCACATTTGTGACGCAAAATACACCTTGGCGCTTACACGCGAGAGCGTCCGCATC 540
 Db 481 AACCACATTTGTGACGCAAAATACACCTTGGCGCTTACACGCGAGAGCGTCCGCATC 540
 Qy 541 GTCCGTGACGACATGCTGTGCGCGGAACACCGGAGGAGTCAATCGAGGCGGACTCC 600
 Db 541 GTCCGTGACGACATGCTGTGCGCGGAACACCGGAGGAGTCAATCGAGGCGGACTCC 600
 Qy 601 GGAGGGCCCTGCTGTCAGGTCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 660
 Db 601 GGAGGGCCCTGCTGTCAGGTCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 660
 Qy 661 GGCAGGGCTGTGCCAGCCCAACCGGCTGGCATCTACACCCGTGTCACTACTATTG 720
 Db 661 GGCAGGGCTGTGCCAGCCCAACCGGCTGGCATCTACACCCGTGTCACTACTATTG 720
 Qy 721 GACTGGATCCACACTATGTCCCAAAAGCGGTGAAGCGGCGCGCGTGTGT 771
 Db 721 GACTGGATCCACACTATGTCCCAAAAGCGGTGAAGCGGCGCGCGTGTGT 771

RESULT 5
 BD211490
 LOCUS 771 bp DNA linear PAT 17-JUL-2003
 DEFINITION Enzymatically-active recombinant human beta-tryptase and method of making same.
 ACCESSION BD211490
 VERSION 1 GI:33021260
 KEYWORDS JP 2002515254-A/4.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Maffitt,M.A., Nilles,A.L. and Friendscho,M.H.
 AUTHORS (bases 1 to 771)
 TITLE Enzymatically-active recombinant human beta-tryptase and method of making same
 JOURNAL Patent: JP 2002515254-A 4 28-MAY-2002;
 COMMENT PROMEGA CORP
 OS Homo sapiens (human)
 PN JP 2002515254-A/4
 PD 28-MAY-2002
 PF 29-OCT-1998 JP 2000549745
 PR 15-MAY-1998 US 09/079970
 PI MARK A MAFFITT, ANDREW L NILES, MARY HAAS PRENDSCHO PC
 C12N15/09, C07K16/40, C12N1/19, C12N9/64, C12P21/08, C12Q1/37// PC
 (C12N9/64, C12R1:645), C12N15/00

CC Strandedness: Single;
 CC Topology: Linear;
 CC Enzymatically-active recombinant human beta-tryptase and method of making
 CC same
 FH key Location/Qualifiers
 FT CDS 7..753
 FT misc signal 7..18.
 FT Location/Qualifiers
 FEATURES
 source 1..771
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 ORIGIN
 Query Match 99.2%; Score 764.6; DB 6; Length 771;
 Best Local Similarity 99.5%; Pred. No. 2.6e-116;
 Matches 767; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 GGGCCCCCTCGAGAAAGAAATCGTGGGGGTGAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
 Db 1 GGGCCCCCTCGAGAAAGAAATCGTGGGGGTGAGGAGGCCCCCAGGAGCAAGTGGCCCTGG 60
 Qy 61 CAGGTGAGCTGAGAGTCCACGGCCCATATCTGGATGCACTTCTCGGGGGGTCTCCCTCATC 120
 Db 61 CAGGTGAGCTGAGAGTCCACGGCCCATATCTGGATGCACTTCTCGGGGGGTCTCCCTCATC 120
 Qy 121 CACCCCGAGTGGGTCTGACCGCGCGCGTGGACCGGACGTCAGGATCTGGCC 180
 Db 121 CACCCCGAGTGGGTCTGACCGCGCGCGTGGACCGGACGTCAGGATCTGGCC 180
 Qy 181 GCCCTCAGGTGCACTGCGGAGCAGCAGCTTCTACTACAGGACCGAGTCTGCCGTC 240
 Db 181 GCCCTCAGGTGCACTGCGGAGCAGCAGCTTCTACTACAGGACCGAGTCTGCCGTC 240
 Qy 241 AGCAGGATCATCTGTCACCCACAGTCTTACACCCCGCAGATCGGAGCGGACATGCCCTG 300
 Db 241 AGCAGGATCATCTGTCACCCACAGTCTTACACCCCGCAGATCGGAGCGGACATGCCCTG 300
 Qy 301 CTGAGGTGAGGAGCGCGTGAAGTCTCCAGGCGCCTACACGCTCACCGTCCGCCCT 360
 Db 301 CTGAGGTGAGGAGCGCGTGAAGTCTCCAGGCGCCTACACGCTCACCGTCCGCCCT 360
 Qy 361 GCCTCAGAGACCTTCCCGCGGAGTCCCGTCTGGGTCACTGGCTGGGGCGATGTGGAC 420
 Db 361 GCCTCAGAGACCTTCCCGCGGAGTCCCGTCTGGGTCACTGGCTGGGGCGATGTGGAC 420
 Qy 421 AATGATGAGCGCTCCCGCGGAGTCCCGTCTGGGTCACTGGCTGGGGCGATGTGGAC 480
 Db 421 AATGATGAGCGCTCCCGCGGAGTCCCGTCTGGGTCACTGGCTGGGGCGATGTGGAC 480
 Qy 481 AACCACATTTGTGACGCAAAATACACCTTGGCGCTTACACGCGAGAGCGTCCGCATC 540
 Db 481 AACCACATTTGTGACGCAAAATACACCTTGGCGCTTACACGCGAGAGCGTCCGCATC 540
 Qy 541 GTCCGTGACGACATGCTGTGCGCGGAACACCGGAGGAGTCAATCGAGGCGGACTCC 600
 Db 541 GTCCGTGACGACATGCTGTGCGCGGAACACCGGAGGAGTCAATCGAGGCGGACTCC 600
 Qy 601 GGAGGGCCCTGCTGTCAGGTCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 660
 Db 601 GGAGGGCCCTGCTGTCAGGTCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 660
 Qy 661 GGCAGGGCTGTGCCAGCCCAACCGGCTGGCATCTACACCCGTGTCACTACTATTG 720
 Db 661 GGCAGGGCTGTGCCAGCCCAACCGGCTGGCATCTACACCCGTGTCACTACTATTG 720
 Qy 721 GACTGGATCCACACTATGTCCCAAAAGCGGTGAAGCGGCGCGCGTGTGT 771
 Db 721 GACTGGATCCACACTATGTCCCAAAAGCGGTGAAGCGGCGCGCGTGTGT 771
 RESULT 6

AX347838
LOCUS AX347838 771 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 5 from Patent WO0198470.
ACCESSION AX347838
VERSION AX347838.1 GI:18495645
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Maffit,M., Niles,A.L. and Haak-Frendscho,M.
AUTHORS Recombinant proteolytic trypsinases, active site mutants thereof, and
TITLE methods of making same
JOURNAL Patent: WO 0198470-A 5 27-DEC-2001;
PROMEGA CORPORATION (US)
FEATURES
source location/Qualifiers
1..771
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
CDS
1..756
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD22417.1"
/db_xref="GI:18495645"
/translation="LEKRIVGQAPRSKWPQVSLRVHGYPMHFGGSLIHPQWVL
TAACVGPDKDLAALRVQLREQLHYQDQLLPVSRILVHPQFYTAQIGAAIALLELE
EPVNVSHVHTVTLPPASETPPPGMPQWVGWDVNDRLPPFPPLKQKVPIMENH
ICDAKYLHGAVTGDDVIRVDRMLCAGNTRDSCQSDGSLVCKVNGTWLQAGVWSV
GEGCAQPNRPGIYTRVITYLDWIHHVYKPE"
ORIGIN
Query Match 99.0%; Score 763; DB 6; Length 771;
Best Local Similarity 99.4%; Pred. No. 4.8e-116;
Matches 766; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 GGGCCCCCTCGAGAAAGAAATCGTGGGGGTGAGAGGCCCCCAGAGCAAGTGCCCTGG 60
DB 1 GGGCCCCCTCGAGAAAGAAATCGTGGGGGTGAGAGGCCCCCAGAGCAAGTGCCCTGG 60
QY 61 CAGGTGAGCCTGAGAGTCCAGCGGCCATCTCTGATGCACTTCTCGGGGGGTCCCTCATC 120
DB 61 CAGGTGAGCCTGAGAGTCCAGCGGCCATCTCTGATGCACTTCTCGGGGGGTCCCTCATC 120
QY 121 CACCCCGAGTGGTGCTGACCGCGCGCGTGTGGGACCGAGCTCAAGGATCTGGCC 180
DB 121 CACCCCGAGTGGTGCTGACCGCGCGCGTGTGGGACCGAGCTCAAGGATCTGGCC 180
QY 181 GCCCTCAGGGTGCAACTCGCGGAGCAGCACCTCTACTACAGGACCACTGCTGCCGTC 240
DB 181 GCCCTCAGGGTGCAACTCGCGGAGCAGCACCTCTACTACAGGACCACTGCTGCCGTC 240
QY 241 AGCAGGATCATCGTGCAACCCAGCTTCTACACCGCCAGATCGGAGCGGACATCGCCCTG 300
DB 241 AGCAGGATCATCGTGCAACCCAGCTTCTACACCGCCAGATCGGAGCGGACATCGCCCTG 300
QY 301 CTGAGCTGGAGGAGCGGTGAAGTCTCCAGCCACGTCACAGCTCAACCTGCCCCCT 360
DB 301 CTGAGCTGGAGGAGCGGTGAAGTCTCCAGCCACGTCACAGCTCAACCTGCCCCCT 360
QY 361 GCCTCAGAGACCTTCCCCCGGGATGCCGTGCTGGGTCACTGGTGGGGGATGTGGAC 420
DB 361 GCCTCAGAGACCTTCCCCCGGGATGCCGTGCTGGGTCACTGGTGGGGGATGTGGAC 420
QY 421 AATGATGAGCGCTCCACCGCCATTCTCTGAAGCAGGTGAAGGTCCCCCATATGGA 480
DB 421 AATGATGAGCGCTCCACCGCCATTCTCTGAAGCAGGTGAAGGTCCCCCATATGGA 480
QY 481 AACCAATTTGTAGCGAAATATACCACTTGGCGCTTACAGGAGACGATCGGCATC 540
DB 481 AACCAATTTGTAGCGAAATATACCACTTGGCGCTTACAGGAGACGATCGGCATC 540

QY 541 GTCCGTGACGACATGCTGTGTGCCGGAACACCCGGAGGGACTCATGCCAGGGGACTCC 600
DB 541 GTCCGTGACGACATGCTGTGTGCCGGAACACCCGGAGGGACTCATGCCAGGGGACTCC 600
QY 601 GGAGGGCCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCGAGGGGGCGTGTGCTCAGCTGG 660
DB 601 GGAGGGCCCCCTGGTGTGCAAGGTGAATGGCACCTGGCTGCGAGGGGGCGTGTGCTCAGCTGG 660
QY 661 GGCAGGGCTGTGCCGACCCCAACCGGCTGGCATCTACACCGTGTCACTTACTTCTT 720
DB 661 GGCAGGGCTGTGCCGACCCCAACCGGCTGGCATCTACACCGTGTCACTTACTTCTT 720
QY 721 GACTGGATCCACCACTATGTCCCAAAAGCCGTGAAGCGGCCGCCGCTCGT 771
DB 721 GACTGGATCCACCACTATGTCCCAAAAGCCGTGAAGCGGCCGCCGCTCGT 771
RESULT 7
AX347855
LOCUS AX347855 771 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 22 from Patent WO0198470.
ACCESSION AX347855
VERSION AX347855.1 GI:18495662
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Maffit,M., Niles,A.L. and Haak-Frendscho,M.
AUTHORS Recombinant proteolytic trypsinases, active site mutants thereof, and
TITLE methods of making same
JOURNAL Patent: WO 0198470-A 22 27-DEC-2001;
PROMEGA CORPORATION (US)
FEATURES
source location/Qualifiers
1..771
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
CDS
1..756
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD22421.1"
/db_xref="GI:18495663"
/translation="LEKRIVGQAPRSKWPQVSLRVHGYPMHFGGSLIHPQWVL
TAACVGPDKDLAALRVQLREQLHYQDQLLPVSRILVHPQFYTAQIGAAIALLELE
EPVNVSHVHTVTLPPASETPPPGMPQWVGWDVNDRLPPFPPLKQKVPIMENH
ICDAKYLHGAVTGDDVIRVDRMLCAGNTRDSCQSDGSLVCKVNGTWLQAGVWSV
GEGCAQPNRPGIYTRVITYLDWIHHVYKPE"
ORIGIN
Query Match 98.8%; Score 761.4; DB 6; Length 771;
Best Local Similarity 99.2%; Pred. No. 8.7e-116;
Matches 765; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 GGGCCCCCTCGAGAAAGAAATCGTGGGGGTGAGAGGCCCCCAGAGCAAGTGCCCTGG 60
DB 1 GGGCCCCCTCGAGAAAGAAATCGTGGGGGTGAGAGGCCCCCAGAGCAAGTGCCCTGG 60
QY 61 CAGGTGAGCCTGAGAGTCCAGCGGCCATCTCTGATGCACTTCTCGGGGGGTCCCTCATC 120
DB 61 CAGGTGAGCCTGAGAGTCCAGCGGCCATCTCTGATGCACTTCTCGGGGGGTCCCTCATC 120
QY 121 CACCCCGAGTGGTGCTGACCGCGCGCGTGTGGGACCGAGCTCAAGGATCTGGCC 180
DB 121 CACCCCGAGTGGTGCTGACCGCGCGCGTGTGGGACCGAGCTCAAGGATCTGGCC 180
QY 181 GCCCTCAGGGTGCAACTCGCGGAGCAGCACCTCTACTACAGGACCACTGCTGCCGTC 240
DB 181 GCCCTCAGGGTGCAACTCGCGGAGCAGCACCTCTACTACAGGACCACTGCTGCCGTC 240


```

QY 241 AGCAGGATCATCTGTCACCCACAGTTCTACACCGCCAGATCGAGCGGACATCGCCCTG 300
Db 241 AGCAGGATCATCTGTCACCCACAGTTCTACACCGCCAGATCGAGCGGACATCGCCCTG 300
QY 301 CTGAGCTGAGAGGCGCGGTGAAGTCTCAGCCACGTCACACGCTCACCCTGCCCT 360
Db 301 CTGAGCTGAGAGGCGCGGTGAAGTCTCAGCCACGTCACACGCTCACCCTGCCCT 360
QY 361 GCCTCAGAGACCTTCCCGCGGGATCGGTGCTGGGTCACTGCTGGGGCGATGTGGAC 420
Db 361 GCCTCAGAGACCTTCCCGCGGGATCGGTGCTGGGTCACTGCTGGGGCGATGTGGAC 420
QY 421 AATGATGAGCGCTTCCACCGCCATTTCTCTGAAGCAGGTGAAGTCCCATATGAA 480
Db 421 AATGATGAGCGCTTCCACCGCCATTTCTCTGAAGCAGGTGAAGTCCCATATGAA 480
QY 481 AACACATTTGTACGCAAAATACCACTTTGGCGCTTACAGGGAGACGATCGGCATC 540
Db 481 AACACATTTGTACGCAAAATACCACTTTGGCGCTTACAGGGAGACGATCGGCATC 540
QY 541 GTCCGTGACGACATGCTGTGCGGGAAACACCGGAGGACTCATGCCAGGGCGACTCC 600
Db 541 GTCCGTGACGACATGCTGTGCGGGAAACACCGGAGGACTCATGCCAGGGCGACTCC 600
QY 601 GGAGGGCCCTGTGTGCAAGGTGAATGGACCTGTGGCTGACAGCGCGGTGCTGAGTGG 660
Db 601 GGAGGGCCCTGTGTGCAAGGTGAATGGACCTGTGGCTGACAGCGCGGTGCTGAGTGG 660
QY 661 GCGAGGGCTGTCCAGCGCCACCGCGCTGGATCTACACCGTGTCACTACTACTTGG 720
Db 661 GCGAGGGCTGTCCAGCGCCACCGCGCTGGATCTACACCGTGTCACTACTACTTGG 720
QY 721 GACTGGATCCACCACTATGTCCTCCCAAAAGCGGTGAAGCGCGCGCGCTCGT 771
Db 721 GACTGGATCCACCACTATGTCCTCCCAAAAGCGGTGAAGCGCGCGCGCTCGT 771

```

```

RESULT 8
AX347871
LOCUS AX347871 771 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 38 from Patent WO0198470.
ACCESSION AX347871
VERSION AX347871.1 GI:18495678
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Maffit,M., Niles,A.L. and Haak-Frendscho,M.
TITLE Recombinant proteolytic tryptases, active site mutants thereof, and methods of making same
JOURNAL Patent: WO 0198470-A 38 27-DEC-2001;
PROMEGA CORPORATION (US)
FEATURES
source location/Qualifiers
1. .771
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
<7..756
/notes="unnamed protein product"
/codon_start=1
/protein_id="CAD22429.1"
/db_xref="GI:18495678"
/db_xref="REMBL:CAD22429"
/translacion="LEKRIVGQAPSKWPMQVSLRVHPYNNHFGSILHPQWVL
TAACVGPDKVIAALRVQLRQHLHYQDLFPVRLIVPQFTAQIGRAIALLELE
EPNVSHVITVILPPASETFPPGMPQWVTGWDVNDRLPPFPPLKQKVPIMENH
ICDAKHLGATGDSVIRVMDLACNTRDSCQSGDGLVCKVNGTWMQAGWSW
GEGCAQPNRFGIYTRVITYLDWIHHYVFKFP"
ORIGIN
Query Match 98.5%; Score 759.8; DB 6; Length 771;

```

```

Best Local Similarity 99.1%; Pred. No. 1.6e-115;
Matches 764; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 GGGCCCTCAGAAAAGATCGTGGGGTTCAGAGGCGCCCGAGGACAAAGTGGCCCTGG 60
Db 1 GGGCCCTCAGAAAAGATCGTGGGGTTCAGAGGCGCCCGAGGACAAAGTGGCCCTGG 60
QY 61 CAGTGAGCTGAGAGTCCACGGCCCATCTGATGACATTTCTGCGGGGGCTCCCTCATC 120
Db 61 CAGTGAGCTGAGAGTCCACGGCCCATCTGATGACATTTCTGCGGGGGCTCCCTCATC 120
QY 121 CACCCAGTGGGTGTGACCGCGGGCGGTGCGTGGGACCGGACGTCFAAGGATCTGGCC 180
Db 121 CACCCAGTGGGTGTGACCGCGGGCGGTGCGTGGGACCGGACGTCFAAGGATCTGGCC 180
QY 181 GCCTCAGGGTGAACCTGCGGAGGACGACCTCTACTACAGGACGACGCTGCTGCCGTC 240
Db 181 GCCTCAGGGTGAACCTGCGGAGGACGACCTCTACTACAGGACGACGCTGCTGCCGTC 240
QY 241 AGCAGGATCATCTGTCGACCCACAGTTCTACACCGCCAGATCGAGCGGCAATCGCCTG 300
Db 241 AGCAGGATCATCTGTCGACCCACAGTTCTACACCGCCAGATCGAGCGGCAATCGCCTG 300
QY 301 CTGAGCTGAGAGGCGCGGTGAAGTCTCAGCCACGTCACACGCTCACCTGCCCT 360
Db 301 CTGAGCTGAGAGGCGCGGTGAAGTCTCAGCCACGTCACACGCTCACCTGCCCT 360
QY 361 GCCTCAGAGACCTTCCCGCGGGATCGGTGCTGGGTCACTGCTGGGGCGATGTGGAC 420
Db 361 GCCTCAGAGACCTTCCCGCGGGATCGGTGCTGGGTCACTGCTGGGGCGATGTGGAC 420
QY 421 AATGATGAGCGCTTCCACCGCCATTTCTCTGAAGCAGGTGAAGTCCCATATGAA 480
Db 421 AATGATGAGCGCTTCCACCGCCATTTCTCTGAAGCAGGTGAAGTCCCATATGAA 480
QY 481 AACACATTTGTACGCAAAATACCACTTTGGCGCTTACAGGGAGACGATCGGCATC 540
Db 481 AACACATTTGTACGCAAAATACCACTTTGGCGCTTACAGGGAGACGATCGGCATC 540
QY 541 GTCCGTGACGACATGCTGTGCGGGAAACACCGGAGGACTCATGCCAGGGCGACTCC 600
Db 541 GTCCGTGACGACATGCTGTGCGGGAAACACCGGAGGACTCATGCCAGGGCGACTCC 600
QY 601 GGAGGGCCCTGTGTGCAAGGTGAATGGACCTGTGGCTGACAGCGCGGTGCTGAGTGG 660
Db 601 GGAGGGCCCTGTGTGCAAGGTGAATGGACCTGTGGCTGACAGCGCGGTGCTGAGTGG 660
QY 661 GCGAGGGCTGTCCAGCGCCACCGCGCTGGATCTACACCGTGTCACTACTACTTGG 720
Db 661 GCGAGGGCTGTCCAGCGCCACCGCGCTGGATCTACACCGTGTCACTACTACTTGG 720
QY 721 GACTGGATCCACCACTATGTCCTCCCAAAAGCGGTGAAGCGCGCGCGCTCGT 771
Db 721 GACTGGATCCACCACTATGTCCTCCCAAAAGCGGTGAAGCGCGCGCGCTCGT 771
RESULT 9
AX347857
LOCUS AX347857 771 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 24 from Patent WO0198470.
ACCESSION AX347857
VERSION AX347857.1 GI:18495664
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Maffit,M., Niles,A.L. and Haak-Frendscho,M.
TITLE Recombinant proteolytic tryptases, active site mutants thereof, and methods of making same
JOURNAL Patent: WO 0198470-A 24 27-DEC-2001;
PROMEGA CORPORATION (US)

```


FEATURES

source

Location/Qualifiers

1..771

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

<7..756

/note="unnamed protein product"

/codon_start=1

/protein_id="CAD22422.1"

/db_xref="GI:18495665"

/db_xref="REMTREMBL:CAD22422"

/translation="LEKRIVGQAPRSKWPQVSLRVHGPYMHFCGSLIHPQWL
TAACHVGPDKDLAALVOLREOHLXYQDQLPVSRITVHPQFVTAQIGADIALLELE
EPVKVSHVHTVTLPPASETPPGMPCWMTGWDVNDRLPPFPPLKQVKVPMENH
ICDAKYHLGATGDDVRIVRDMCLCAGNTRDSCQDAGGFLVCKVNGTWLQAGVWSW
GEGCAQENRPGIYTRVYILDWIIHHYVKKP"

ORIGIN

Query Match 97.9%; Score 755; DB 6; Length 771;
Best Local Similarity 98.7%; Pred. No. 9.9e-115;
Matches 761; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 GGGCCCCCTCGAGAAAAGAAATCGTGGGGGTGAGAGGCCCCCAGAGCAAGTGGCCCTGG 60
DB 1 GGGCCCCCTCGAGAAAAGAAATCGTGGGGGTGAGAGGCCCCCAGAGCAAGTGGCCCTGG 60

QY 61 CAGGTGACCTGAGAGTCCAGGCCCATCTACTGGATGCACTTCTCGGGGGCTCCCTCATC 120
DB 61 CAGGTGACCTGAGAGTCCAGGCCCATCTACTGGATGCACTTCTCGGGGGCTCCCTCATC 120

QY 121 CACCCCCAGTGGGTGCTGACCGCCGCGCGTGGCGGACCGGACCTCAAGGATCTGGCC 180
DB 121 CACCCCCAGTGGGTGCTGACCGCGACGCACTGGTGGGACCGGACCTCAAGGATCTGGCC 180

QY 181 GCCCTCAGGTGCAACTCGCGGAGCAGCACCTCTACTACGAGGACCACTGCTGCGGTC 240
DB 181 GCCCTCAGGTGCAACTCGCGGAGCAGCACCTCTACTACGAGGACCACTGCTGCGGTC 240

QY 241 AGCAGGATCATCTGTCACCGCCGCGTGGCGGACCGGACCTCAAGGATCTGGCC 300
DB 241 AGCAGGATCATCTGTCACCGCCGCGTGGCGGACCGGACCTCAAGGATCTGGCC 300

QY 301 CTGGAGCTGGAGGAGCGGTGAAGTCTCCAGCCACGCTCCACAGGACCACTGCTGCGGTC 360
DB 301 CTGGAGCTGGAGGAGCGGTGAAGTCTCCAGCCACGCTCCACAGGACCACTGCTGCGGTC 360

QY 361 GCCTCAGAGACCTTCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGGAC 420
DB 361 GCCTCAGAGACCTTCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGGAC 420

QY 421 AATGATGAGCGCTCCCAACCGCCATTTCTCTGAAGCAGGTGAAGGTCCCATATGAA 480
DB 421 AATGATGAGCGCTCCCAACCGCCATTTCTCTGAAGCAGGTGAAGGTCCCATATGAA 480

QY 481 AACCACATTTGTGAGCGAAAATACCACTTGGCGCTTACCGGAGACGAGTCCGCATC 540
DB 481 AACCACATTTGTGAGCGAAAATACCACTTGGCGCTTACCGGAGACGAGTCCGCATC 540

QY 541 GTCGCTGACGATCTGTGTGCGGGAAACACCGGAGGAGTCACTGTCAGGGGAGTCC 600
DB 541 GTCGCTGACGATCTGTGTGCGGGAAACACCGGAGGAGTCACTGTCAGGGGAGTCC 600

QY 601 GGAGGCCCCCTGGTGTGAAGTGAATGGCACTGGCTGCGGCGGGGTGGTCAAGTGG 660
DB 601 GGAGGCCCCCTGGTGTGAAGTGAATGGCACTGGCTGCGGCGGGGTGGTCAAGTGG 660

QY 661 GGCGAGGCTGTGCTGCGGACCCCAACCGGCTGGCATCTACCCCGTGTCACTACTTTG 720
DB 661 GGCGAGGCTGTGCTGCGGACCCCAACCGGCTGGCATCTACCCCGTGTCACTACTTTG 720

QY 721 GACTGATCCACCACTATGTCCCCAAAAGCGGTGAAGCGGCGCGCTGCT 771
DB 721 GACTGATCCACCACTATGTCCCCAAAAGCGGTGAAGCGGCGCGCTGCT 771

RESULT 10

AX347859
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

AX347859
Sequence 26 from Patent WO0198470.
AX347859
AX347859.1 GI:18495666
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1
Maffit, M., Niles, A.L. and Haak-Frendscho, M.
Recombinant proteolytic trypsin, active site mutants thereof, and
methods of making same
Patent: WO 0198470-A 26 27-DEC-2001;
PROMEGA CORPORATION (US)
Location/Qualifiers
1..771
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
<7..756
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD22422.1"
/db_xref="GI:18495667"
/db_xref="REMTREMBL:CAD22422"
/translation="LEKRIVGQAPRSKWPQVSLRVHGPYMHFCGSLIHPQWL
TAACHVGPDKDLAALVOLREOHLXYQDQLPVSRITVHPQFVTAQIGADIALLELE
EPVKVSHVHTVTLPPASETPPGMPCWMTGWDVNDRLPPFPPLKQVKVPMENH
ICDAKYHLGATGDDVRIVRDMCLCAGNTRDSCQDAGGFLVCKVNGTWLQAGVWSW
GEGCAQENRPGIYTRVYILDWIIHHYVKKP"

ORIGIN

Query Match 97.9%; Score 755; DB 6; Length 771;
Best Local Similarity 98.7%; Pred. No. 9.9e-115;
Matches 761; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 GGGCCCCCTCGAGAAAAGAAATCGTGGGGGTGAGAGGCCCCCAGAGCAAGTGGCCCTGG 60
DB 1 GGGCCCCCTCGAGAAAAGAAATCGTGGGGGTGAGAGGCCCCCAGAGCAAGTGGCCCTGG 60

QY 61 CAGGTGACCTGAGAGTCCAGGCCCATCTACTGGATGCACTTCTGCGGGGCTCCCTCATC 120
DB 61 CAGGTGACCTGAGAGTCCAGGCCCATCTACTGGATGCACTTCTGCGGGGCTCCCTCATC 120

QY 121 CACCCCCAGTGGGTGCTGACCGCCGCGTGGCGGACCGGACCTCAAGGATCTGGCC 180
DB 121 CACCCCCAGTGGGTGCTGACCGCGACGCACTGGTGGGACCGGACCTCAAGGATCTGGCC 180

QY 181 GCCCTCAGGTGCAACTCGCGGAGCAGCACCTCTACTACGAGGACCACTGCTGCGGTC 240
DB 181 GCCCTCAGGTGCAACTCGCGGAGCAGCACCTCTACTACGAGGACCACTGCTGCGGTC 240

QY 241 AGCAGGATCATCTGTCACCGCCGCGTGGCGGACCGGACCTCAAGGATCTGGCC 300
DB 241 AGCAGGATCATCTGTCACCGCCGCGTGGCGGACCGGACCTCAAGGATCTGGCC 300

QY 301 CTGGAGCTGGAGGAGCGGTGAAGTCTCCAGCCACGCTCCACAGGACCACTGCTGCGGTC 360
DB 301 CTGGAGCTGGAGGAGCGGTGAAGTCTCCAGCCACGCTCCACAGGACCACTGCTGCGGTC 360

QY 361 GCCTCAGAGACCTTCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGGAC 420
DB 361 GCCTCAGAGACCTTCCCCCGGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGGAC 420

QY 421 AATGATGAGCGCTCCCAACCGCCATTTCTCTGAAGCAGGTGAAGGTCCCATATGAA 480
DB 421 AATGATGAGCGCTCCCAACCGCCATTTCTCTGAAGCAGGTGAAGGTCCCATATGAA 480

```

QY 481 AACCACTTTGTGACGCAAAATACCACTTGGCGCTACACGGGAGACGCTCCGCATC 540
Db 481 AACCACTTTGTGACGCAAAATACCACTTGGCGCTACACGGGAGACGCTCCGCATC 540
QY 541 GTCGCTGACGACATGCTGTGTGCGCGAAACACCGGAGGACTCATGCCAGGGCGACTCC 600
Db 541 GTCGCTGACGACATGCTGTGTGCGCGAAACACCGGAGGACTCATGCCAGGAGACGCC 600
QY 601 GGAGGGCCCTGTGTGTCAGAGTGAATGGCACTGGCTGACGGCGGGCGTGGTCACTGG 660
Db 601 GGCGGACCACTGGTGTGCAAGTGAATGGCACTGGCTGACGGCGGGCGTGGTCACTGG 660
QY 661 GGCAGGGCTGTGCCAGCCCAACCGGCTGGCATCTACACCCCTGTCACTACTACTTTG 720
Db 661 GGCAGGGCTGTGCCAGCCCAACCGGCTGGCATCTACACCCCTGTCACTACTACTTTG 720
QY 721 GACTGGATCCACACTATGTCCCAAAAGCCGTGAAGCGCGCCCGCTCGT 771
Db 721 GACTGGATCCACACTATGTCCCAAAAGCCGTGAAGCGCGCCCGCTCGT 771

RESULT 11
AX347873
LOCUS AX347873 771 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 40 from Patent WO0198470.
ACCESSION AX347873
VERSION AX347873.1 GI:18495680
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Maffit, M., Niles, A.L. and Haak-Frendscho, M.
TITLE Recombinant proteolytic trypsinases, active site mutants thereof, and
methods of making same
JOURNAL Patent: WO 0198470-A 40 27-DEC-2001;
PROMEGA CORPORATION (US)
FEATURES
Location/Qualifiers
source 1..771
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
<1..756
/notes="unnamed protein product"
/codon_start=1
/protein_id="CAD22430.1"
/db_xref="GI:18495681"
/db_xref="REMBL:CAD22430"
/translation="GLEKRIVGQEPKRWQVSLRVHGYWVHFGGSLHPQW
VLTAAHCVDPKDLAALRVQLRQHLVYQDLPLVSRIVHPOFYTAQIGADIALLE
LEPYNVSSHVHTVLPASSETFPPGMCWNTGMDVNDRLPPPLKQVPIKME
NHICDAKYLHGYATGDDVRLVRDMLCAGNTRDSCQDAGGLVCKVNGTLQAGV
SWEGCAQPNRPIGYTRVYLDLHIVHVPKKP"

ORIGIN
Query Match 97.7%; Score 753.4; DB 6; Length 771;
Best Local Similarity 98.6%; Pred. No. 1.8e-114;
Matches 760; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GGGCCCCCAGAAAAGATCGTGGGGGTGACGAGGCCCGCCAGAGCAAGTGGCCCTGG 60
Db 1 GGGCCCCCAGAAAAGATCGTGGGGGTGACGAGGCCCGCCAGAGCAAGTGGCCCTGG 60
QY 61 CAGGTGAGCTGAGAGTCCACGGCCCATCTGGATGCATCTCTCGGGGGCTCCCTCATC 120
Db 61 CAGGTGAGCTGAGAGTCCACGGCCCATCTGGATGCATCTCTCGGGGGCTCCCTCATC 120
QY 121 CACCCCGAGTGGGTGCTGACCGCGCGCGTGGTGGGACCGGACGTCGAGGATCTGGCC 180
Db 121 CACCCCGAGTGGGTGCTGACCGCGCGCGTGGTGGGACCGGACGTCGAGGATCTGGCC 180
QY 181 GCCCTCAGGGTGCNACTGCGGGGACACACCTCTACTACAGGACGAGCTGCTCCCGGTC 240

```

```

Db 181 GCCCTCAGGGTGCNACTGCGGGAGCAGCACTCTACTACAGGACGAGCTGCTCCCGGTC 240
QY 241 AGCAGGATCATCGTGCACCCACAGTTCTACACGCCCCAGATCGGAGCGGACATCGCCCTG 300
Db 241 AGCAGGATCATCGTGCACCCACAGTTCTACACGCCCCAGATCGGAGCGGACATCGCCCTG 300
QY 301 CTGGAGCTGAGGAGCGGCTGAGGTTCTCCAGCCACGTCACACGCTCACCTCCGCCCT 360
Db 301 CTGGAGCTGAGGAGCGGCTGAGGTTCTCCAGCCACGTCACACGCTCACCTCCGCCCT 360
QY 361 GCCTCAGAGACCTTCCCTCCCGGGGATGCCGTGTGGGTCACTGGCTGGGGGATGTGGAC 420
Db 361 GCCTCAGAGACCTTCCCTCCCGGGGATGCCGTGTGGGTCACTGGCTGGGGGATGTGGAC 420
QY 421 AATGATGAGGCGCTCCACCGCCATTTCTCTGAAGCAGGTGAAGTCCCCATATGGA 480
Db 421 AATGATGAGGCGCTCCACCGCCATTTCTCTGAAGCAGGTGAAGTCCCCATATGGA 480
QY 481 AACCACTTTGTGACGCAAAATACCACTTGGCGCTACACGGGAGACGCTCCGCATC 540
Db 481 AACCACTTTGTGACGCAAAATACCACTTGGCGCTACACGGGAGACGCTCCGCATC 540
QY 541 GTCGCTGACGACATGCTGTGTGCGCGAAACACCGGAGGACTCATGCCAGGGCGACTCC 600
Db 541 GTCGCTGACGACATGCTGTGTGCGCGAAACACCGGAGGACTCATGCCAGGGCGAGCC 600
QY 601 GGAGGGCCCTGTGTGTCAGAGTGAATGGCACTGGCTGACGGCGGGCGTGGTCACTGG 660
Db 601 GGCGGACCTGTGTGTCAGAGTGAATGGCACTGGCTGACGGCGGGCGTGGTCACTGG 660
QY 661 GGCAGGGCTGTGCCAGCCCAACCGGCTGGCATCTACACCCCTGTCACTACTACTTTG 720
Db 661 GGCAGGGCTGTGCCAGCCCAACCGGCTGGCATCTACACCCCTGTCACTACTACTTTG 720
QY 721 GACTGGATCCACACTATGTCCCAAAAGCCGTGAAGCGCGCCCGCTCGT 771
Db 721 GACTGGATCCACACTATGTCCCAAAAGCCGTGAAGCGCGCCCGCTCGT 771

RESULT 12
AX347875
LOCUS AX347875 771 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 42 from Patent WO0198470.
ACCESSION AX347875
VERSION AX347875.1 GI:18495682
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Maffit, M., Niles, A.L. and Haak-Frendscho, M.
TITLE Recombinant proteolytic trypsinases, active site mutants thereof, and
methods of making same
JOURNAL Patent: WO 0198470-A 42 27-DEC-2001;
PROMEGA CORPORATION (US)
FEATURES
Location/Qualifiers
source 1..771
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
<7..756
/notes="unnamed protein product"
/codon_start=1
/protein_id="CAD22431.1"
/db_xref="GI:18495683"
/db_xref="REMBL:CAD22431"
/translation="LEKRIVGQEPKRWQVSLRVHGYWVHFGGSLHPQWV
TAAHCVDPKDLAALRVQLRQHLVYQDLPLVSRIVHPOFYTAQIGADIALLE
EPYNVSSHVHTVLPASSETFPPGMCWNTGMDVNDRLPPPLKQVPIKMEH
ICDAKYLHGYATGDDVRLVRDMLCAGNTRDSCQDAGGLVCKVNGTLQAGVSW
EGCAQPNRPIGYTRVYLDLHIVHVPKKP"

```

ORIGIN

Query Match 97.7%; Score 753.4; DB 6; Length 771;
Best Local Similarity 98.6%; Pred. No. 1.8e-114;
Matches 760; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GGGCCCCCGAGAAAGAAATCGTCGGGGGTCAGAGAGCCCCCAGAGCAAGTGCGCCCTGG 60
DB 1 GGGCCCCCGAGAAAGAAATCGTCGGGGTCAGAGAGCCCCCAGAGCAAGTGCGCCCTGG 60

QY 61 CAGGTGAGCTGAGAGTCCAGGCCCATCTCTGATGACCTTCTGCGGGGGTCCCTCATC 120
DB 61 CAGGTGAGCTGAGAGTCCAGGCCCATCTCTGATGACCTTCTGCGGGGGTCCCTCATC 120

QY 121 CACCCCCAGTGGTCTGACCGCGCGCTGCGGGACCGGACGCTCAAGATCTGGCC 180
DB 121 CACCCCCAGTGGTCTGACCGCGCGCTGCGGGACCGGACGCTCAAGATCTGGCC 180

QY 181 GCCTCAGGTGCAACTCGGGAGCAGCACCTCTACTACAGGACCAAGCTGTGCGGGTC 240
DB 181 GCCTCAGGTGCAACTCGGGAGCAGCACCTCTACTACAGGACCAAGCTGTGCGGGTC 240

QY 241 AGCAGGATCATCTGTCACCCACAGTCTTACACGCCCGAGATCGAGCGGACATCGCCCTG 300
DB 241 AGCAGGATCATCTGTCACCCACAGTCTTACACGCCCGAGATCGAGCGGACATCGCCCTG 300

QY 301 CTGAGCTGGAGGACCGGTGAACTCTCCAGCCACGTCACAGCTCACCTGCCCCCT 360
DB 301 CTGAGCTGGAGGACCGGTGAACTCTCCAGCCACGTCACAGCTCACCTGCCCCCT 360

QY 361 GCCTCAGAGACCTTCCCCCGGGATGCGGTGCTGGGTCACTGGCTGGGGGATGTGGAC 420
DB 361 GCCTCAGAGACCTTCCCCCGGGATGCGGTGCTGGGTCACTGGCTGGGGGATGTGGAC 420

QY 421 AATGATGAGCGCTCCACCGGCATTTCTCTGAAGCAGGTGAAGTCCCATATGAA 480
DB 421 AATGATGAGCGCTCCACCGGCATTTCTCTGAAGCAGGTGAAGTCCCATATGAA 480

QY 481 AACACATTTGTGACGCAAAATACCACTTGGCGCTTACCGGGAGAGAGCTCGGCATC 540
DB 481 AACACATTTGTGACGCAAAATACCACTTGGCGCTTACCGGGAGAGAGCTCGGCATC 540

QY 541 GTCCGTGACGACATCTGTGTGCGGGAAACACCGGAGGACTCATGCGAGGGGACTCC 600
DB 541 GTCCGTGACGACATCTGTGTGCGGGAAACACCGGAGGACTCATGCGAGGAGAGCC 600

QY 601 GGAGGCGCTGTGTGCAAGGTGAATGGACCTGGCTGCGAGGGGGGTGTGAGCTGG 660
DB 601 GGAGGCGCTGTGTGCAAGGTGAATGGACCTGGCTGCGAGGGGGGTGTGAGCTGG 660

QY 661 GCGGAGGCTGTGCGCCAGCCCAACCGGCTGGCATCTACCCGCTGTCACTACTCTTG 720
DB 661 GCGGAGGCTGTGCGCCAGCCCAACCGGCTGGCATCTACCCGCTGTCACTACTCTTG 720

QY 721 GACTGGATCCCACTATGTCCCAAAAGCGGTGAAGCGCCGCGCT 771
DB 721 GACTGGATCCCACTATGTCCCAAAAGCGGTGAAGCGCCGCGCT 771

RESULT 13

AX347861
LOCUS AX347861 735 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 28 from Patent WO0198470.
ACCESSION AX347861
VERSION AX347861.1 GI:18495668
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 Maffei, M., Niles, A.L. and Haak-Frendscho, M.
AUTHORS Recombinant proteolytic tryptases, active site mutants thereof, and
TITLE

JOURNAL

Patent: WO 0198470-A 28 27-DEC-2001;
PROMEGA CORPORATION (US)
Location/Qualifiers
1. 735

FEATURES

source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
<1..>735
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD22424.1"
/db_xref="GI:18495668"
/db_xref="EMBL:CAD22424"

CDS

/translation="IVGGDEAPRKPQVSLRVHPYWMHPCGSLIHPQVLTAA
CVGPDKDLAALRLVQLRQHLIYQDLPLPVSRIIVHPQFYTAQIGADIALLELPEVK
VSSHVHTVTLPPASETFPGMVCWGTGMDVNDERLPPFLKQKVPINENHICDA
KYLHGAIVTGDVIRVDDMLCAGNTRDSCQDGGPLVCKVNGTWLQAGVVSWGEGC
AQPNRPGIYTRVTYVLDWIHHVVPKP"

ORIGIN

Query Match 95.3%; Score 735; DB 6; Length 735;
Best Local Similarity 100.0%; Pred. No. 2e-111;
Matches 735; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ATCTGCGGGGTCAAGAGGCCGCCAGGAGCAAGTGGCCCTGGCAGGTGAGCTGAGATC 78
DB 1 ATCTGCGGGGTCAAGAGGCCGCCAGGAGCAAGTGGCCCTGGCAGGTGAGCTGAGATC 60

QY 79 CACGCCCATACTGGATGCACTTCTGCGGGGGTCCCTCATCCACCCCGAGTGGGTGCTG 138
DB 61 CACGCCCATACTGGATGCACTTCTGCGGGGGTCCCTCATCCACCCCGAGTGGGTGCTG 120

QY 139 ACCGCGCGGGTCTGCGGGACCGGACGCTCAAGATCTGGCGCCCTCAGGGTGCAATG 198
DB 121 ACCGCGCGGGTCTGCGGGACCGGACGCTCAAGATCTGGCGCCCTCAGGGTGCAATG 180

QY 199 CGGAGAGCAGCACTCTACTACGAGGACGCTGCGGTGCGGTGAGGATCATCGTGAC 258
DB 181 CGGAGAGCAGCACTCTACTACGAGGACGCTGCGGTGCGGTGAGGATCATCGTGAC 240

QY 259 CCACAGTTCTACACCGCCCGAGATCGAGCGGACATCGCCCTGCTGGAGCTGGAGAGCG 318
DB 241 CCACAGTTCTACACCGCCCGAGATCGAGCGGACATCGCCCTGCTGGAGCTGGAGAGCG 300

QY 319 GTGAAGTCTCCAGCAGCTCCACGCTGACCTGCGCCCTGCTGAGACCTTCCCT 378
DB 301 GTGAAGTCTCCAGCAGCTCCACGCTGACCTGCGCCCTGCTGAGACCTTCCCT 360

QY 379 CCGGGATGCGCTGCTGGTCACTGGTGGGGCGATGCGGCAATGATGAGCGCTCCCA 438
DB 361 CCGGGATGCGCTGCTGGTCACTGGTGGGGCGATGCGGCAATGATGAGCGCTCCCA 420

QY 439 CCGCCATTTCTCTGAAGCAGGTGAAGTCCCAATAATGAAAAACCACTTTGTGACGCA 498
DB 421 CCGCCATTTCTCTGAAGCAGGTGAAGTCCCAATAATGAAAAACCACTTTGTGACGCA 480

QY 499 AATACCACTTGGCGCTTACCGGAGAGAGAGCTCGGCAATGCTCGGTGAGCAATGCTG 558
DB 481 AATACCACTTGGCGCTTACCGGAGAGAGAGCTCGGCAATGCTCGGTGAGCAATGCTG 540

QY 559 TGTCCGGGAACACCGGAGGAGCTCATGCGAGGGGACCTCCGAGGGGCCCTGCTGTGC 618
DB 541 TGTCCGGGAACACCGGAGGAGCTCATGCGAGGGGACCTCCGAGGGGCCCTGCTGTGC 600

QY 619 AAGTGAATGSCACTTGGCTGCGGCGGGTGTGCTGAGCTGGGGCGAGGGGTGTGCCAG 678
DB 601 AAGTGAATGSCACTTGGCTGCGGCGGGTGTGCTGAGCTGGGGCGAGGGGTGTGCCAG 660

QY 679 CCNAACCGGCTGGCATCTACACCGGTGTCACCTACTCTACTTGGACTGGATCCACATAT 738
DB 661 CCNAACCGGCTGGCATCTACACCGGTGTCACCTACTCTACTTGGACTGGATCCACATAT 720

```

QY 739 GTCCCAAAAAGCG 753
Db 721 GTCCCAAAAAGCG 735

RESULT 14
AX347877
LOCUS AX347877 735 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 44 from Patent WO0198470.
ACCESSION AX347877
VERSION AX347877.1 GI:18495684
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Maffei, M., Niles, A.L. and Haak-Frendscho, M.
TITLE Recombinant proteolytic trypsinases, active site mutants thereof, and
METHODS of making same
JOURNAL Patent: WO 0198470-A 44 27-DEC-2001;
PROMEGA CORPORATION (US)
FEATURES
Location/Qualifiers
source 1..735
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
<1..>735
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD22432.1"
/db_xref="GI:18495685"
/db_xref="REMTREMBL:CAD22432"
/translation="IVGQAPRSKQWVSLRVHGYWHPFGGSLIHPQWLTAA
CVGPDVNDLALRYLQELHYDQLLPVHFPYTAQIGADIALLELEFPV
VSHRVHTVTPPASETPPGWPCWVTGWGDVNDRLPFPPLKQVXPVMEINHICDA
KYLHGVATGDIVRVDMLCAGNTRDSQGDGGLVCKVNGTWLQAGVVSNGEG
AQPNRPGIYRVTVYLDLIIHYVPKE"

ORIGIN
Query Match 95.1%; Score 733.4; DB 6; Length 735;
Best Local Similarity 99.9%; Pred. No. 3.6e-111;
Matches 734; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 ATCTCGGGGTGAGAGGCCCCCAGAGCAAGTGGCCCTGCGAGGTGAGCTGAGAGTC 78
Db 1 ATCTCGGGGTGAGAGGCCCCCAGAGCAAGTGGCCCTGCGAGGTGAGCTGAGAGTC 60

QY 79 CACGGCCCATCTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCACTGGGTGCTG 138
Db 61 CACGGCCCATCTGGATGCACTTCTGCGGGGGCTCCCTCATCCACCCCACTGGGTGCTG 120

QY 139 ACCGCGGGGTGCGTGGGACCGGACGTCAAGATCTGGCGCCCTCAGGGTGAACCTG 198
Db 121 ACCGCGGGGTGCGTGGGACCGGACGTCAAGATCTGGCGCCCTCAGGGTGAACCTG 180

QY 199 CGGAGAGCAGCACTTACTACAGACCAAGTCTGTCGGGTGAGAGATCATGTCAC 258
Db 181 CGGAGAGCAGCACTTACTACAGACCAAGTCTGTCGGGTGAGAGATCATGTCAC 240

QY 259 CCACAGTTCTACACGGCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGAGCG 318
Db 241 CCACAGTTCTACACGGCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGAGCG 300

QY 319 GTGAGGTCTCAGCAGGTCCACAGTCACTCCCTGCGCCCTGCTCAGACCTTCCC 378
Db 301 GTGAGGTCTCAGCAGGTCCACAGTCACTCCCTGCGCCCTGCTCAGACCTTCCC 360

QY 379 CCGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGCAATGATGAGCGCTCCCA 438
Db 361 CCGGGATGCCGTGCTGGGTCACTGGCTGGGGCGATGTGGCAATGATGAGCGCTCCCA 420

QY 439 CCGCCATTTCTCTGAAGAGGTGAAGGTCCCAATATGGAACCAACATTTGTGACGCA 498

```

```

Db 421 CCGCCATTTCTCTGAAGCAGGTGAAGTCCCCATAATGAAAACACATTTGTGACGCA 480
QY 499 AATATACACCTTGGCGCTACACGGGAGACGCTCGCATGCTCGTACGACATCTG 558
Db 481 AATATACACCTTGGCGCTACACGGGAGACGCTCGCATGCTCGTACGACATCTG 540

QY 559 TGTGCGGGGAACACCGGAGGAGTCAATGCCAGGGGACTCCGGAGGGCCCTGCTGTC 618
Db 541 TGTGCGGGGAACACCGGAGGAGTCAATGCCAGGGGACTCCGGAGGGCCCTGCTGTC 600
QY 619 AAGTGAATGCGACCTTGGCTGCGAGGGGCGTGTGCTGAGCTGGGGCGAGGGGTGTGCCAG 678
Db 601 AAGTGAATGCGACCTTGGCTGCGAGGGGCGTGTGCTGAGCTGGGGCGAGGGGTGTGCCAG 660

QY 679 CCNAACCGGCTGGCATCTACACCCGCTGACCTACCTACTGTTGAGTGGATCCACCATAT 738
Db 661 CCNAACCGGCTGGCATCTACACCCGCTGACCTACTACTTGGACTGGATCCACCATAT 720
QY 739 GTCCCAAAAAGCG 753
Db 721 GTCCCAAAAAGCG 735

RESULT 15
LOCUS AR080461 1128 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 15 from patent US 5968782.
ACCESSION AR080461
VERSION AR080461.1 GI:10007196
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1128)
AUTHORS Stevens, R.L.
TITLE Mast cell protease that cleaves fibrinogen
JOURNAL Patent: US 5968782-A 15 19-OCT-1999;
FEATURES
Location/Qualifiers
source 1..1128
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 94.8%; Score 731; DB 6; Length 1128;
Best Local Similarity 98.7%; Pred. No. 8.3e-111;
Matches 737; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 17 GAATCGTCGGGGTTCAGAGGCCCCCAGAGCAAGTGGCCCTGCGAGGTGAGAGTC 76
Db 87 GCATCGTTGGGGTTCAGAGGCCCCCAGAGCAAGTGGCCCTGCGAGGTGAGAGTC 146

QY 77 TCCACGGCCCATCTGATGCACTTCTCGGGGGCTCCCTCATCACCCCACTGGGTGC 136
Db 147 TCCACGGCCCATCTGATGCACTTCTCGGGGGCTCCCTCATCACCCCACTGGGTGC 206

QY 137 TGACCGCGCGGTGCGTGGGACCGGACGTCAGAGATCTGGCCGCTCAGGGTGAAC 196
Db 207 TGACCGCGCGCATCTGCGTGGGACCGGACGTCAGAGATCTGGCCGCTCAGGGTGAAC 266

QY 197 TCGGGGAGCAGCACTTCTACTACAGGACCAAGTGTGTCGGGTGAGAGATCATGTC 256
Db 267 TCGGGGAGCAGCACTTCTACTACAGGACCAAGTGTGTCGGGTGAGAGATCATGTC 326

QY 257 ACCACAGTCTTACACCGCCAGATCGGAGCGGACATCGCCCTGCTGAGCTGGAGGAGC 316
Db 327 ACCACAGTCTTACACCGCCAGATCGGAGCGGACATCGCCCTGCTGAGCTGGAGGAGC 386

QY 317 CGGTGAAGGTCTCCAGCCACGTCACCGGTCACTGTCGGGTGAGAGATCATGTC 376
Db 387 CGGTGAAGGTCTCCAGCCACGTCACCGGTCACTGTCGGGTGAGAGATCATGTC 446

QY 377 CCGCGGGATGCGGTGCTGGGTGCTGCTGGGGGATGTGACATATGAGCGCCCTCC 436

```

[illegible]

Search completed: July 22, 2004, 12:27:24
Job time : 5134 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 22, 2004, 12:27:31 ; Search time 569 Seconds

(without alignments)
6623.689 Million cell updates/sec

Title: US-09-598-982-20

Perfect score: 771

Sequence: 1 gggccctcgagaaagaat.....cgtgaagcggcgcgtcgt 771

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3216467 seqs, 2444149694 residues

Total number of hits satisfying chosen parameters: 6432934

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	731	94.8	1143	16	US-10-352-684A-47
2	731	94.8	1145	17	US-10-287-226-93
3	730.4	94.7	828	17	US-10-287-226-91
4	726.2	94.2	1081	9	US-09-954-456-2126
5	726.2	94.2	1081	10	US-09-960-706-680
6	726.2	94.2	1081	10	US-09-873-319-427
7	726.2	94.2	1081	10	US-09-873-367C-155
8	718.2	94.2	1081	17	US-10-275-505-27
9	718.2	93.2	2662	17	US-09-873-367C-714
10	700	90.8	828	17	US-10-287-226-89
11	686.2	89.0	1154	16	US-10-352-684A-45
12	686.2	89.0	1158	13	US-10-116-802-240
13	678	87.9	858	17	US-10-287-226-87
14	463	60.1	1187	17	US-10-275-505-22

15	287.4	37.3	846	10	US-09-813-432-11	Sequence 11, Appl
16	287.4	37.3	846	13	US-10-246-583-11	Sequence 11, Appl
17	287.4	37.3	846	16	US-10-174-364-11	Sequence 11, Appl
18	287.4	37.3	846	17	US-10-689-832-11	Sequence 11, Appl
19	275	35.7	383	10	US-09-918-995-6378	Sequence 6378, Ap
20	252.4	32.7	948	13	US-10-150-813-15	Sequence 15, Appl
21	252.4	32.7	948	13	US-10-139-854-15	Sequence 15, Appl
22	252.4	32.7	948	15	US-10-131-409-15	Sequence 15, Appl
23	252.4	32.7	948	16	US-10-150-811-15	Sequence 15, Appl
24	236.4	30.7	858	13	US-10-150-813-21	Sequence 21, Appl
25	236.4	30.7	858	13	US-10-139-854-21	Sequence 21, Appl
26	236.4	30.7	858	15	US-10-131-409-21	Sequence 21, Appl
27	236.4	30.7	858	16	US-10-150-811-21	Sequence 21, Appl
28	233.4	30.3	873	15	US-10-117-323-2	Sequence 2, Appli
29	231.6	30.0	843	13	US-10-150-813-25	Sequence 25, Appl
30	231.6	30.0	843	13	US-10-139-854-25	Sequence 25, Appl
31	231.6	30.0	843	15	US-10-131-409-25	Sequence 25, Appl
32	231.6	30.0	843	16	US-10-150-811-25	Sequence 25, Appl
33	230	29.8	978	15	US-10-311-955-1	Sequence 1, Appli
C 34	223.2	28.9	616	9	US-09-954-456-2242	Sequence 2242, Ap
C 35	223.2	28.9	616	10	US-09-960-706-74	Sequence 74, Appl
C 36	223.2	28.9	616	10	US-09-873-319-51	Sequence 51, Appl
C 37	223.2	28.9	616	10	US-09-873-367C-545	Sequence 545, App
38	221.8	28.8	870	13	US-10-150-813-19	Sequence 19, Appl
39	221.8	28.8	870	13	US-10-139-854-19	Sequence 19, Appl
40	221.8	28.8	870	15	US-10-131-409-19	Sequence 19, Appl
41	221.8	28.8	870	16	US-10-150-811-19	Sequence 19, Appl
42	218.8	28.4	1958	17	US-10-311-035-29	Sequence 29, Appl
43	201.4	26.1	780	15	US-10-266-035-3	Sequence 3, Appli
44	201.4	26.1	783	17	US-10-391-364-22	Sequence 22, Appl
45	201.4	26.1	980	15	US-10-266-035-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

- US-10-352-684A-47
- Sequence 47, Application US/10352684A
- Publication No. US20030215452A1
- GENERAL INFORMATION:
- APPLICANT: Millennium Pharmaceuticals Inc.
- APPLICANT: Carroll, Joseph M.
- APPLICANT: Healy, Aileen
- APPLICANT: Welch, Nadine S.
- APPLICANT: Kelly, Louise M.
- TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
- TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
- TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
- TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
- TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
- FILE REFERENCE: MP102-019P1RNOMIN
- CURRENT APPLICATION NUMBER: US/10352,684A
- CURRENT FILING DATE: 2003-01-28
- PRIOR APPLICATION NUMBER: US 60/354,333
- PRIOR FILING DATE: 2002-02-04
- PRIOR APPLICATION NUMBER: US 60/360,258
- PRIOR FILING DATE: 2002-02-28
- PRIOR APPLICATION NUMBER: US 60/364,476
- PRIOR FILING DATE: 2002-03-15
- PRIOR APPLICATION NUMBER: US 60/375,626
- PRIOR FILING DATE: 2002-04-26
- PRIOR APPLICATION NUMBER: US 60/386,494
- PRIOR FILING DATE: 2002-06-06
- PRIOR APPLICATION NUMBER: US 60/390,965
- PRIOR FILING DATE: 2002-06-24
- PRIOR APPLICATION NUMBER: US 60/392,480
- PRIOR FILING DATE: 2002-06-28
- PRIOR APPLICATION NUMBER: US 60/394,128
- PRIOR FILING DATE: 2002-07-03
- PRIOR APPLICATION NUMBER: US 60/399,783
- PRIOR FILING DATE: 2002-07-31
- PRIOR APPLICATION NUMBER: US 60/403,221

```
; PRIOR FILING DATE: 2002-08-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(833)
US-10-352-684A-47

Query Match          94.8%; Score 731; DB 16; Length 1143;
Best Local Similarity 98.0%; Pred. No. 4.4e-133;
Matches 740; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 17 GAATCGTCGGGGTTCAGAGAGCCCGCCAGGAGCAAGTGGCCCTGCGAGTGAGCTGAGAG 76
Db 94 GCATCGTTGGGGTTCAGAGAGCCCGCCAGGAGCAAGTGGCCCTGCGAGTGAGCTGAGAG 153
QY 77 TCACGGCCCATACTGATGCACTTCTCGGGGGCTCCCTCATCCACCCAGTGGGTGC 136
Db 154 TCACGGCCCATACTGATGCACTTCTCGGGGGCTCCCTCATCCACCCAGTGGGTGC 213
QY 137 TGACCGCGCGGCTGCGTGGGACCGGACGTCAGGATCTGGCCGCTCAGGCTGCAAC 196
Db 214 TGACCGCGCGGCTGCGTGGGACCGGACGTCAGGATCTGGCCGCTCAGGCTGCAAC 273
QY 197 TGGGGAGAGACCTCTTACTACAGGACCAAGTGTGCGGGTTCAGGAGATATCTGTGC 256
Db 274 TGGGGAGAGACCTCTTACTACAGGACCAAGTGTGCGGGTTCAGGAGATATCTGTGC 333
QY 257 ACCACAGTTCTACACCGCCAGATCGGAGGGACATGCGCTGCTGAGCTGAGAGGC 316
Db 334 ACCACAGTTCTACACCGCCAGATCGGAGGGACATGCGCTGCTGAGCTGAGAGGC 393
QY 317 CGGTGAAGGTCTCCAGGACCGTCCACACGCTCAGCTTCCCTGCTGCTCAGAGACCTTC 376
Db 394 CGGTGAAGGTCTCCAGGACCGTCCACACGCTCAGCTTCCCTGCTGCTCAGAGACCTTC 453
QY 377 CCCCAGGATGCGGTGTGGGTCTACTGCTGGGGGATGTGGAATATGATGAGCGCTCC 436
Db 454 CCCCAGGATGCGGTGTGGGTCTACTGCTGGGGGATGTGGAATATGATGAGCGCTCC 513
QY 437 CACCGCATTTCTCTGAGCAGGTGAAGTCCCATTAATGGAATGGAATTTGTGACG 496
Db 514 CACCGCATTTCTCTGAGCAGGTGAAGTCCCATTAATGGAATGGAATTTGTGACG 573
QY 497 CAAATATACCATTTGGGGCTTACACGGGAGACGATCCCGCATCGTCCGTGACGACATGC 556
Db 574 CAAATATACCATTTGGGGCTTACACGGGAGACGATCCCGCATCGTCCGTGACGACATGC 633
QY 557 TGTGTGCGGGAACACCGGAGGATCATGCCAGGGGATCTCCGGAGGGCCCTGTGTGT 616
Db 634 TGTGTGCGGGAACACCGGAGGATCATGCCAGGGGATCTCCGGAGGGCCCTGTGTGT 693
QY 617 GCAAGTGAATGCACTTGGGTGACGGCGGCTGCTGAGTGGGGGAGGGCTGTGCCC 676
Db 694 GCAAGTGAATGCACTTGGGTGACGGCGGCTGCTGAGTGGGGGAGGGCTGTGCCC 753
QY 677 AGCCCAACCGGCTGGCATCTTACACCCGCTGTCACTTACTTGGATGGATCCACCACT 736
Db 754 AGCCCAACCGGCTGGCATCTTACACCCGCTGTCACTTACTTGGATGGATCCACCACT 813
QY 737 ATGTCCCAAAAGCCGTGAAGCGCCCGCGCTGT 771
Db 814 ATGTCCCAAAAGCCGTGAAGCGCCCGCGCTGT 848

RESULT 2
US-10-287-226-93
; Sequence 93, Application US/10287226
```

```
; Publication No. US20040086875A1
; GENERAL INFORMATION:
; APPLICANT: Agee, Michele L.,
; APPLICANT: Alsobrook, John P.,
; APPLICANT: Berghs, Constance,
; APPLICANT: Boldog, Ference,
; APPLICANT: Burgess, Catherine E.,
; APPLICANT: Chant, John S.,
; APPLICANT: Chaudhuri, Amitabha,
; APPLICANT: Dipippo, Vincent A.,
; APPLICANT: Edinger, Shlomit R.,
; APPLICANT: Eisen, Andrew,
; APPLICANT: Ellerman, Karen,
; APPLICANT: Gangolli, Esha A.,
; APPLICANT: Gorman, Linda,
; APPLICANT: Gerlach, Valerie,
; APPLICANT: Ji, Weizhen,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Khrantsov, Nikolai,
; APPLICANT: Li, Li,
; APPLICANT: Malyankar, Uriel M.,
; APPLICANT: MacDougall, John R.,
; APPLICANT: Mezes, Peter S.,
; APPLICANT: Miller, Charles E.,
; APPLICANT: Millet, Isabelle,
; APPLICANT: Ooi, Chean Eng,
; APPLICANT: Ort, Tatiana,
; APPLICANT: Padigaru, Muralidhara,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rastelli, Luca,
; APPLICANT: Rieger, Daniel K.,
; APPLICANT: Rothenberg, Mark E.,
; APPLICANT: Shenoy, Suresh G.,
; APPLICANT: Spaderna, Steven K.,
; APPLICANT: Spytek, Kimberley A.,
; APPLICANT: Taupier, Jr., Raymond J.,
; APPLICANT: Vernet, Corine A.M.,
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-480C
; CURRENT APPLICATION NUMBER: US/10/287,226
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: 60/334,421
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,392
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/360,148
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/364,000
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/404,821
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/334,526
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,409
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/364,227
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/334,027
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/331,641
; PRIOR FILING DATE: 2001-11-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 673
; SOFTWARE: Curaseq version 0.1
; SEQ ID NO 93
; LENGTH: 1145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (8)...(832)
```


US-10-287-226-93

```

Query Match      94.8%; Score 731; DB 17; Length 1145;
Best Local Similarity 98.7%; Pred. No. 4.4e-193;
Matches 737; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 17 GAATCGTCGGGGTFCAGAGAGCCCGCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
Db 96 GCATCGTGGGGTFCAGAGAGCCCGCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 155

Qy 77 TCCACGGCCCATCTGATGATCTTCTCGGGGGCTCCCTCATCCACCCCGAGTGGTGC 136
Db 156 TCCACGGCCCATCTGATGATCTTCTCGGGGGCTCCCTCATCCACCCCGAGTGGTGC 215

Qy 137 TGACCGCGGGCGTGGTGGGACCGGAGCTCAAGGATCTGGCCGCCCTCAGGTGCAAC 196
Db 216 TGACCGCGAGCGCATGGGTGGGACCGGAGCTCAAGGATCTGGCCGCCCTCAGGTGCAAC 275

Qy 197 TCGGGAGCAGCAGCTCTACTTACCAGGACCAAGCTGCTGCCGCTCAGCAGGATCATCTGTC 256
Db 276 TCGGGAGCAGCAGCTCTACTTACCAGGACCAAGCTGCTGCCGCTCAGCAGGATCATCTGTC 335

Qy 257 ACCACAGTTCTTACCGCCCGCAGATCGGAGCGGATCGCCCTCTGGAGCTGAGGAGC 316
Db 336 ACCACAGTTCTTACCGCCCGCAGATCGGAGCGGATCGCCCTCTGGAGCTGAGGAGC 395

Qy 317 CGGTGAAGGTCTCCAGCCAGCTCCACAGGTCACCGCTGCCCGCCCTCAGGACCTTC 376
Db 396 CGGTGAAGGTCTCCAGCCAGCTCCACAGGTCACCGCTGCCCGCCCTCAGGACCTTC 455

Qy 377 CCGCGGGATCGCTGCTGGTCACTGGCTGGGGCGATGTGCAATGATGAGCGCCTCC 436
Db 456 CCGCGGGATCGCTGCTGGTCACTGGCTGGGGCGATGTGCAATGATGAGCGCCTCC 515

Qy 437 CACCGCATTTCTTCTGAAGCAGTGAAGTCCCAATGATGAGGAGGAGGAGGAGG 496
Db 516 CACCGCATTTCTTCTGAAGCAGTGAAGTCCCAATGATGAGGAGGAGGAGGAGG 575

Qy 497 CAATATCACCTTGGCGCTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 556
Db 576 CAATATCACCTTGGCGCTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 635

Qy 557 TGTGTGCGGGAAACACCGGAGGAGTCACTCCAGGAGGAGTCCCGGAGGGCCCTGGTGT 616
Db 636 TGTGTGCGGGAAACACCGGAGGAGTCACTCCAGGAGGAGTCCCGGAGGGCCCTGGTGT 695

Qy 617 GCAAGGTGAATGGACCTGGCTGACGGGCGGCTGGTGGTGGGGGAGGGCTGTGCCC 676
Db 696 GCAAGGTGAATGGACCTGGCTGACGGGCGGCTGGTGGTGGGGGAGGGCTGTGCCC 755

Qy 677 AGCCCAACCGGCGTGGCATCTACACCGGTGTCACCTACTTCTGACTGGATCCACCACT 736
Db 756 AGCCCAACCGGCGTGGCATCTACACCGGTGTCACCTACTTCTGACTGGATCCACCACT 815

Qy 737 ATGTCCCAAAAGCCGTGAAGCGGCC 763
Db 816 ATGTCCCAAAAGCCGTGAAGCGGCC 842

```

RESULT 3
 US-10-287-226-91
 ; Sequence 91, Application US/10287226
 ; Publication No. US20040086875A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agee, Michele L.,
 ; APPLICANT: Alsbrook, John P.,
 ; APPLICANT: Berghs, Constance,
 ; APPLICANT: Boldog, Ference,
 ; APPLICANT: Burgess, Catherine E.,
 ; APPLICANT: Chant, John S.,
 ; APPLICANT: Chaudhuri, Amitabha,
 ; APPLICANT: DiPippo, Vincent A.,
 ; APPLICANT: Edinger, Shlomit R.,

```

; APPLICANT: Eisen, Andrew,  

; APPLICANT: Ellerman, Karen,  

; APPLICANT: Gangolli, Esna A.,  

; APPLICANT: Gorman, Linda,  

; APPLICANT: Gerlach, Valerie,  

; APPLICANT: Ji, Weizhen,  

; APPLICANT: Kekuda, Ramesh,  

; APPLICANT: Khrantsov, Nikolai,  

; APPLICANT: Li, Li,  

; APPLICANT: Malyankar, Uriel M.,  

; APPLICANT: MacDougall, John R.,  

; APPLICANT: Mezes, Peter S.,  

; APPLICANT: Miller, Charles E.,  

; APPLICANT: Millet, Isabelle,  

; APPLICANT: Ooi, Chean Eng,  

; APPLICANT: Ort, Tatiana,  

; APPLICANT: Padigar, Muralidhara,  

; APPLICANT: Patturajan, Meera,  

; APPLICANT: Rastelli, Luca,  

; APPLICANT: Rieger, Daniel K.,  

; APPLICANT: Rothenberg, Mark E.,  

; APPLICANT: Shenoy, Suresh G.,  

; APPLICANT: Spaderna, Steven K.,  

; APPLICANT: Spytek, Kimberley A.,  

; APPLICANT: Taupier, Jr., Raymond J.,  

; APPLICANT: Vernet, Corine A.M.,  

; APPLICANT: Zerhusen, Bryan D.,  

; APPLICANT: Zhong, Mei  

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  

; FILE REFERENCE: 21402-480C  

; CURRENT APPLICATION NUMBER: US/10/287,226  

; PRIOR FILING DATE: 2002-11-04  

; PRIOR APPLICATION NUMBER: 60/334,421  

; PRIOR FILING DATE: 2001-11-30  

; PRIOR APPLICATION NUMBER: 60/354,392  

; PRIOR FILING DATE: 2002-02-04  

; PRIOR APPLICATION NUMBER: 60/360,148  

; PRIOR FILING DATE: 2002-02-27  

; PRIOR APPLICATION NUMBER: 60/364,000  

; PRIOR FILING DATE: 2002-03-13  

; PRIOR APPLICATION NUMBER: 60/404,821  

; PRIOR FILING DATE: 2002-08-20  

; PRIOR APPLICATION NUMBER: 60/334,526  

; PRIOR FILING DATE: 2001-11-30  

; PRIOR APPLICATION NUMBER: 60/354,409  

; PRIOR FILING DATE: 2002-02-04  

; PRIOR APPLICATION NUMBER: 60/364,227  

; PRIOR FILING DATE: 2002-03-13  

; PRIOR APPLICATION NUMBER: 60/334,027  

; PRIOR FILING DATE: 2001-11-28  

; PRIOR APPLICATION NUMBER: 60/331,641  

; PRIOR FILING DATE: 2001-11-20  

; Remaining Prior Application data removed - See File Wrapper or PALM.  

; NUMBER OF SEQ ID NOS: 673  

; SOFTWARE: CuraseqList version 0.1  

; SEQ ID NO 91  

; LENGTH: 828  

; TYPE: DNA  

; ORGANISM: Homo sapiens  

; FEATURE:  

; NAME/KEY: CDS  

; LOCATION: (1)..(825)  

; US-10-287-226-91

```

Query Match 94.7%; Score 730.4; DB 17; Length 828;
 Best Local Similarity 99.2%; Pred. No. 6.1e-193;
 Matches 734; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

 Qy 17 GAATCGTCGGGGTFCAGAGAGCCCGCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
 Db 89 GCATCGTGGGGTFCAGAGAGCCCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 148
 Qy 77 TCCACGGCCCATCTGATGATCTTCTCGGGGGCTCCCTCATCCACCCCGAGTGGTGC 136

Db 726 AGCCCAACCGCGCTGCGCATCTTAACCCGCTGTCACCTACTTGGACTGGATCCACCCT 785

QY 737 ATGTCCCCCAAAAAGCGTGAAGCGGC 763
 |||||
 Db 786 ATGTCCCAAAAAGCGTGAAGCGGC 812
 |||||

RESULT 6
 US-09-873-319-427
 ; Sequence 427, Application US/09873319A
 ; Publication No. US20030134324A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Munger, William E.
 ; APPLICANT: Kulkarni, Prakash
 ; APPLICANT: Getzenberg, Robert H.
 ; APPLICANT: Waga, Iwao
 ; APPLICANT: Yamamoto, Jun
 ; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic
 ; TITLE OF INVENTION: Hyperplasia Using Gene Expression Profiles
 ; FILE REFERENCE: 44921-5029-US
 ; CURRENT APPLICATION NUMBER: US/09/873,319A
 ; CURRENT FILING DATE: 2001-06-05
 ; EARLIER APPLICATION NUMBER: US 60/223,323
 ; EARLIER FILING DATE: 2000-08-07
 ; NUMBER OF SEQ ID NOS: 755
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 427
 ; LENGTH: 1081
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Genbank Accession No. US20030134324A1 M33493
 US-09-873-319-427

Query Match 94.2%; Score 726.2; DB 10; Length 1081;
 Best Local Similarity 98.3%; Pred. No. 9.3e-192;
 Matches 734; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 17 GAATCGTCGGGGGTACGAGGCCCCAGAGCAAGTGGCCCTGGCAGGTGAGCCTCAGAG 76
 |||||
 Db 66 GCATCGTTGGGGTACGAGGCCCCAGAGCAAGTGGCCCTGGCAGGTGAGCCTCAGAG 125
 |||||

QY 77 TCCACGGCCCATACTCGATGCATCTTCGGGGGGCTCCCTCATCCACCCCGAGTGGGTGC 136
 |||||
 Db 126 TCGCGACCGATACTGGATGCATCTTCGGGGGGTCCCTCATCCACCCCGAGTGGGTGC 185
 |||||

QY 137 TGACCGCGCGGGTTCGCTGGACCGGACGTCAAGATCTGGCCGCCCTCAGGGTGCAC 196
 |||||
 Db 186 TGACCGCAGCGCACTCGCTGGGACCGGACGTCAAGGATCTGGCCGCCCTCAGGGTGCAC 245
 |||||

QY 197 TGGCGGAGCAGCACCTCTACTACCGAGGACAGTCTGCCGGTTCAGCAGGATCATCGTC 256
 |||||
 Db 246 TGGCGGAGCAGCACCTCTACTACCGAGGACAGTCTGCCGGTTCAGCAGGATCATCGTC 305
 |||||

QY 257 ACCCAGATTCTACACCGCCCGATCGGACGGACATCGCCCTCTGTGGAGCTGGAGGAGC 316
 |||||
 Db 306 ACCCAGATTCTACACCGCCCGATCGGACGGACATCGCCCTCTGTGGAGCTGGAGGAGC 365
 |||||

QY 317 CGGTGAAGTCTCCAGCAGCTCCACCGGTCACTGCCCTGCCCTCGCTCAGAGACCTTCC 376
 |||||
 Db 366 CGGTGAAGTCTCCAGCAGCTCCACCGGTCACTGCCCTGCCCTCGCTCAGAGACCTTCC 425
 |||||

QY 377 CCGCGGGATGCGGTCTGGGTCACTGGTGGGGCGATGAGCATGATGAGCGCCTCC 436
 |||||
 Db 426 CCGCGGGATGCGGTCTGGGTCACTGGTGGGGCGATGAGCATGATGAGCGCCTCC 485
 |||||

QY 437 CACCGCATTTCTCTGAAGCAGGTGAAGGTCCCATATGAAACCAATTTGTGAGC 496
 |||||
 Db 486 CACCGCATTTCTCTGAAGCAGGTGAAGGTCCCATATGAAACCAATTTGTGAGC 545
 |||||

QY 497 CAAATACCACCTTGGCGCTTACCGGGAGACGATCCGCGCATCGTCCGTGACGACATGC 556
 |||||
 Db 546 CAAATACCACCTTGGCGCTTACCGGGAGACGATCCGCGCATCGTCCGTGACGACATGC 605
 |||||

557 TGTGTGCGGGAAACACCCGAGGAGCTCATCCAGGCGGACTCCGGAGGCGCCCTGGTGT 616
 606 TGTGTGCGGGAAACACCCGAGGAGCTCATCCAGGCGGACTCCGGAGGCGCCCTGGTGT 665
 617 GCAAGGTGAATGACACTGCTGCTGCAGGCGGCGTGTGTCAGCTGGGGGAGGGTGTGCC 676
 666 GCAAGGTGAATGACACTGCTGCTGCAGGCGGCGTGTGTCAGCTGGGGGAGGGTGTGCC 725
 677 AGCCCAACCGGCTGCGATCTACACCGCTGTCACCTACTTACTTGGATCGATCCACACT 736
 726 AGCCCAACCGGCTGCGATCTACACCGCTGTCACCTACTTACTTGGATCGATCCACACT 785
 737 ATGTCCCAAAAGCCGTGAAGCGGC 763
 786 ATGTCCCAAAAGCCGTGAGTCAGGC 812

RESULT 7
 US-09-873-367C-155
 ; Sequence 155, Application US/09873367C
 ; Publication No. US20030165839A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Paul
 ; APPLICANT: Soppet, Daniel
 ; APPLICANT: Endress, Gregory
 ; APPLICANT: Augustus, Meena
 ; APPLICANT: Ebner, Reinhard
 ; APPLICANT: Carter, Kenneth
 ; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
 ; FILE OF INVENTION: Signature Gene Sets
 ; FILE REFERENCE: 689290-64
 ; CURRENT FILING DATE: 2003-04-29
 ; PRIOR APPLICATION NUMBER: U.S. 60/236,891
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: U.S. 60/236,842
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: U.S. 60/244,867
 ; PRIOR FILING DATE: 2000-11-01
 ; PRIOR APPLICATION NUMBER: U.S. 60/245,084
 ; PRIOR FILING DATE: 2000-11-01
 ; NUMBER OF SEQ ID NOS: 1067
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 155
 ; LENGTH: 1081
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-873-367C-155

Query Match 94.2%; Score 726.2; DB 10; Length 1081;
 Best Local Similarity 98.3%; Pred. No. 9.3e-192;
 Matches 734; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

17 GAATCGTGGGGTCAAGAGGCGCCCGAGGAGCAAGTGGCGGCTCCCTCATCCACCCAGTGGGTGC 76
 66 GCATCGTGGGGTCAAGAGGCGCCCGAGGAGCAAGTGGCGGCTCCCTCATCCACCCAGTGGGTGC 125
 77 TCACCGGCGGCTGAGTGCATCTTCTCGGGGCTCCCTCATCCACCCAGTGGGTGC 136
 126 TCGGAGCCGATGAGTGCATCTTCTCGGGGCTCCCTCATCCACCCAGTGGGTGC 185
 137 TGACCGCGGCGGCTGAGTGCATCTTCTCGGGGCTCCCTCATCCACCCAGTGGGTGC 196
 186 TGACCGCGGCGGCTGAGTGCATCTTCTCGGGGCTCCCTCATCCACCCAGTGGGTGC 245
 197 TGCGGGGAGCAGCTTACTTACAGGAGCAGTGTGCTGCGGTCAGGAGTATCTGTC 256
 246 TGCGGGGAGCAGCTTACTTACAGGAGCAGTGTGCTGCGGTCAGGAGTATCTGTC 305
 257 ACCACAGTTCATACACCGCCAGATCGAGGCGGACATCGCCCTGCTGAGCTGGAGGAGC 316
 306 ACCACAGTTCATACACCGCCAGATCGAGGCGGACATCGCCCTGCTGAGCTGGAGGAGC 365

317 CGTGAAGGTCTCCAGCCAGCTCCACACGCTCACCCCTGCCCCCTGCTCAGAGACCTTCC 376
 366 CGTGAAGGTCTCCAGCCAGCTCCACACGCTCACCCCTGCCCCCTGCTCAGAGACCTTCC 425
 377 CCCCAGGATGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 436
 426 CCCCAGGATGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 485
 437 CACCGCATTTCTCTGAAGCAGTGAAGTCCCATATATGGAACCAACCATTTGTGACG 496
 486 CACCGCATTTCTCTGAAGCAGTGAAGTCCCATATATGGAACCAACCATTTGTGACG 545
 497 CAAATACACCTTGGCGCTTACACGGGAGACGACGCTCCCGCATCTGCTGCTGCTGCTGCT 556
 546 CAAATACACCTTGGCGCTTACACGGGAGACGACGCTCCCGCATCTGCTGCTGCTGCTGCT 605
 557 TGTGTGCGGGAAACACCCGAGGAGCTCATGCGAGGCGGACTCCGGAGGCGCCCTGGTGT 616
 606 TGTGTGCGGGAAACACCCGAGGAGCTCATGCGAGGAGCTCATGCGAGGCGCCCTGGTGT 665
 617 GCAAGGTGAATGACACTGCTGCTGCAGGCGGCGTGTGTCAGCTGGGGGAGGGTGTGCC 676
 666 GCAAGGTGAATGACACTGCTGCTGCAGGCGGCGTGTGTCAGCTGGGGGAGGGTGTGCC 725
 677 AGCCCAACCGGCTGCGATCTACACCGCTGTCACCTACTTACTTGGATCGATCCACACT 736
 726 AGCCCAACCGGCTGCGATCTACACCGCTGTCACCTACTTACTTGGATCGATCCACACT 785
 737 ATGTCCCAAAAGCCGTGAAGCGGC 763
 786 ATGTCCCAAAAGCCGTGAGTCAGGC 812

RESULT 8
 US-09-873-367C-714
 ; Sequence 714, Application US/09873367C
 ; Publication No. US20030165839A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Paul
 ; APPLICANT: Soppet, Daniel
 ; APPLICANT: Endress, Gregory
 ; APPLICANT: Augustus, Meena
 ; APPLICANT: Ebner, Reinhard
 ; APPLICANT: Carter, Kenneth
 ; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
 ; FILE OF INVENTION: Signature Gene Sets
 ; FILE REFERENCE: 689290-84
 ; CURRENT FILING DATE: 2003-04-29
 ; PRIOR APPLICATION NUMBER: U.S. 60/236,891
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: U.S. 60/236,842
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: U.S. 60/244,867
 ; PRIOR FILING DATE: 2000-11-01
 ; PRIOR APPLICATION NUMBER: U.S. 60/245,084
 ; NUMBER OF SEQ ID NOS: 1067
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 714
 ; LENGTH: 1081
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-873-367C-714

Query Match 94.2%; Score 726.2; DB 10; Length 1081;
 Best Local Similarity 98.3%; Pred. No. 9.3e-192;
 Matches 734; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

17 GAATCGTGGGGTCAAGAGGCGCCCGAGGAGCAAGTGGCGGCTCCCTGCGAGCTGAGAG 76
 66 GCATCGTGGGGTCAAGAGGCGCCCGAGGAGCAAGTGGCGGCTCCCTGCGAGCTGAGAG 125

QY 77 TCCACGGCCCATACATGATGACATCTCTGCGGGGCTCCCTCATCCACCCCAAGTGGGTGC 136
Db |||
QY 126 TCCGCGACGATACATGATGACATCTCTGCGGGGCTCCCTCATCCACCCCAAGTGGGTGC 185
Db |||
QY 137 TGACCGCGCGCGGTGCGTGGGACCGGACGTCGAGATCTGGCCGCTCAGGGTGCAAC 196
Db |||
QY 186 TGACCGCGCGCGGTGCGTGGGACCGGACGTCGAGATCTGGCCGCTCAGGGTGCAAC 245
QY 197 TGCGGAGACGACCTCTACTACAGGACCGGACGTCGCGGTGAGGATCATCGTGC 256
Db |||
QY 246 TGCGGAGACGACCTCTACTACAGGACCGGACGTCGCGGTGAGGATCATCGTGC 305
QY 257 ACCACAGTCTTACACCGCCAGATCGGAGCGGACATCGCCCTGCTGAGCTGGAGGAGC 316
Db |||
QY 306 ACCACAGTCTTACACCGCCAGATCGGAGCGGACATCGCCCTGCTGAGCTGGAGGAGC 365
QY 317 CGGTGAAGGTCTCAGCGACGTCGACAGGTGACCGTCCGCGGCTCAGAGCTTCC 376
Db |||
QY 366 CGGTGAAGGTCTCAGCGACGTCGACAGGTGACCGTCCGCGGCTCAGAGCTTCC 425
QY 377 CCCGCGGATGCGGTGCGGTGCTGCGTGGGCGGATCGCCCTGCTGAGCTGGAGGAGC 436
Db |||
QY 426 CCCGCGGATGCGGTGCGGTGCTGCGTGGGCGGATCGCCCTGCTGAGCTGGAGGAGC 485
QY 437 CACCGCATTTCTCTGAAGCAGGTGAAGGTCCCATTAATGAAACCCACATTTGTGAGC 496
Db |||
QY 486 CACCGCATTTCTCTGAAGCAGGTGAAGGTCCCATTAATGAAACCCACATTTGTGAGC 545
QY 497 CAAATACACCTTGGGCGCTACAGGAGAGGAGCGTCCGATCGTCCGTGACGACATGC 556
Db |||
QY 546 CAAATACACCTTGGGCGCTACAGGAGAGGAGCGTCCGATCGTCCGTGACGACATGC 605
QY 557 TGTGTGCGGGAACACCGGAGGAGTCTATGCGAGGAGCGTCCGAGGCGGCTGTCGCC 616
Db |||
QY 606 TGTGTGCGGGAACACCGGAGGAGTCTATGCGAGGAGCGTCCGAGGCGGCTGTCGCC 665
QY 617 GCAAGGTGAATGGACCTTGGCTGAGGCGGCGGTGGTCACTGGGCGGAGGCGCTGTCGCC 676
Db |||
QY 666 GCAAGGTGAATGGACCTTGGCTGAGGCGGCGGTGGTCACTGGGCGGAGGCGCTGTCGCC 725
QY 677 AGCCCAACCGGCTGGGATCTACAGGCGGCTGTCAGTCTTGAATGCAACCACT 736
Db |||
QY 726 AGCCCAACCGGCTGGGATCTACAGGCGGCTGTCAGTCTTGAATGCAACCACT 785
QY 737 ATGTCCCAAAAGCGTGAAGCGCC 763
Db |||
QY 786 ATGTCCCAAAAGCGTGAAGCGCC 812

RESULT 9

US-10-275-505-27
; Sequence 27, Application US/10275505
; Publication No. US20040081961A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DELEGANE, Angelo M.; LAL, Preeti G.
; APPLICANT: HAPALIA, April J.A.; PATTERSON, Chandra
; APPLICANT: WALIA, Narinder K.; KEARNEY, Liam
; APPLICANT: TRIBOULEY, Catherine M.; KHAN, Farrah A.
; APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Valda; ELLIOTT, Vicki S.
; APPLICANT: NGUYEN, Daniel B.; GANDHI, Ameena R.
; APPLICANT: YANG, Junning; HERNANDEZ, Roberto
; APPLICANT: POLICKY, Jennifer L.; LU, Dyung Aina M.
; APPLICANT: REDDY, Roopa M.; YUE, Henry
; APPLICANT: TANG, Y. Tom
; TITLE OF INVENTION: PROTEASES
; FILE REFERENCE: PI-0085 USN
; CURRENT APPLICATION NUMBER: US/10/275,505
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: PCT/US01/14651
; PRIOR FILING DATE: 2001-05-04

; PRIOR APPLICATION NUMBER: 60/209,402
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 60/207,477
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/205,803
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: 60/203,566
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 60/202,082
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PERL Program
; SEQ ID NO 27
; LENGTH: 2662
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7472460CB1
US-10-275-505-27

Query Match 93.2%; Score 718.2; DB 17; Length 2662;
Best Local Similarity 98.2%; Pred. No. 1.7e-189;
Matches 726; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 17 GAATCGTCGGGGTCCAGGAGCGCCCGGAGCAAGTGGCCCTGGCAGTGAGCTGAGAG 76
Db 699 GCATCGTTGGGGGTCCAGGAGCGCCCGGAGCAAGTGGCCCTGGCAGTGAGCTGAGAG 758
QY 77 TCCACGGCCCATACATGATGACATCTCTGCGGGGCTCCCTCATCCACCCCAAGTGGGTGC 136
Db 759 TCCGCGACGATACATGATGACATCTCTGCGGGGCTCCCTCATCCACCCCAAGTGGGTGC 818
QY 137 TGACCGCGCGCGGTGCGTGGGACCGGACGTCGAGGATCTGGCCGCTCAGGGTGCAAC 196
Db 819 TGACCGCGCGCGGTGCGTGGGACCGGACGTCGAGGATCTGGCCGCTCAGGGTGCAAC 878
QY 197 TGCGGAGACGACCTCTACTACCGGAGCGGCTGCTGCCGCTCAGGAGGATCATCGTGC 256
Db 879 TGCGGAGACGACCTCTACTACCGGAGCGGCTGCTGCCGCTCAGGAGGATCATCGTGC 938
QY 257 ACCACAGATTTCTACACCGCCAGATCGGAGCGGACATCGCCCTGCTGAGCTGGAGGAGC 316
Db 939 ACCACAGATTTCTACACCGCCAGATCGGAGCGGACATCGCCCTGCTGAGCTGGAGGAGC 998
QY 317 CGGTGAAGGTCTCAGCGACGTCGACAGGTGACCGTCCGCGGCTCAGAGACCTTCC 376
Db 999 CGGTGAAGGTCTCAGCGACGTCGACAGGTGACCGTCCGCGGCTCAGAGACCTTCC 1058
QY 377 CCCGCGGATGCGGTGCGGTGCTGCGTGGGCGGATCGCCCTGCTGAGCTGGAGGAGC 436
Db 1059 CCCGCGGATGCGGTGCGGTGCTGCGTGGGCGGATCGCCCTGCTGAGCTGGAGGAGC 1118
QY 437 CACCGCATTTCTCTGAAGCAGGTGAAGGTCCCATTAATGAAACCCACATTTGTGAGC 496
Db 1119 CACCGCATTTCTCTGAAGCAGGTGAAGGTCCCATTAATGAAACCCACATTTGTGAGC 1178
QY 497 CAAATACACCTTGGGCGCTACAGGAGCGGACGTCGCGGATCGTCCGTGACGACATGC 556
Db 1179 CAAATACACCTTGGGCGCTACAGGAGCGGACGTCGCGGATCGTCCGTGACGACATGC 1238
QY 557 TGTGTGCGGGAACACCGGAGGAGTCTGTCGAGGCGGCTCCGAGGCGGCTGCTGTGT 616
Db 1239 TGTGTGCGGGAACACCGGAGGAGTCTGTCGAGGCGGCTCCGAGGCGGCTGCTGTGT 1298
QY 617 GCAAGGTGAATGGACCTTGGCTGAGGCGGCGGTGCTGAGTGGGCGGAGGCTGTGCC 676
Db 1299 GCAAGGTGAATGGACCTTGGCTGAGGCGGCGGTGCTGAGTGGGCGGAGGCTGTGCC 1358
QY 677 AGCCCAACCGGCTGGGATCTACACCGGCTGCACTACTACTTGGATGCAACCACT 736
Db 1359 AGCCCAACCGGCTGGGATCTACACCGGCTGCACTACTACTTGGATGCAACCACT 1418

QY 737 ATGTCCCAAAAGCCGTG 755
Db 1419 ATGTCCCAAAAGCCGTG 1437

RESULT 10

US-10-287-226-89

; Sequence 89, Application US/10287226

; Publication No. US20040086875A1

; GENERAL INFORMATION:

; APPLICANT: Agee, Michele L.,

; APPLICANT: Alsobrook, John P.,

; APPLICANT: Bergs, Constance,

; APPLICANT: Boldog, Ference,

; APPLICANT: Burgess, Catherine E.,

; APPLICANT: Chant, John S.,

; APPLICANT: Chaudhuri, Amitabha,

; APPLICANT: DiPippo, Vincent A.,

; APPLICANT: Edinger, Shlomit R.,

; APPLICANT: Eisen, Andrew,

; APPLICANT: Ellerman, Karen,

; APPLICANT: Gangolli, Esha A.,

; APPLICANT: Gorman, Linda,

; APPLICANT: Gerlach, Valerie,

; APPLICANT: Ji, Weizhen,

; APPLICANT: Kekuda, Rameesh,

; APPLICANT: Kuramsov, Nikolai,

; APPLICANT: Li, Li,

; APPLICANT: Malyankar, Uriel M.,

; APPLICANT: MacDougall, John R.,

; APPLICANT: Mezes, Peter S.

; APPLICANT: Miller, Charles E.,

; APPLICANT: Millet, Isabelle,

; APPLICANT: Ooi, Chean Eng,

; APPLICANT: Ort, Tatiana,

; APPLICANT: Padigar, Muralidhara,

; APPLICANT: Patturajan, Meera,

; APPLICANT: Rastelli, Luca,

; APPLICANT: Rieger, Daniel K.,

; APPLICANT: Rothenberg, Mark E.,

; APPLICANT: Shenoy, Suresh G.,

; APPLICANT: Spaderna, Steven K.,

; APPLICANT: Spytek, Kimberley A.,

; APPLICANT: Taupier, Jr., Raymond J.,

; APPLICANT: Vernet, Corine A.M.,

; APPLICANT: Zethusen, Bryan D.,

; APPLICANT: Zhong, Mei

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 21402-480C

; CURRENT APPLICATION NUMBER: US/10/287,226

; PRIOR FILING DATE: 2002-11-04

; PRIOR APPLICATION NUMBER: 60/334,421

; PRIOR FILING DATE: 2001-11-30

; PRIOR APPLICATION NUMBER: 60/354,392

; PRIOR FILING DATE: 2002-02-04

; PRIOR APPLICATION NUMBER: 60/360,148

; PRIOR FILING DATE: 2002-02-27

; PRIOR APPLICATION NUMBER: 60/364,000

; PRIOR FILING DATE: 2002-03-13

; PRIOR APPLICATION NUMBER: 60/404,821

; PRIOR FILING DATE: 2002-08-20

; PRIOR APPLICATION NUMBER: 60/334,526

; PRIOR FILING DATE: 2001-11-30

; PRIOR APPLICATION NUMBER: 60/354,409

; PRIOR FILING DATE: 2002-02-04

; PRIOR APPLICATION NUMBER: 60/364,227

; PRIOR FILING DATE: 2002-03-13

; PRIOR APPLICATION NUMBER: 60/334,027

; PRIOR FILING DATE: 2001-11-28

; PRIOR APPLICATION NUMBER: 60/331,641

; PRIOR FILING DATE: 2001-11-20

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 673

; SOFTWARE: CuraSeqList version 0.1

; SEQ ID NO 89

; LENGTH: 828

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(825)

US-10-287-226-89

Query Match

90.8%; Score 700; DB 17; Length 828;

Best Local Similarity 96.6%; Pred. No. 1.7e-184;

Matches 715; Conservative

0; Mismatches 25; Indels 0; Gaps 0;

QY 17 GAATCGTCGGGGCTCAGGAGGCCGCCAGGAGCAAGTGGCCCTGCAGGTGAGCCTGAGAG 76

Db 89 GCATTGTTGGGGGAGAGAGGCCGCCAGGAGCAAGTGGCCCTGCAGGTGAGCCTGAGAG 148

QY 77 TCCACGGCCCATACTGCGATGCACCTTCTGCGGGGGCTCCCTCATCCACCCAGTGGGTGC 136

Db 149 TCCGGGGCCCATACTGCGATGCACCTTCTGCGGGGGCTCCCTCATCCACCCAGTGGGTGC 208

QY 137 TGACCGCCCGGGCGTGGTGGGACCGGACGCTCAAGGATCTGGCGGCCCTCAGGGTGAAC 196

Db 209 TAAACCGCGCGCACTGCGTGGAAACCGGACATCAAGGATCTGGCGGCCCTCAGGGTGAAC 268

QY 197 TCGGGAGAGCAGCACCTTCTACTACGAGCAGCAGCTGTGCGCGTCCAGCAGGATCATCTGC 256

Db 269 TCGGGAGAGCAGCACCTTCTACTACGAGCAGCAGCTGTGCGCGTCCAGCAGGATCATCTGC 328

QY 257 ACCACAGTTTCTACACCGCCAGATCGGAGCGGACATCGCCCTGCTGAGCTGAGGAGC 316

Db 329 ACCACAGTTTCTACATCATCCAGACCGGGCGGACATCGCCCTGCTGAGCTGAGGAGC 388

QY 317 CGGTGAAGGTCTCAGCCAGCTCCACAGGTCACTCCCTGCGCCCTGCTCAGAGACCTTCC 376

Db 389 CCGTGAACATCTCCAGCCACATCCACAGGTCACTCCCTGCGCCCTGCTCAGAGACCTTCC 448

QY 377 CCGGGGATGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 436

Db 449 CCGGGGATGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 508

QY 437 CACGCCATTTCCTCTGAAGCAGGTGAAGTCCCATTAATGGAACCAACATTTGTGACG 496

Db 509 CACGCCATTTCCTCTGAAGCAGGTGAAGTCCCATTAATGGAACCAACATTTGTGACG 568

QY 497 CAAATAACCACTTGGCGCTTACCGGAGACGAGCTCCGATCGTCCGTGACGACATGC 556

Db 569 CAAATAACCACTTGGCGCTTACCGGAGACGAGCTCCGATCGTCCGTGACGACATGC 628

QY 557 TGTGTGCGGGAACACCGGAGGAGTCAATGCCAGGCGACTCCGGAGGGGCCCTGGTGT 616

Db 629 TGTGTGCGGGAACACCGGAGGAGTCAATGCCAGGCGACTCCGGAGGGGCCCTGGTGT 688

QY 617 GCAAGGTGAATGGCACCTGGCTGACGCGGCGGTGGTCAAGTGGGGGAGGGCTGTGCC 676

Db 689 GCAAGGTGAATGGCACCTGGCTGACGCGGCGGTGGTCAAGTGGGGGAGGGCTGTGCC 748

QY 677 AGCCCAACCGGCTGGGATCTTACACCGGTGTCACTACTTACTTGGATCCACCACT 736

Db 749 AGCCCAACCGGCTGGGATCTTACACCGGTGTCACTACTTACTTGGATCCACCACT 808

QY 737 ATGTCCCAAAAGCCGTGA 756

Db 809 ATGTCCCAAAAGCCGTGA 828

RESULT 11

US-10-352-684A-45

; Sequence 45, Application US/10352684A

; Publication No. US20030215452A1

; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals Inc.

```
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; APPLICANT: Weich, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1873, 13051, 1847, 1849,
; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
; FILE REFERENCE: MF102-019P1RNOMIM
; CURRENT APPLICATION NUMBER: US/10/352,684A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/364,476
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)...(845)
; US-10-352-684A-45

Query Match      89.0%; Score 686.2; DB 16; Length 1154;
Best Local Similarity 94.3%; Pred. No. 1.2e-180;
Matches 712; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 17 GAATCGTCGGGGGTACAGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
Db 106 GTATCGTCGGGGGTACAGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 165

Qy 77 TCCAGGGCCCATCTGATGATGACTTCTCGGGGGGCTCCCTCATCCACCCCGAGTGGGTGC 136
Db 166 TCCGCGACCGGATCTGATGATGACTTCTCGGGGGGCTCCCTCATCCACCCCGAGTGGGTGC 225

Qy 137 TGACCGCGCGCGCTGCTGGGACCGGACGTCAGGATCTGCGCGGCTCAGCAGGATCATCGTGC 196
Db 226 TGACCGCGCGCGCTGCTGGGACCGGACGTCAGGATCTGCGCGGCTCAGCAGGATCATCGTGC 285

Qy 197 TCGGGAGGAGCAGCCTCTACTACAGGACGAGTGGCGGCTGCGCGGCTCAGCAGGATCATCGTGC 256
Db 286 TCGGGAGGAGCAGCCTCTACTACAGGACGAGTGGCGGCTGCGCGGCTCAGCAGGATCATCGTGC 345

Qy 317 CGGTGAAGGTCTCCAGGACGCTCCACAGGTCACCGCTGCGCGGCTGCGCGGCTCAGCAGGATCATCGTGC 376
Db 406 CGGTGAAGGTCTCCAGGACGCTCCACAGGTCACCGCTGCGCGGCTGCGCGGCTCAGCAGGATCATCGTGC 465

Qy 377 CCGCGGGGATGCGGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCCTCC 436
Db 377 CCGCGGGGATGCGGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCCTCC 436

; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; APPLICANT: Weich, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1873, 13051, 1847, 1849,
; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
; FILE REFERENCE: MF102-019P1RNOMIM
; CURRENT APPLICATION NUMBER: US/10/352,684A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/364,476
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)...(845)
; US-10-352-684A-45

Query Match      89.0%; Score 686.2; DB 13; Length 1158;
Best Local Similarity 94.9%; Pred. No. 1.2e-180;
Matches 709; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 17 GAATCGTCGGGGGTACAGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
Db 106 GTATCGTCGGGGGTACAGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 165

Qy 77 TCCAGGGCCCATCTGATGATGACTTCTCGGGGGGCTCCCTCATCCACCCCGAGTGGGTGC 136
Db 166 TCCGCGACCGGATCTGATGATGACTTCTCGGGGGGCTCCCTCATCCACCCCGAGTGGGTGC 225

Qy 137 TGACCGCGCGCGCTGCTGGGACCGGACGTCAGGATCTGCGCGGCTCAGCAGGATCATCGTGC 196
Db 226 TGACCGCGCGCGCTGCTGGGACCGGACGTCAGGATCTGCGCGGCTCAGCAGGATCATCGTGC 285

Qy 197 TCGGGAGGAGCAGCCTCTACTACAGGACGAGTGGCGGCTGCGCGGCTCAGCAGGATCATCGTGC 256
Db 286 TCGGGAGGAGCAGCCTCTACTACAGGACGAGTGGCGGCTGCGCGGCTCAGCAGGATCATCGTGC 345

Qy 257 ACCCAGACGTTCTACATATCCAGATCGGAGCGGATATCGCCCTGCTGGAGCTGGAGGAGC 405
Db 316 ACCCAGACGTTCTACATATCCAGATCGGAGCGGATATCGCCCTGCTGGAGCTGGAGGAGC 465

Qy 317 CGGTGAAGGTCTCCAGGACGCTCCACAGGTCACCGCTGCGCGGCTGCGCGGCTCAGCAGGATCATCGTGC 376
Db 406 CGGTGAAGGTCTCCAGGACGCTCCACAGGTCACCGCTGCGCGGCTGCGCGGCTCAGCAGGATCATCGTGC 465

Qy 377 CCGCGGGGATGCGGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCCTCC 436
Db 377 CCGCGGGGATGCGGTGCTGGGTCACTGGCTGGGGCGATGTGGACAATGATGAGCGCCCTCC 436
```


Db 346 ACCACAGTTCTATCATCCAGACTGAGCGGATATCGCCCTGCTGAGCTGGAGGAGC 405
 QY 317 CGGTGAAGGTCTCAGCCAGCTCCACACGCTCACTCCCTGCCCCCTGCTCAGAGACCTTCC 376
 Db 406 CCGTGAACATCTCAGCCGCTCCACACGCTCACTCCCTGCCCCCTGCTCAGAGACCTTCC 465
 QY 377 CCCCCGGGATGCCGTGCTGGGTCACTGGCTGGGCGCATGTGGAACAATGATGAGCCCTCC 436
 Db 466 CCCCCGGGATGCCGTGCTGGGTCACTGGCTGGGCGCATGTGGAACAATGATGAGCCCTCC 525
 QY 437 CACGGCCATTCTCTGAACGAGTGAAGTCCCATTAATGGAACCAATTTGTGACG 496
 Db 526 CACGGCCATTCTCCCTGAACGAGTGAAGTCCCATTAATGGAACCAATTTGTGACG 585
 QY 497 CAAATACACCTTGGCGCTTACACGGGAGACGAGTCCCATCTCGTCCGTGAGCACATGC 556
 Db 586 CAAATACACCTTGGCGCTTACACGGGAGACGAGTCCCATCTCGTCCGTGAGCACATGC 645
 QY 557 TGTGTGCGGGAAACACCCGAGGAGTCTATGCCAGGCGGACTCGGAGGCGCCCTGTGTGT 616
 Db 646 TGTGTGCGGGAAACACCCGAGGAGTCTCTCTCAAGGCGGACTCTGAGGCGCCCTGTGTGT 705
 QY 617 GCAGGTGATGACCTGCTGCTGAGGAGTCTGAGGCGGCTGCTGAGGCGGAGGCTGTGCC 676
 Db 706 GCAAGGTGAATGGACCTGCTGCTGAGGCGGCTGCTGAGGCGGAGGCTGTGCC 765
 QY 677 AGCCCAACCGCGCTGGCATCTACACCGCGTGTCTACTACTACTTGGACTGGATCCACACT 736
 Db 766 AGCCCAACCGCGCTGGCATCTACACCGCGTGTCTACTACTACTTGGACTGGATCCACACT 825
 QY 737 ATGTCCCCAAAGCGCGTGAAGCGGC 763
 Db 826 ATGTCCCCAAAGCGCGTGAAGCGGC 852

RESULT 13

US-10-287-226-87
 ; Sequence 87, Application US/10287226
 ; Publication No. US20040086875A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agee, Michele L.,
 ; APPLICANT: Alsbrook, John P.,
 ; APPLICANT: Berghs, Constance,
 ; APPLICANT: Boldog, Ferenc,
 ; APPLICANT: Burgess, Catherine E.,
 ; APPLICANT: Chant, John S.,
 ; APPLICANT: Chaudhuri, Amitabha,
 ; APPLICANT: Dipippo, Vincent A.,
 ; APPLICANT: Edinger, Shlomit R.,
 ; APPLICANT: Eisen, Andrew,
 ; APPLICANT: Ellerman, Karen,
 ; APPLICANT: Gangolli, Esha A.,
 ; APPLICANT: Gorman, Linda,
 ; APPLICANT: Gerlach, Valerie,
 ; APPLICANT: Ji, Weizhen,
 ; APPLICANT: Kekuda, Ramesh,
 ; APPLICANT: Khramtsov, Nikolai,
 ; APPLICANT: Li, Li,
 ; APPLICANT: Malyankar, Uriel M.,
 ; APPLICANT: MacDougall, John R.,
 ; APPLICANT: Mezes, Peter S.,
 ; APPLICANT: Miller, Charles E.,
 ; APPLICANT: Millet, Isabelle,
 ; APPLICANT: Ooi, Chean Eng,
 ; APPLICANT: Ort, Tatiana,
 ; APPLICANT: Padigaru, Muralidhara,
 ; APPLICANT: Patturajan, Meera,
 ; APPLICANT: Rastelli, Luca,
 ; APPLICANT: Rieger, Daniel K.,
 ; APPLICANT: Rothenberg, Mark E.,
 ; APPLICANT: Shenoy, Suresh G.,
 ; APPLICANT: Spaderna, Steven K.,
 ; APPLICANT: Spytek, Kimberley A.,

Query Match 87.9%; Score 678; DB 17; Length 858;
 Best Local Similarity 96.3%; Pred. No. 2.2e-178;
 Matches 722; Conservative 0; Mismatches 10; Indels 18; Gaps 2;

QY 17 GAATCGTGGGGGTTCAGGAGGCCCCCAGGAGCAAGTGGCCCTTGGCAGGTGAGCCTGAGAG 76
 Db 120 GCATCGTGGGGGTTCAGGAGGCCCCCAGGAGCAAGTGGCCCTTGGCAGGTGAGCCTGAGAG 179
 QY 77 TCACGGCCCCATCTAGTATGACTTCTGGGGGGCTCCCTCATCCACCCCGAGTGGGTGC 136
 Db 180 TCACGGCCCCATCTAGTATGACTTCTGGGGGGCTCCCTCATCCACCCCGAGTGGGTGC 239
 QY 137 TGACCGCGCGGTGGTGGGACCGGACGCTCAAGGATCTGGCGCCCTCAGGGTGCAAC 196
 Db 240 TGACCGCGCGGTGGTGGGACCGGACGCTCAAGGATCTGGCGCCCTCAGGGTGCAAC 299
 QY 197 TGGCGGAGCAGACCTCTACTACAGGACCGAGTGTGGCGGTGAGCAGGATCATCGTGC 256
 Db 300 TGGCGGAGCAGACCTCTACTACAGGACCGAGTGTGGCGGTGAGCAGGATCATCGTGC 359
 QY 257 ACCACAGTTCTACACCGCCAGATCGGAGGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
 Db 360 ACCACAGTTCTACACCGCCAGATCGGAGGGACATCGCCCTGCTGGAGCTGGAGGAGC 419
 QY 317 CGGTGAAGGTCTCAGGCAAGTCCACACGGTCACTCCCTGCCCCCTGCTCAGAGACCTTCC 376
 Db 420 CGGTGAAGGTCTCAGGCAAGTCCACACGGTCACTCCCTGCCCCCTGCTCAGAGACCTTCC 479
 QY 377 CCCCCGGGATGCCGTGCTGGGTCACTGGCTGGGCGCATGTGGAACAATGATGAGGCGCTCC 436
 Db 480 CCCCCGGGATGCCGTGCTGGGTCACTGGCTGGGCGCATGTGGAACAATGATGAGGCGCTCC 524
 QY 437 CACGCCATTTCCTCTGGAAGCAGGTGAAGTCCCCCATTAATGAACCAACCATTTGTGACG 496

; APPLICANT: Taupier, Jr., Raymond J.,
 ; APPLICANT: Vernet, Corine A.M.,
 ; APPLICANT: Zerhusen, Bryan D.,
 ; APPLICANT: Zhong, Mei
 ; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 21402-480C
 ; CURRENT APPLICATION NUMBER: US/10/287,226
 ; CURRENT FILING DATE: 2002-11-04
 ; PRIOR APPLICATION NUMBER: 60/334,421
 ; PRIOR FILING DATE: 2001-11-30
 ; PRIOR APPLICATION NUMBER: 60/354,392
 ; PRIOR FILING DATE: 2002-02-04
 ; PRIOR APPLICATION NUMBER: 60/360,148
 ; PRIOR FILING DATE: 2002-02-27
 ; PRIOR APPLICATION NUMBER: 60/364,000
 ; PRIOR FILING DATE: 2002-03-13
 ; PRIOR APPLICATION NUMBER: 60/404,821
 ; PRIOR FILING DATE: 2002-08-20
 ; PRIOR APPLICATION NUMBER: 60/334,526
 ; PRIOR FILING DATE: 2001-11-30
 ; PRIOR APPLICATION NUMBER: 60/354,409
 ; PRIOR FILING DATE: 2002-02-04
 ; PRIOR APPLICATION NUMBER: 60/364,227
 ; PRIOR FILING DATE: 2002-03-13
 ; PRIOR APPLICATION NUMBER: 60/334,027
 ; PRIOR FILING DATE: 2001-11-28
 ; PRIOR APPLICATION NUMBER: 60/331,641
 ; PRIOR FILING DATE: 2001-11-20
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 673
 ; SOFTWARE: Curaseqlist version 0.1
 ; SEQ ID NO 87
 ; LENGTH: 858
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (8)..(844)
 ; US-10-287-226-87

Db 525 CACGCCATTTCTCTGAAGCAGGTGAAGGTCCCAATAATGAAACACACATTTGTGACG 584
QY 497 CAAAATACCACTTGGCGCCTACACGGGAGAGAGTCCGATCGTTCGTGACGACATGC 556
Db 585 CAAAATACCACTTGGCGCCTACACGGGAGAGAGTCCGATCGTTCGTGACGACATGC 644
QY 557 TGTGTGCGGGGAAACACCGGAGGAGTCAATGC--CAGGGGCACTCCCGAGGGGCCCTGG 613
Db 645 TGTGTGCGGGGAAACACCGGAGGAGTCAATGCCAGCAGGGGCACTCCCGAGGGGCCCTGG 704
QY 614 TGTGAAGGTGAATGGGCACTTGGCTGCGAGGCGGGGCTGGTGAAGTGGGGCGAGGCTGTG 673
Db 705 TGTGAAGGTGAATGGGCACTTGGCTGCGAGGCGGGGCTGGTGAAGTGGGGCGAGGCTGTG 764
QY 674 CCCAGCCCAACCGGCTGGCACTTACACCCGCTGTCACCTACTTACTTGGACTGGATCCACC 733
Db 765 CCCAGCCCAACCGGCTGGCACTTACACCCGCTGTCACCTACTTACTTGGACTGGATCCACC 824
QY 734 ACTATGTCCCCAAAAGCGTGAAGCGGCC 763
Db 825 ACTATGTCCCCAAAAGCGTGAAGTCAAGC 854

RESULT 14

US-10-275-505-22
; Sequence 22, Application US/10275505
; Publication No. US20040081961A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DELEGANE, Angelo M.; IAL, Preeti G.
; APPLICANT: HAFALIA, April J.A.; PATTERSON, Chandra
; APPLICANT: WALIA, Narinder K.; KEARNEY, Liam
; APPLICANT: TRIBOULEY, Catherine M.; KHAN, Farrah A.
; APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.
; APPLICANT: AZIMZAL, faldia; ELLIOTT, Vicki S.
; APPLICANT: NGUYEN, Danniell B.; GANDHI, Ameena R.
; APPLICANT: YANG, Junning; HERNANDEZ, Roberto
; APPLICANT: POLICKY, Jennifer L.; LU, Dyung Aina M.
; APPLICANT: REDDY, Roopa M.; YUE, Henry
; APPLICANT: TANG, Y. Tom
; TITLE OF INVENTION: PROTEASES
; FILE REFERENCE: PI-0085 USN
; CURRENT APPLICATION NUMBER: US/10/275,505
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: PCT/US01/14651
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/209,402
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 60/207,477
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/205,803
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: 60/203,566
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 60/202,082
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PERL Program
; SEQ ID NO 22
; LENGTH: 1187
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 3897384CB1
US-10-275-505-22

Query Match 60.1%; Score 463; DB 17; Length 1187;
Best Local Similarity 76.4%; Pred. No. 1.2e-118;
Matches 568; Conservative 0; Mismatches 175; Indels 0; Gaps 0;
QY 14 AAGAATGTGCGGGGTGAGGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGA 73

Db 258 AAGCATTTGTGGGGGACAGGAGGACATGGGAACAAGTGGCCCTGGCAGGTGACCTGC 317
QY 74 GAGTCCACGGCCCATATCTGGATGACATCTTCTGCGGGGGTCTCCCTCATCAOCCOCCAGTGG 133
Db 318 GTGCCAATGACACCTTACTTGGATGCAATTTCTGCGGTGGCTCCCTCATCAOCCOCCAGTGG 377
QY 134 TGCTGACCGCGCGGCGTGGGACCGGACGTCAGGATCTGCGCCCTCAGGGTGC 193
Db 378 TGCTGACCGCGGCACTGTGTGGGACCGGATGTTGTGACCCCAAGGTTCAGAGTAC 437
QY 194 AACTCGGGGACAGCACCTCTACTACAGGACCACTGCTGCGGTGACGAGGATCATCG 253
Db 438 AGCTCCGTAAGCAGTACCTCTATTACCATGACCACTGATGACTGTGAGCCAGATCATCA 497
QY 254 TGACCCACAGTTCTACACCCGCCAGATCGGAGCGGACATCGCCCTGTGTGAGGTGGAGG 313
Db 498 CACACCCCGACTTCTACATCTGTCAGGATGGGAGACATTTGCCCTGCTGAAACTCACA 557
QY 314 AGCGGTGAAGTCTCCAGCCACGTCACACGCTCACTGCGCCCTGCTCAGAGCT 373
Db 558 ACCGTGTGAACATTTCTGACTATGTCCACCTGTCCTCCCTTACCTCTGCTCAGAGCT 617
QY 374 TCCCGCGGGGATGCCGTGTGGGTCACTGCTGGGGGATGTGGACAATGATGAGCGCC 433
Db 618 TCCCGCTCAGGAACGTTGTGCTGGGTGACAGGCTGGGGTAAATCGACAAATGTTGAAC 677
QY 434 TCCCGCGGCAATTTCTCTGAAAGCAGGTGAAGTCCCATTAATGAAACCAATTTGTG 493
Db 678 TGCGGCCACCAATTTCTTTGAAAGGAGGTGCAAGTTCCCATATAGAAAACCACTTTGTG 737
QY 494 ACGCAAAATACCACTTGGCGCTTACACGGGAGAGGAGTCCGATCGTCCGTGACGACA 553
Db 738 ACTTGAAGTATCAAAAGGTCTCATACAGGTGACAATGTCCAGATGACA 797
QY 554 TGCTGTGTGCGGGGAAACACCGGAGGAGTCACTGCCAGGGGAGTCCCGAGGGGCCCTGG 613
Db 798 TGCTGTGTGTGGGAATGAAGGACATGACTCTCCAGGGGAGTCCCGGAGGACTCTG 857
QY 614 TGTCAAGGTGAATGGCACCTGCGTGTGAGGCGGCGTGGTCACTGCGGCGGAGGGCTGTG 673
Db 858 TCTCAAGGTAGAAGACACCTGCTGTCAGGCGAGCGTGGTCACTGCGGCTGAGGGCTGTG 917
QY 674 CCCAGCCCAACCGGCTGGGATCTACACCGGTGTCACCTACTTACTTGGACTGGATCCACC 733
Db 918 CACAGCCCAACAGGCTGGGATCTACACCGGCTGTCACCTACTTACTTGGACTGGATCCACC 977
QY 734 ACTATGTCCCCAAAAGCGCTGA 756
Db 978 ACTATGTCCCCAAGGACTTCTGA 1000

RESULT 15

US-09-813-432-11
; Sequence 11, Application US/09813432
; Publication No. US20030148485A1
; GENERAL INFORMATION:
; APPLICANT: Taupier Jr., Raymond J
; APPLICANT: Majmuder, Kamud
; APPLICANT: Spaderna, Steven K
; APPLICANT: Smithson, Glenda
; APPLICANT: Mezes, Peter S
; APPLICANT: Vernet, Corine A. M.
; TITLE OF INVENTION: No. US20030148485A1el Polypeptides and Amino Acids Encoding Same
; FILE REFERENCE: 15966-729
; CURRENT APPLICATION NUMBER: US/09/813,432
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,836
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/193,843
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 846
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-813-432-11

Query Match 37.3%; Score 287.4; DB 10; Length 846;
Best Local Similarity 62.6%; Pred. No. 6.9e-70;
Matches 469; Conservative 0; Mismatches 271; Indels 9; Gaps 1;
QY 17 GATTCGTGGGGTTCAGAGGCCCCAGAGCAAGTGGCCCTGGCAGGTGAGCTGAGAG 76
Db 94 GCATTTGGGGGGCCACAATGCCCCCGGGGAAGTGGCCGTGGCAGGTGAGCTGAGGG 153
QY 77 TCCACGGCC-----CATACTGGATGACTTCTCGGGGGTCCCTCATCCACCCCC 127
Db 154 TCTACAGTACCCTGGGCCCTCTGGGGCCACATCTGTGGGGTCCCTCATCCACCCCC 213
QY 128 AGTGGGTGCTACCGCGCGCGTGGGACCGGACGTCAGGATCTGGCCGCCCTCA 187
Db 214 AGTGGGTGCTGACTGTGCTGCCACTGCATTTCTGGAAGGACACCGGTCCTACCC 273
QY 188 GGGTGCAACTGGGGGAGGACCTCTACTACAGGACAGCTGCTGCGGTGAGCAGGA 247
Db 274 GGAATCCACGCTGGGGAGCTGTATCTCTACGGGGCGCGGGGCTCTGAACGTCAGCCGA 333
QY 248 TCATCGTGCAACCCACAGTTCTACACCGCCAGATCGGAGCGGACATCGCCCTGCTGGAGC 307
Db 334 TCATCGTGCAACCCCACTATGTCTACTCGGGGCTGGGTGCGGATGTGGCCCTGCTCCAGC 393
QY 308 TGGAGGAGCGGGTGAAGGTCTCCAGCCACGTCCTCACCGTCAACCTGCCCCCTGCCCTAG 367
Db 394 TGGTGAGCCCCATGATCGAGCCGCTAATGTGAGGACGGTCAAGCTCTCCCGGCTCTCGC 453
QY 368 AGACTTTCCTCCCGGGGATGCGGTGCTGGGTCACTGGCTGGGGCGATGTGACATGATG 427
Db 454 TGGAGCTCACCCCGAAGGACAGTGTGGGTGACTGGCTGGGGAGCGATCAGGATGTTCG 513
QY 428 AGCGCCCTCCACCGCATTTCTCTGAAGCAGGTGAAGTCCCATATGGAACACACA 487
Db 514 AGTCGTGCGCGCGCCCTACCGCTGACAGAGGCGAGTGTGAGGTGCTGGAGAACGCCG 573
QY 488 TTTGTGACGCAAAATACACCTTGGCGCTTACACGGGAGCAGCTCCGCATCGTCCGTG 547
Db 574 TCTGTGAGCAGCCCTACCGCAACGCTCAGGGCACACTGGGGCACCGGCGAGCTCATCTGG 633
QY 548 ACAGCATGCTGTGGCGGGAACACCGGAGGACTCATGCGAGGAGCTCCGAGGGCC 607
Db 634 ATGACATGCTGTGCGCGGACGAGGCGCGAGACTCTCTGTCAGGGTACTCCGCGGCC 693
QY 608 CCTTGGTGTCAAGGTGAATGGCACTGGCTGACGGCGGGGTGTGTGAGCTGGGGCCAGG 667
Db 694 CTCTGGTCTGAGGCTGCGGGGTCTTGGCGCTGCTGGGGGTGTGAGCTGGGGCTACG 753
QY 668 GCTGTGCCAGCCCAACCGGCGCTGGCATCTACACCGGTGTACCTACTACTTGGACTGGA 727

Db 754 GCTGTACCTCGGGGACTTTCCCGGGTCTACACCCACGTCAGATCTAGTGTCTCTGGA 813
QY 728 TCCACCACTATGTCCCCCAAAAGCCGTGA 756
Db 814 TCCTGCAGCAAGTCGGGGAGTTGCCCTGA 842

Search completed: July 22, 2004, 15:20:33
Job time : 572 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 22, 2004, 10:46:50 ; Search time 90 Seconds
(without alignments)
4754.079 Million cell updates/sec

Title: US-09-598-982-20

Perfect score: 771

Sequence: 1 gggccctcgagaaagaat.....cgtgaagcggcgccgctgct 771

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	764.6	99.2	771	3	US-09-079-970A-4
2	731	94.8	1128	2	US-09-016-366A-20
3	731	94.8	1128	2	US-08-978-404B-15
4	731	94.8	1137	2	US-09-016-366A-18
5	731	94.8	1137	2	US-08-978-404B-13
6	728.6	94.5	735	3	US-09-079-970A-1
7	726.2	94.2	1081	2	US-09-016-366A-22
8	726.2	94.2	1081	2	US-08-978-404B-17
9	686.2	89.0	1154	2	US-09-016-366A-16
10	686.2	89.0	1154	2	US-08-978-404B-11
11	477.2	61.9	1219	2	US-08-978-404B-7
12	469.6	60.9	1108	2	US-09-016-366A-14
13	469.6	60.9	1108	2	US-08-978-404B-20
14	463	60.1	1031	2	US-08-978-404B-1
15	445.6	57.8	1103	2	US-09-016-366A-24
16	444	57.6	1097	2	US-08-978-404B-4
17	371	48.1	2259	3	US-08-845-998-3
18	371	48.1	2259	3	US-09-206-537-3
19	371	48.1	2259	3	US-08-430-854-3
20	369.4	47.9	2218	3	US-08-845-998-5
21	369.4	47.9	2218	3	US-09-206-537-5
22	369.4	47.9	2218	3	US-09-430-854-5
23	271.8	35.3	1095	2	US-08-978-404B-9
24	201.4	26.1	980	4	US-09-023-942A-30
25	201.4	26.1	1110	4	US-09-386-653A-1
26	199.8	25.9	1212	4	US-09-620-312D-431
27	193.8	25.1	1130	4	US-09-386-653A-8

Sequence 1, Appli
Sequence 8, Appli
Sequence 13, Appli
Sequence 19, Appli
Sequence 29, Appli
Sequence 2, Appli
Sequence 8, Appli
Sequence 7, Appli
Sequence 1, Appli
Sequence 28, Appli
Sequence 262, App
Sequence 262, App
Sequence 262, App
Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 256, App

ALIGNMENTS

RESULT 1
US-09-079-970A-4
; Sequence 4, Application US/09079970A
; Patent No. 6274366
; GENERAL INFORMATION:
; APPLICANT: Maffitt, Mark A.
; APPLICANT: Niles, Andrew L.
; APPLICANT: Haak-Frendscho, Mary
; TITLE OF INVENTION: Enzymatically-Active Recombinant Human
; TITLE OF INVENTION: Beta-Tryptase and Method of Making Same
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Intellectual Property Department
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WISCONSIN
; COUNTRY: U.S.A.
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/079,970A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Leone, Joseph T.
; REGISTRATION NUMBER: 37,170
; REFERENCE/DOCKET NUMBER: 34506.073
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7..753
; FEATURE:
; NAME/KEY: misc_signal


```

; FILING DATE: 05-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1137 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-016-366A-18

Query Match          94.8%; Score 731; DB 2; Length 1137;
Best Local Similarity 98.7%; Pred. No. 2.1e-158;
Matches 737; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 17 GAATCGTCGGGGTCAGAGGCCCCCAGGACCAAGTGGCCCTGGCAGGTGAGCTGAGAG 76
Db 85 GCATCGTCGGGGTCAGAGGCCCCCAGGACCAAGTGGCCCTGGCAGGTGAGCTGAGAG 144

Qy 77 TCCACGGCCCATACTGGATGCACTTCTCGGGGGGCTCCCTCATCCACCCCGAGTGGGTGC 136
Db 145 TCCACGGCCCATACTGGATGCACTTCTCGGGGGGCTCCCTCATCCACCCCGAGTGGGTGC 204

Qy 137 TGACCGCGGGCGCTGGTGGGACCGGACGTCACAGGATCTGGCGCGCCCTCAGGGTGCAAC 196
Db 205 TGACCGCGGGCGCTGGTGGGACCGGACGTCACAGGATCTGGCGCGCCCTCAGGGTGCAAC 264

Qy 197 TCGCGGAGCAGCAGCTTACTTACCAGGACCAAGTGTCTGCCGGTCAGCAGGATCATCGTGC 256
Db 265 TCGCGGAGCAGCAGCTTACTTACCAGGACCAAGTGTCTGCCGGTCAGCAGGATCATCGTGC 324

Qy 257 ACCACAGTTCACACCGCCCATCGAGCGGACATCGCCCTGCTGGAGCTGGAGAGC 316
Db 325 ACCACAGTTCACACCGCCCATCGAGCGGACATCGCCCTGCTGGAGCTGGAGAGC 384

Qy 317 CGGTGAAGGTCTCAGCGACGTCACACGTCACGTCACGTCGCCCCCTGCTCAGACCTTCC 376
Db 385 CGGTGAAGGTCTCAGCGACGTCACACGTCACGTCACGTCGCCCCCTGCTCAGACCTTCC 444

Qy 377 CCGCGGGATGCGCTGCTGGTGTGCTACTGCTGGGGCGATGTGCAATGATCAGCGCTCC 436
Db 445 CCGCGGGATGCGCTGCTGGTGTGCTACTGCTGGGGCGATGTGCAATGATCAGCGCTCC 504

Qy 437 CACCGCCATTTCCTCTGAAGCAGGTGAAGTTCCTCCATAATGGAACCAACATTTGTGACG 496
Db 505 CACCGCCATTTCCTCTGAAGCAGGTGAAGTTCCTCCATAATGGAACCAACATTTGTGACG 564

Qy 497 CAAATACACCTTGGCGCCCTACAGGAGACGACGTCGCGATCGTCCGTGACGACATGC 556
Db 565 CAAATACACCTTGGCGCCCTACAGGAGACGACGTCGCGATCGTCCGTGACGACATGC 624

Qy 557 TGTGTGCGGGAACACCGGAGGACTCATCCAGGGGACTTCCGAGGGGCCCTTGGTGT 616
Db 625 TGTGTGCGGGAACACCGGAGGACTCATCCAGGGGACTTCCGAGGGGCCCTTGGTGT 684

Qy 617 GCAAGGTGAATGGACCTTGGCTGAGCGGGCGTGGTTCAGTGGGGCGAGGGCTGTGCC 676
Db 685 GCAAGGTGAATGGACCTTGGCTGAGCGGGCGTGGTTCAGTGGGGCGAGGGCTGTGCC 744

Qy 677 AGCCCAACCGCTGGATCTACACCGCTGTACCTACTTACTTGGATCGATCCACACT 736
Db 745 AGCCCAACCGCTGGATCTACACCGCTGTACACCGCTGTACCTACTTGGATCGATCCACACT 804

Qy 737 ATGTCCCCCAAAAGCGTGAAGCGGCC 763
Db 805 ATGTCCCCCAAAAGCGTGAAGCGGCC 831

```

```

RESULT 5
US-08-978-404B-13
; Sequence 13, Application US/08978404B
; Patent No. 5968782
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
; TITLE OF INVENTION: FLBRINOGEN
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,404B
; FILING DATE: 25-NOV-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/032,354
; FILING DATE: 04-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1137 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-978-404B-13

```

```

Query Match          94.8%; Score 731; DB 2; Length 1137;
Best Local Similarity 98.7%; Pred. No. 2.1e-158;
Matches 737; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 17 GAATCGTCGGGGTCAGAGGCCCCCAGGACCAAGTGGCCCTGGCAGGTGAGCTGAGAG 76
Db 85 GCATCGTCGGGGTCAGAGGCCCCCAGGACCAAGTGGCCCTGGCAGGTGAGCTGAGAG 144

Qy 77 TCCACGGCCCATACTGGATGCACTTCTCGGGGGGCTCCCTCATCCACCCCGAGTGGGTGC 136
Db 145 TCCACGGCCCATACTGGATGCACTTCTCGGGGGGCTCCCTCATCCACCCCGAGTGGGTGC 204

Qy 137 TGACCGCGGGCGCTGGTGGGACCGGACGTCACAGGATCTGGCGCGCCCTCAGGGTGCAAC 196
Db 205 TGACCGCGGGCGCTGGTGGGACCGGACGTCACAGGATCTGGCGCGCCCTCAGGGTGCAAC 264

Qy 197 TCGCGGAGCAGCAGCTTACTTACCAGGACCAAGTGTCTGCCGGTCAGCAGGATCATCGTGC 256
Db 265 TCGCGGAGCAGCAGCTTACTTACCAGGACCAAGTGTCTGCCGGTCAGCAGGATCATCGTGC 324

Qy 257 ACCACAGTTCACACCGCCCATCGAGCGGACATCGCCCTGCTGGAGCTGGAGAGC 316
Db 325 ACCACAGTTCACACCGCCCATCGAGCGGACATCGCCCTGCTGGAGCTGGAGAGC 384

Qy 317 CGGTGAAGGTCTCAGCGACGTCACACGTCACGTCACGTCGCCCCCTGCTCAGACCTTCC 376
Db 385 CGGTGAAGGTCTCAGCGACGTCACACGTCACGTCACGTCGCCCCCTGCTCAGACCTTCC 444

```

QY 377 CCCCCGGGATGCCGTGGTGGTCACTGGCTGGGGGATGTGACAAATGATGAGCGCTCC 436
Db 445 CCCCCGGGATGCCGTGGTGGTCACTGGCTGGGGGATGTGACAAATGATGAGCGCTCC 504
QY 437 CACCCCAATTCCTCTGAAGCAGGTGAAGGTCCCATTAATGAAACACACATTTGTGAGC 496
Db 505 CACCCCAATTCCTCTGAAGCAGGTGAAGGTCCCATTAATGAAACACACATTTGTGAGC 564
QY 497 CAAATATACCTTGGCGCTTACACGGGAGAGAGCTCGGATCGTCCGTGACGACATGC 556
Db 565 CAAATATACCTTGGCGCTTACACGGGAGAGAGCTCGGATCGTCCGTGACGACATGC 624
QY 557 TGTGTGCGGGGAAACCCCGAGGAGTCAATGCGAGGGGACTCCGGAGGGGCCCTGGTGT 616
Db 625 TGTGTGCGGGGAAACCCCGAGGAGTCAATGCGAGGGGACTCCGGAGGGGCCCTGGTGT 684
QY 617 GCAAGGTGAATGGACCTTGGCTGTCAGGCGGGGCTGGTCACTGGGGCGAGGCTGTGCC 676
Db 685 GCAAGGTGAATGGACCTTGGCTGTCAGGCGGGGCTGGTCACTGGGGCGAGGCTGTGCC 744
QY 677 AGCCCAACCGGCTGGGATCTACACCCGTGTACCTACTTGGACTGGATCCACACT 736
Db 745 AGCCCAACCGGCTGGGATCTACACCCGTGTACCTACTTGGACTGGATCCACACT 804
QY 737 ATGTCCCCCAAAAGCGTGAAGCGGCC 763
Db 805 ATGTCCCCCAAAAGCGTGAAGTCAAGC 831

RESULT 6

US-09-079-970A-1
; Sequence 1, Application US/09079970A
; Patent No. 6274366
; GENERAL INFORMATION:
; APPLICANT: Maffitt, Mark A.
; APPLICANT: Niles, Andrew L.
; APPLICANT: Haak-Frendscho, Mary
; TITLE OF INVENTION: Enzymatically-Active Recombinant Human
; TITLE OF INVENTION: Beta-Tryptase and Method of Making Same
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WISCONSIN
; COUNTRY: U.S.A.
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Leone, Joseph T.
; REGISTRATION NUMBER: 37,170
; REFERENCE/DOCKET NUMBER: 34506.073
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 735 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..735
US-09-079-970A-1

Query Match 94.5%; Score 728.6; DB 3; Length 735;
Best Local Similarity 99.5%; Pred. No. 6.8e-158;
Matches 731; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 19 ATCGTCGGGGGTGAGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 78
Db 1 ATCGTCGGGGGTGAGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAGTC 60
QY 79 CACGCCCATACTGGATGCACTTCTGCGGGGGTCCCTCATCCACCCCAAGTGGGTGCTG 138
Db 61 CACGCCCATACTGGATGCACTTCTGCGGGGGTCCCTCATCCACCCCAAGTGGGTGCTG 120
QY 139 ACCGCCGGCGGTGGTGGGACCGGACGTCAAGGATCTGGCGGCCCTCAGGGTGAAGTC 198
Db 121 ACCGCCGGCGGTGGTGGGACCGGACGTCAAGGATCTGGCGGCCCTCAGGGTGAAGTC 180
QY 199 CGGAGCAGCAGCACCTCTACTACAGGACCGAGTGTGCGGTCAGCAGGATCATCGTGAC 258
Db 181 CGGAGCAGCAGCACCTCTACTACAGGACCGAGTGTGCGGTCAGCAGGATCATCGTGAC 240
QY 259 CCACAGTTCTACACGGCCAGATCGGAGCGACATGCGCCCTGGAGCTGGAGGAGCG 318
Db 241 CCACAGTTCTACACGGCCAGATCGGAGCGACATGCGCCCTGGAGCTGGAGGAGCG 300
QY 319 GTGAAGTCTCCAGCCAGTCCACACGGTCACTGCGCCCTGCGCTCAGACACCTTCCCC 378
Db 301 GTGAAGTCTCCAGCCAGTCCACACGGTCACTGCGCCCTGCGCTCAGACACCTTCCCC 360
QY 379 CCGGGGATGCGGTGCTGGGTCACTGGGTGGGGCGATGTGGACAATGATGAGCGCTCCCA 438
Db 361 CCGGGGATGCGGTGCTGGGTCACTGGGTGGGGCGATGTGGACAATGATGAGCGCTCCCA 420
QY 439 CCGCCATTTCTCTGAAGCAGGTGAAGTCCCCATAATGAAAAACCAATTGTGACGCA 498
Db 421 CCGCCATTTCTCTGAAGCAGGTGAAGTCCCCATAATGAAAAACCAATTGTGACGCA 480
QY 499 AAATACACCTTGGCGCTACACGGGAGACGACGTGCGCATCGTCCGTGACGACATGCTG 558
Db 481 AAATACACCTTGGCGCTACACGGGAGACGACGTGCGCATCGTCCGTGACGACATGCTG 540
QY 559 TGTGCGGGAAACCCCGAGGAGTCACTGCGCGGCGACTCCGGAGGGCCCTCGTGTGTC 618
Db 541 TGTGCGGGAAACCCCGAGGAGTCACTGCGCGGCGACTCCGGAGGGCCCTCGTGTGTC 600
QY 619 AAGTGAATGGACCTTGGCTGACGGGGGGTGTGCTAGCTGGGGCGAGGGCTGTGCCAG 678
Db 601 AAGTGAATGGACCTTGGCTGACGGGGGGTGTGCTAGCTGGGGCGAGGGCTGTGCCAG 660
QY 679 CCCAACCGGCTGGCATCTACACCGGTGTCACCTACTTGGACTGGATCCACACTAT 738
Db 661 CCCAACCGGCTGGCATCTACACCGGTGTCACCTACTTGGACTGGATCCACACTAT 720
QY 739 GTCCCCCAAAAGCGC 753
Db 721 GTCCCCCAAAAGCGC 735

RESULT 7

US-09-016-366A-22
; Sequence 22, Application US/09016366A
; Patent No. 5955431
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; APPLICANT: Huang, Chifu
; TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
; ANTI-SENSE: INHIBITORS

NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ For Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1081 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-016-366A-22

Query Match 94.2%; Score 726.2; DB 2; Length 1081;
Best Local Similarity 98.3%; Pred. No. 2.6e-157;
Matches 734; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 17 GAATCGTGGGGTCAGAGGCCCCCAGGAGCAAGTGGCCCTGCGAGGTGAGCTGAGAG 76
DB 66 GCATCGTTGGGGTTCAGAGGCCCCCAGGAGCAAGTGGCCCTGCGAGGTGAGCTGAGAG 125
QY 77 TCACAGGCCCATCTGATGCACTTCTCGGGGGCTCCCTCATCCACCCCGAGTGGGTGC 136
DB 126 TCCGCGACCATGATGATGACACTTCTCGGGGGGCTCCCTCATCCACCCCGAGTGGGTGC 185
QY 137 TGACCCCGCGCGCGTGGTGGGACCGGACGTCAGAGGATCTGGCCGCCCTCAGGGGTGCAAC 196
DB 186 TGACCCCGCGCGCGTGGTGGGACCGGACGTCAGAGGATCTGGCCGCCCTCAGGGGTGCAAC 245
QY 197 TCGGGGAGCAGCAGCTTACTTACAGGACAGCTGCTGCGGTGAGGATCATCGTGC 256
DB 246 TCGGGGAGCAGCAGCTTACTTACAGGACAGCTGCTGCGGTGAGGATCATCGTGC 305
QY 257 ACCACAGGTTCTACACCGCCAGATCGGAGCGGACATCGCCCTGCTGAGCTGAGGAGC 316
DB 306 ACCACAGGTTCTACACCGCCAGATCGGAGCGGACATCGCCCTGCTGAGCTGAGGAGC 365
QY 317 CGGTGAAGGTCTCAGGACAGCTCCACAGCGTCAACCTGCGCCCTGCTGAGGACCTTCC 376
DB 366 CGGTGAAGGTCTCAGGACAGCTCCACAGCGTCAACCTGCGCCCTGCTGAGGACCTTCC 425
QY 377 CCGCGGGATGCGGTGCTGGTGCATGCTGGGGGATGTGGACAATGATGAGCGCTCC 436
DB 426 CCGCGGGATGCGGTGCTGGTGCATGCTGGGGGATGTGGACAATGATGAGCGCTCC 485
QY 437 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTGCCCATTAATGAAACACACATTTGTGACG 496
DB 486 CACCGCCATTTCCTCTGAAGCAGGTGAAGGTGCCCATTAATGAAACACACATTTGTGACG 545

QY 497 CAAAATACCACTTGGCGCTACACGGGAGACGAGTCCCATCTGCTGAGCAATGC 556
DB 546 CAAAATACCACTTGGCGCTACACGGGAGACGAGTCCCATCTGCTGAGCAATGC 605
QY 557 TGTGTGCGGGGAACACCGGAGGACTCATGCCAGGGGAGTCCGGAGGGCCCTGCTGT 616
DB 606 TGTGTGCGGGGAACACCGGAGGACTCATGCCAGGGGAGTCCGGAGGGCCCTGCTGT 665
QY 617 GCAAGGTGAATGGCACCCTGCTGCAGGGCGGCTGTGTCACTGGGGGAGGGCTGTGCC 676
DB 666 GCAAGGTGAATGGCACCCTGCTGCAGGGCGGCTGTGTCACTGGGGGAGGGCTGTGCC 725
QY 677 AGCCCAACCGGCTGCGATCTACACCGGTGTCACTTACTTGGATGATCCACACT 736
DB 726 AGCCCAACCGGCTGCGATCTACACCGGTGTCACTTACTTGGATGATCCACACT 785
QY 737 ATGTCCCAAAAGCCGTGAAGCGGC 763
DB 786 ATGTCCCAAAAGCCGTGAAGCGGC 812

RESULT 8
US-08-978-404B-17
Sequence 17, Application US/08978404B
Patent No. 5968782
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINOGEN
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1081 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-978-404B-17

Query Match 94.2%; Score 726.2; DB 2; Length 1081;
Best Local Similarity 98.3%; Pred. No. 2.6e-157;
Matches 734; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 17 GAATCGTGGGGTTCAGAGGCCCCCAGGAGCAAGTGGCCCTGCGAGGTGAGCTGAGAG 76
DB 66 GCATCGTTGGGGTTCAGAGGCCCCCAGGAGCAAGTGGCCCTGCGAGGTGAGCTGAGAG 125

77 TCCACGGCCCACTAGTGTGCTTCTGCGGGGCTCCCTCATCAACCCCAAGTGGTGC 136
Db TCCGCGACCGATAGTGTGCTTCTGCGGGGCTCCCTCATCAACCCCAAGTGGTGC 185
QY TGACCGCGCGCGTGTGCGGACCGGAGCTCAAGATCTGCGCGCCCTCAGGGTGCAAC 196
Db TGACCGCGCGCGTGTGCGGACCGGAGCTCAAGATCTGCGCGCCCTCAGGGTGCAAC 245
QY TCGCGGAGCAGCACTCTTACTACAGGACCGTGTGCGGCGGATCGCCCTGCTGGAGCTGGAGGAGC 256
Db TCGCGGAGCAGCACTCTTACTACAGGACCGTGTGCGGCGGATCGCCCTGCTGGAGCTGGAGGAGC 305
QY ACCCACAGTCTTACACCGCCCAAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
Db ACCCACAGTCTTACACCGCCCAAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 365
QY CGGTGAAGGTCTCCAGCAGCTTCACAGGTTCACAGGTTCACAGGTTCACAGGTTCACAGGTTCAC 376
Db CGGTGAAGGTCTCCAGCAGCTTCACAGGTTCACAGGTTCACAGGTTCACAGGTTCACAGGTTCAC 425
QY CCGCGGGGATGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 436
Db CCGCGGGGATGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 485
QY CACCGCCATTCTCTGTAAGCAGGTGAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 496
Db CACCGCCATTCTCTGTAAGCAGGTGAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 545
QY CAAATATACCTTGGCGCTTACACGGGAGGAGCTGCGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 556
Db CAAATATACCTTGGCGCTTACACGGGAGGAGCTGCGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 605
QY TGTGTGCGGGGAAACACCGGAGGAGCTCATGCGGAGGAGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGT 616
Db TGTGTGCGGGGAAACACCGGAGGAGCTCATGCGGAGGAGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGT 665
QY GCAAGGTGAATGGCACTTGGCTGCGAGGCGGCGTGTGCTGCGAGGCGGAGGAGGAGGAGGAGGAGGAGT 676
Db GCAAGGTGAATGGCACTTGGCTGCGAGGCGGCGTGTGCTGCGAGGCGGAGGAGGAGGAGGAGGAGGAGT 725
QY AGCCCAACCGGCTGGATCTACACCGCTGTACACCGCTGTACACCGCTGTACACCGCTGTACACCGCTGT 736
Db AGCCCAACCGGCTGGATCTACACCGCTGTACACCGCTGTACACCGCTGTACACCGCTGTACACCGCTGT 785
QY ATGTCTCCCAAAAGCGTGAAGCGGCC 763
Db ATGTCTCCCAAAAGCGTGAAGCGGCC 812

RESULT 9

US-09-016-366A-16

Sequence 16, Application US/09016366A

Patent No. 5955431

GENERAL INFORMATION:

APPLICANT: Stevens, Richard L.

APPLICANT: Huang, Chifu

TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE

TITLE OF INVENTION: INHIBITORS

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESS: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: MA

COUNTRY: U.S.A.

ZIP: 02210-2211

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016.366A

FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-016-366A-16

Query Match 89.0%; Score 686.2; DB 2; Length 1154;
Best Local Similarity 94.3%; Pred. No. 3.7e-148;
Matches 712; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 17 GAATGTCGGGGTCAAGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCTGAGAG 76
Db 106 GTATGTCGGGGTCAAGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCTGAGAG 165
QY 77 TCCACGGCCCACTAGTGTGCTTCTGCGGGGCTCCCTCATCAACCCCAAGTGGTGC 136
Db 166 TCCGCGACCGATAGTGTGCTTCTGCGGGGCTCCCTCATCAACCCCAAGTGGTGC 225
QY 137 TGACCGCGCGCGTGTGCGGACCGGAGCTCAAGATCTGCGCGCCCTCAGGGTGCAAC 196
Db 226 TGACCGCGCGCGTGTGCGGACCGGAGCTCAAGATCTGCGCGCCCTCAGGGTGCAAC 285
QY 197 TCGCGGAGCAGCACTCTTACTACAGGACCGGAGCTGCTGCGGCTGAGGAGTCACTGTGC 256
Db 286 TCGCGGAGCAGCACTCTTACTACAGGACCGGAGCTGCTGCGGCTGAGGAGTCACTGTGC 345
QY 257 ACCACAGTCTTACACCGCCAGATCGGAGCGGAGCATCGCCCTGCTGAGCTGGAGGAGC 316
Db 346 ACCACAGTCTTACATCAAGAGCTGAGGAGGAGTATCGCCCTGCTGAGCTGGAGGAGC 405
QY 317 CGGTGAAGGTCTCCAGGACCGTCCACAGCTCAACCGCTGCGCCCTGCTGAGAGCTTCC 376
Db 406 CCGTGAACATCTCCAGCGCGCTCCACAGCTCAATGCTGCGCCCTGCTGAGAGCTTCC 465
QY 377 CCGCGGGATGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 436
Db 466 CCGCGGGATGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 525
QY 437 CACCGCCATTCTCTGAAAGCAGGTGAAGGTGCTCCCATTAATGTAAGGAGGAGGAGGAGGAGGAGGAGT 496
Db 526 CACCGCCATTCTCTGAAAGCAGGTGAAGGTGCTCCCATTAATGTAAGGAGGAGGAGGAGGAGGAGGAGT 585
QY 497 CAAATATACCTTGGCGCTTACACGGGAGGAGCTGCTGCGATCGTGGTGGAGGAGGAGGAGGAGGAGT 556
Db 586 CAAATATACCTTGGCGCTTACACGGGAGGAGCTGCTGCGATCGTGGTGGAGGAGGAGGAGGAGGAGT 645
QY 557 TGTGTGCGGGGAAACACCGGAGGAGCTCATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 616
Db 646 TGTGTGCGGGGAAACACCGGAGGAGCTCATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 705
QY 617 GCAAGGTGAATGGCACTTGGCTGCGAGGCGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 676
Db 706 GCAAGGTGAATGGCACTTGGCTGCGAGGCGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 765
QY 677 AGCCCAACCGGCTGGATCTTACACCGCTGTACACCGCTGTACACCGCTGTACACCGCTGTACACCGCTGT 736
Db 766 AGCCCAACCGGCTGGATCTTACACCGCTGTACACCGCTGTACACCGCTGTACACCGCTGTACACCGCTGT 825

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-978-404B-7

Query Match 61.9%; Score 477.2; DB 2; Length 1219;
Best Local Similarity 77.1%; Pred. No. 2.2e-100;
Matches 581; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

```
QY 6 CCTGAGAAAGAAATCTGCGGGGTGAGAGGCCCGCCAGAGCAAGTGGCCCTGGCAGGT 65
Db 260 CCAAGAGTGGGGCATTTGTTGGGGGACAGAGGACCTCTGGGAACAAGTGGCCCTGGCAGGT 319
QY 66 GAGCTGAGAGTCCACCGCCCATCTGATGACACTTCTGCGGGGCTCCCTCATCCACC 125
Db 320 GAGCTTCTGTCCTGATGAACCTACTGAGGCAATTTCTGCGGGCTCCCTCATCCACC 379
QY 126 CAGTGGGTGCTGACCGCGCGGCGTGGTGGGACCGGACGTCAGAGATCTGGCGCCCT 185
Db 380 ACAGTGGGTGCTACCGCGGCACACTGTGTGGACCGACTATTGCTGATCCCAACAGGT 439
QY 186 CAGGTGCAACTGCGGGAGCAGCACTCTACTACAGGACCACTGCTGCGCGGTGAGAG 245
Db 440 CAGAGTACAGTTTCAAAAGCAAGTACCTCTATTACCACGACCACTGCTGGGTGTGAGCG 499
QY 246 GATCATGTCGACCCACACAGTTCTACACCGCCGAGATCGGAGCGGACATCGCCCTGCTGA 305
Db 500 GATCATCACACCGGACATTTCTATGCCACCAGATGGGGCGGACATGCGCTACTTGA 559
QY 306 GCTGAGAGCGCGTGAAGGTCTCAGACCACTGTCACACAGGTCACTGCGCCCTGCTC 365
Db 560 GCTCAAGAACCTGTAAACATTTCCAGGCATGTCCACCCGCTCTCCCTGCTGCTGCTC 619
QY 366 AGAGACCTTCCCGCGGGATGCCGTGCTGGTCACTGCTGGGCGGATGTGCAATGA 425
Db 620 AGAGACCTTCCCGCTCAGGAACATTTGCTGGGTGACAGCTGGGGAACATCGAATGA 679
QY 426 TGAGCGCTTCCACCGCATTTCTCTGAAGCAGGTGAAGTCCCGCATTAATGGAACCA 485
Db 680 TGTGAGCTTCCACCGCATTTCTCTGAGAGAGTGAAGTCCCGCTGCTGGAACCA 739
QY 486 CATTGTGACGCAAAATACCACTTTGGCGCTTACACGGGAGACGACGTCGCGATCGTCG 545
Db 740 GCTTTGTGACCTGAAGTATCAAAAGGTGTCTACACGGGACACATCCACATTTGTCG 799
QY 546 TGACAGATGCTGTGTGCGGGAACACCGGAGGACTCATGCCAGGGGACTCCGGAGG 605
Db 800 AGACGACATGCTGTGTGCGGAACGAAGGACACGACTCTTCCAGGGGTGACTCCGGAGG 859
QY 606 GCGCTGCTGTCAGAGTGAATGGCACCTGCTGAGCGGGCGTGGTCACTGGGGCGA 665
Db 860 ACCTTGTGTCAGAGTAAACGTTACTGCTGTCAGGAGAGTGTGCTGAGTGGGGTGA 919
QY 666 GGGTGTGCCAGCCCAACCGGCTGGGATCTACACCGGTGTCACCTACTACTTGGACTG 725
Db 920 GGGTGTGCTGTCGCCCAACAGGCTGGCATCTACACTCGGGTCACTTATTCTGGAATG 979
QY 726 GATCCACACTATGTCGCCAAAGACCGGTGAGC 759
Db 980 GATCCACCGCTATGTCGCCAAAGACTTCTGAATC 1013
```

RESULT 12

US-09-016-366A-14

Sequence 14, Application US/09016366A

Patent No. 5955431

GENERAL INFORMATION:

APPLICANT: Stevens, Richard L.

APPLICANT: Huang, Chifu

TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE

TITLE OF INVENTION: INHIBITORS

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA

COUNTRY: U.S.A.

ZIP: 02210-2211

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016.366A

FILING DATE: January 30, 1998

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/037,090

FILING DATE: 05-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Plumer, Elizabeth R.

REGISTRATION NUMBER: 36,637

REFERENCE/DOCKET NUMBER: B0801/7093

TELEPHONE: 617-720-3500

TELEFAX: 617-720-2441

TELEX:

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 1108 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-09-016-366A-14

Query Match 60.9%; Score 469.6; DB 2; Length 1108;
Best Local Similarity 77.2%; Pred. No. 1.2e-98;
Matches 571; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

```
QY 17 GAATGTCGGGGTTCAGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCTGAGAG 76
Db 125 GCATGTCGGGAGGACATGAGGCTTCTGAGAGTAAGTGGCCCTGGCAGGTGAGCTGAGAT 184
QY 77 TCCAGGCGCCATCTGATGACACTTCTGCGGGGCTCCCTCATCCACCCAGTGGGTGC 136
Db 185 TTAATTAACACTCTGATACATTTCTCGGAGGCTCTCTCATCCACCAAGTGGGTGC 244
QY 137 TGACCGCGCGCGTGTGCGGACCGGACGTCAGGATCTGGCCGCCCTCAGGGTGAAC 196
Db 245 TCACCTGCGGCACACTGTGTGGGACCGCACATCAAAAGCCACAGCTCTTCGGGTGCAGC 304
QY 197 TCGGGAGCAGCAGCTCTACTACAGGACAGCTGCTGCGCGGTGAGGAGTATCTGTCG 256
Db 305 TTGCTGAGCAGTATCTATCTATGATGAGGACAGCTCTCTTTTGAACCGGATCTGTTG 364
QY 257 ACCACAGCTTCTACACCGCCAGATCGGAGCGGACATCGCCCTGCTGAGCTGGAGGAGC 316
Db 365 ACCCCCACTATTACACCGCCAGGCTGGGGGAGAGCTTGCCCTGCTGAGCTTGAAGTCC 424
QY 317 CGGTGAAGGTCTCCAGCCACGTCACACGCTCACCCCTGCCCTCCCTCAGAGACCTTCC 376
Db 425 CTGTGAATGTCTCCACCCATATCCACCCCATATCCCTGCCCTCCCTCGGAGACCTTCC 484
QY 377 CCGCGGAGTCCGCTGCTGGGTCACTGCTGGGGGATGTGGAATATGAGGCGCTTCC 436
Db 485 CCGCTGGGACATCTGCTGGGTGACAGGCTGGGGGAGCAATTGATTAATGACGAGCTCTCC 544
QY 437 CACGCGCATTTCTCTGAAGCAGTGAAGTCCCATTAATGAAGAACACCATTTCTGAGC 496
Db 545 CACCTCTTATCTCTGAAGCAAGTGAAGGTTCCCAATTGTGGAAGAACAGCTTGTGTGAC 604
QY 497 CAAATACCACTTGGCGCCCTACACGGGAGAGCAGCTCCGATCGCTGAGACGATGC 556
```


APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1031 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-978-404B-1

Query Match 60.1%; Score 463; DB 2; Length 1031;
Best Local Similarity 76.4%; Pred. No. 3.8e-97;
Matches 568; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

QY 14 AAGAGATCGTCGGGGTCAAGAGGCCCCCAGAGCAAGTGGCCCTGGCAGGTGAGCCTGA 73
Db |||||
QY 106 AAGGCATTGTGGGGGACAGAGGACACATGGGAAAGTGGCCCTGGCAGGTGAGCCTGC 165
Db |||||
QY 74 GAGTCCAGCGCCCTACTGATGATGCTCTGCGGGGCTCCCTCATCCACCCCAAGTGGG 133
Db |||||
QY 166 GTGCCAATGACACTTACTGATGATCTTCTGGGTGGCTCCCTCATCCACCCACAGTGGG 225
Db |||||
QY 134 TGCTGACCGCCCGCGGTGCGTGGGACCGGACGTCAAGGATCTGCGCCCTCAGGGTGC 193
Db |||||
QY 226 TGCTCACTCGCGCACACTGTGGGACCGGATGTTGCTGACCCCAAGGTGACAGTAC 285
Db |||||
QY 194 AACTCGGGAGACACACTTACTACACAGGACCTGCTGCGGTGAGCAGGTATCGG 253
Db |||||
QY 286 AGCTCCGTAAGCAGTACCTCTATTAACCATGACCACTGTGATGCTGAGCCAGATCA 345
Db |||||
QY 254 TGACCCACAGTTCTACACCGCCAGATCGGAGCGACATCGCCCTGTGGAGCTGGAGG 313
Db |||||
QY 346 CACACCCGACTTCTAGATGCTCAGGATGGGACAGATTCGCCCTGTGAACCTCAAA 405
Db |||||
QY 314 AGCGGTGAAGTCTCCAGCACGCTCCACAGGTCAACCTGCGCCCTGCGCTCAGAGACT 373
Db |||||
QY 406 ACCCTGTGAACATTTCTGACTATGTCCACCCCTGTCCCTCTGCTCAGAGACT 465
Db |||||
QY 374 TCCCGCGGGGATCGCGTCTGCTGGTCACTGCTGCGGGGATGTGACAAATGATGAGCGCC 433
Db |||||
QY 466 TCCCTTCAGGAACGTGTGCTGGGTGACAGGCTGGGGTAAATCGACAAATGTTAAACC 525
Db |||||
QY 434 TCCACCGCCCTTTCTCTGAAGCAGGTGAAGTCCCATATGAAACCAACACATTTGTG 493
Db |||||
QY 526 TGCGGCCACCAATTCCTTTGAAGGAGGTGCAAGTTCCTATTAAGAAACCACTTTGTG 585
Db |||||
QY 494 ACGCAAAATACACCTTGGCGGCTTACACGGAGACGAGTCCGATCGTCCGTGACGACA 553
Db |||||
QY 586 ACTTGAAGTATACAAAGGTCTCATACAGGTGACAAATGTCCATTTGTCGAGATGACA 645
Db |||||
QY 554 TGCTGTGCGGGACACACCGGAGGACTCATGCGAGGGGACTCCCGAGGGGCCCTGG 613
Db |||||
QY 646 TGCTGTGCTGGGAATGAAGACATGACTCTCTGCGAGGGGACTCCCGAGGACCTCTGG 705
Db |||||
QY 614 TGTCAGAGTGAATGGCACTTGGTGTGACGGGGGGGCTGCTGAGTGGGGGCGAGGCTGTG 673
Db |||||
QY 706 TCTCAAGGTAGAGACACCTTGGCTGACAGGACGAGGTGCTGAGTGGGGTGAAGGCTGTG 765
Db |||||
QY 674 CCGAGCCCAACGGGCTGGGATCTACACCCGTGACCTTACTTGTGACTGGATCCACC 733
Db |||||
QY 766 CACAGCCCAACAGGCTGGCATCTACACCCGGGTCACTTACTTGTGACTGGATCCACC 825
Db |||||
QY 734 ACTATGTCCTCCCAAGGCGTGA 756
Db |||||
QY 826 ACTATGTCCTCCCAAGGACTTCTGA 848
Db |||||

RESULT 15

US-09-016-366A-24
Sequence 24, Application US/09016366A
Patent No. 5955431
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
NUMBER OF INVENTORS: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1103 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-016-366A-24

Query Match 57.8%; Score 445.6; DB 2; Length 1103;
Best Local Similarity 75.1%; Pred. No. 3.7e-93;
Matches 556; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

QY 17 GAATCGTGGGGGTCAAGAGGCCCCCAGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
Db |||||
QY 102 GCATTGTGGGAGGACGAGAGGCTTCTGAAAGTAAGTGGCCCTGGCAGGTGAGCCTGAGAT 161
Db |||||
QY 77 TCCAGGCCCATATGATGATGCTCTGCGGGGGCTCCCTCATCACCCCAAGTGGGTGC 136
Db |||||
QY 162 TTAATTCAGCTTCTGATGATCTCTGTCGGGCTCCCTCATCACCCCAAGTGGGTGC 221
Db |||||
QY 137 TGACCGCGCGGCTGCTGGGACCGGACGTCAGGATCTGCGCCCTCAGGGTGCAC 196
Db |||||
QY 222 TCATCTGGGCACACTGTGTGGACTGCATCAAAAGCCAGAGCTCTTCGCTGTACAGC 281
Db |||||
QY 197 TGGGGAGCAGCCTCTTACTTACAGGACCAAGTGTGTCGGCTCAGCAGGATCATCGTGC 256
Db |||||
QY 282 TCTGTGAGCAGTATCTATCTATCTATCGGACCAAGTGTGACTGTGAACCGGACCTGTGTC 341
Db |||||
QY 257 ACCCAGAGTCTTACACCGCCAGATCGAGGGGACATGCGCCCTGCTGAGGTGAGGAGC 316
Db |||||
QY 342 ACCCCCACTACTACACAGTGGAGATGGGGCAGACATTTGCCCTGCTGAGCTTGAGAACC 401
Db |||||
QY 317 CGGTGAAGGTCTCCAGCCAGCTCCACAGGTCAACCTGCCCCCTGCTCAGAGACCTTCC 376
Db |||||

[illegible]

Search completed: July 22, 2004, 13:26:09
Job time : 93 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 22, 2004, 09:37:10 / Search time 522 Seconds
(without alignments)
6274.637 Million cell updates/sec

Title: US-09-598-982-20
Perfect score: 771
Sequence: 1 gggccctcgagaaagaat.....cgtgaagcggcgcgcgtcgt 771

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 29Jan04: *
1: Geneseqn1980s: *
2: Geneseqn1990s: *
3: Geneseqn2000s: *
4: Geneseqn2001s: *
5: Geneseqn2001bs: *
6: Geneseqn2002s: *
7: Geneseqn2003as: *
8: Geneseqn2003bs: *
9: Geneseqn2003cs: *
10: Geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	771	100.0	771	6	AAS20775 DNA encod
2	769.4	99.8	771	6	AAS20783 DNA encod
3	764.6	99.2	771	3	Aaz40175 Human bet
4	764.6	99.2	771	6	AAS20765 DNA encod
5	763	99.0	771	6	AAS20763 DNA encod
6	761.4	98.8	771	6	AAS20776 DNA encod
7	759.8	98.5	771	6	AAS20784 DNA encod
8	755	97.9	771	6	AAS20778 DNA encod
9	755	97.9	771	6	AAS20777 DNA encod
10	753.4	97.7	771	6	AAS20786 DNA encod
11	753.4	97.7	771	6	AAS20785 DNA encod
12	735	95.3	735	6	AAS20779 DNA encod
13	733.4	95.1	735	6	AAS20787 DNA encod
14	731	94.8	1128	2	Aav44330 Human mas
15	731	94.8	1128	2	Aav42712 Human mas
16	731	94.8	1137	2	Aav44329 Human mas
17	731	94.8	1137	2	Aav42711 Human mas
18	731	94.8	1137	3	Aa34957 Human ade
19	731	94.8	1137	3	Aaf21079 Human low
20	731	94.8	1137	7	ABZ96773 Human nuc
21	731	94.8	1143	3	Aa34955 Human ade
22	731	94.8	1143	3	Aaf21077 Human low
23	731	94.8	1143	7	ABZ96771 Human nuc

24	731	94.8	1145	3	AAA34956 Human ade
25	731	94.8	1145	3	Aaf21078 Human low
26	731	94.8	1145	7	ABZ96772 Human nuc
27	731	94.8	17133	3	AAA34962 Human ade
28	731	94.8	17133	3	Aaf21084 Human low
29	731	94.8	17133	7	ABZ96778 Human nuc
30	728.6	94.5	735	3	Aaz40172 Human bet
31	728.6	94.5	735	6	AAS20766 DNA encod
32	727	94.3	735	6	AAS20760 DNA encod
33	726.2	94.2	1081	2	AAV44331 Human mas
34	726.2	94.2	1081	2	AAV42713 Human mas
35	726.2	94.2	1081	3	AAA34960 Human ade
36	726.2	94.2	1081	3	AAF21082 Human low
37	726.2	94.2	1081	6	ABL62377 Colon ade
38	726.2	94.2	1081	6	ABL66816 Lung canc
39	726.2	94.2	1081	6	ABL61818 Colon ade
40	726.2	94.2	1081	6	ABK35580 Gene TP52
41	726.2	94.2	1081	6	ABK64532 Human ben
42	726.2	94.2	1081	7	ABZ96776 Human nuc
43	725.4	94.1	735	6	AAS20780 DNA encod
44	723.8	93.9	735	6	AAS20788 DNA encod
45	719	93.3	735	6	AAS20782 DNA encod

ALIGNMENTS

RESULT 1
AAS20775
ID AAS20775 standard; DNA; 771 BP.
XX
AC AAS20775;
XX
DT 09-APR-2002 (first entry)
XX
DE DNA encoding human beta-II tryptase active site mutant H44A #1.
XX
KW Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW enzyme; mutant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200198470-A2.
XX
PD 27-DEC-2001.
XX
PF 20-JUN-2001; 2001WO-US019681.
XX
PR 21-JUN-2000; 2000US-00598982.
XX
PA (PROM-) PROMEGA CORP.
XX
PI Maffit M, Niles AL, Haak-Frendscho M;
XX
DR WPI; 2002-114578/15.
XX
P-PSDB; AAU12009.
XX
PT DNA construct for producing enzymatically-inactive proteolytic tryptase,
PT comprises DNA sequence encoding proteolytic tryptase having an active
PT site mutation.
XX
PS Claim 7; Page 83-84; 126pp; English.
XX
CC The present invention relates to recombinant human proteolytic tryptases,
CC active site mutants of these tryptases and the methods for producing
CC these. The method involves the production of a DNA expression construct
CC comprising a promoter operably linked to a secretion signal sequence
CC which is operably linked to a DNA sequence encoding a proteolytic
CC tryptase with an active site mutation (the construct drives expression of
CC a mature proteolytic tryptase that lacks enzymatic activity due to the
CC active site mutation, in hosts transformed to contain the construct). The
CC method is useful for producing enzymatically-active beta-II tryptase. The

CC active site mutants of proteolytic trypsin provide a tool to investigate
 CC the structural and functional properties of the protease and its
 CC enzymatic activity, and for modelling studies. The enzymatically-active,
 CC recombinant proteolytic trypsin produced are useful as an antigen to
 CC generate anti-human trypsin antibodies and in drug screening for
 CC compounds which act as trypsin inhibitors, antagonists, agonists, etc.
 CC AAS20775-AAS20790 encode for recombinant human beta-II trypsin active
 CC site mutants
 XX Homo sapiens.
 XX Synthetic.
 XX WO200198470-A2.
 XX 27-DEC-2001.
 XX 20-JUN-2001; 2001WO-US019681.
 XX 21-JUN-2000; 2000US-00598982.
 XX (PROM-) PROMEGA CORP.
 XX Maffit M, Niles AL, Haak-Frendscho M;
 XX WPI; 2002-114578/15.
 XX P-ESDB; AAU12017.
 XX DNA construct for producing enzymatically-inactive proteolytic trypsin,
 XX comprises DNA sequence encoding proteolytic trypsin having an active
 XX site mutation.
 XX Claim 7; Page 104-105; 126pp; English.

Query Match 100.0%; Score 771; DB 6; Length 771;
 Best Local Similarity 100.0%; Pred. No. 1.3e-147;
 Matches 771; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCCCCCTCGAGAAAGAAATCGTGGGGGTGAGAGGCCCCCAGAGCAAGTGCCCTGG 60
 Db 1 GGGCCCCCTCGAGAAAGAAATCGTGGGGGTGAGAGGCCCCCAGAGCAAGTGCCCTGG 60
 QY 61 CAGGTGAGCCTGAGAGTCCACGGCCCATCTACTGGATGCACTTCTGGGGGGTCCCTCATC 120
 Db 61 CAGGTGAGCCTGAGAGTCCACGGCCCATCTACTGGATGCACTTCTGGGGGGTCCCTCATC 120
 QY 121 CACCCCTCAGTGGGTGCTACCGCCCGCGCGTGTGGGACCGGACGTCAGAGATCTGGCC 180
 Db 121 CACCCCTCAGTGGGTGCTACCGCCCGCGCGTGTGGGACCGGACGTCAGAGATCTGGCC 180
 QY 181 GCGCTCAGGTGCACTGCGGGGAGGAGCAGCCTTACTACAGGACGAGTCTGCGCGTC 240
 Db 181 GCGCTCAGGTGCACTGCGGGGAGGAGCAGCCTTACTACAGGACGAGTCTGCGCGTC 240
 QY 241 AGCAGGATCATCGTGCACCCAGTCTTACACCGCCAGATCGGAGCGGACATCGCCCTG 300
 Db 241 AGCAGGATCATCGTGCACCCAGTCTTACACCGCCAGATCGGAGCGGACATCGCCCTG 300
 QY 301 CTGAGCTGAGAGGAGCGGTGAGGTCTCCAGCCAGCTGTCACGCTCACCCCTGCCCCCT 360
 Db 301 CTGAGCTGAGAGGAGCGGTGAGGTCTCCAGCCAGCTGTCACGCTCACCCCTGCCCCCT 360
 QY 361 GCCTCAGAGAGCTTCCCGCCCGGATGCGGTGCTGGGTCACTGGTGGGGGATGTGGAC 420
 Db 361 GCCTCAGAGAGCTTCCCGCCCGGATGCGGTGCTGGGTCACTGGTGGGGGATGTGGAC 420
 QY 421 AATGATGAGCCCTCCACCGCCATTTCTCTGAAGCAGGTGAAGTCCCATATGAA 480
 Db 421 AATGATGAGCCCTCCACCGCCATTTCTCTGAAGCAGGTGAAGTCCCATATGAA 480
 QY 481 AACCAATTTGTAGCGAAATATACCACTTGGCGCTTACAGGAGAGCAGTTCGGATC 540
 Db 481 AACCAATTTGTAGCGAAATATACCACTTGGCGCTTACAGGAGAGCAGTTCGGATC 540
 QY 541 GTCCGTGACGATGCTGTGTCGGGAACACCGGAGGACTCATGCGAGGAGTCC 600
 Db 541 GTCCGTGACGATGCTGTGTCGGGAACACCGGAGGACTCATGCGAGGAGTCC 600
 QY 601 GGAGGGCCCTGCTGTGAAGGTGAATGGACCTGGTGCAGGGGGGGTGTGAGCTGG 660
 Db 601 GGAGGGCCCTGCTGTGAAGGTGAATGGACCTGGTGCAGGGGGGGTGTGAGCTGG 660
 QY 661 GGAGGGCTGTGCGCCAGCCCAACCGGCTGGCATCTACACCGGTGTACCTACTCTG 720
 Db 661 GGAGGGCTGTGCGCCAGCCCAACCGGCTGGCATCTACACCGGTGTACCTACTCTG 720
 QY 721 GACTGATCCACCATATGTCCCCAAAAGCCGTGAAGCGGCGCGCTGT 771
 Db 721 GACTGATCCACCATATGTCCCCAAAAGCCGTGAAGCGGCGCGCTGT 771

RESULT 2
 AAS20783
 ID AAS20783 standard; DNA; 771 BP.
 XX
 AC AAS20783;

XX 09-APR-2002 (first entry)
 XX DNA encoding human beta-II trypsin active site mutant H44A #3.
 XX Human; proteolytic trypsin; protease; recombinant beta-II trypsin;
 XX enzyme; mutant; ds.
 XX Homo sapiens.
 XX Synthetic.
 XX WO200198470-A2.
 XX 27-DEC-2001.
 XX 20-JUN-2001; 2001WO-US019681.
 XX 21-JUN-2000; 2000US-00598982.
 XX (PROM-) PROMEGA CORP.
 XX Maffit M, Niles AL, Haak-Frendscho M;
 XX WPI; 2002-114578/15.
 XX P-ESDB; AAU12017.
 XX DNA construct for producing enzymatically-inactive proteolytic trypsin,
 XX comprises DNA sequence encoding proteolytic trypsin having an active
 XX site mutation.
 XX Claim 7; Page 104-105; 126pp; English.

The present invention relates to recombinant human proteolytic trypsin,
 active site mutants of these trypsin and the methods for producing
 these. The method involves the production of a DNA expression construct
 comprising a promoter operably linked to a secretion signal sequence
 which is operably linked to a DNA sequence encoding a proteolytic
 trypsin with an active site mutation (the construct drives expression of
 a mature proteolytic trypsin that lacks enzymatic activity due to the
 active site mutation, in hosts transformed to contain the construct). The
 method is useful for producing enzymatically-active beta-II trypsin. The
 active site mutants of proteolytic trypsin provide a tool to investigate
 the structural and functional properties of the protease and its
 enzymatic activity, and for modelling studies. The enzymatically-active,
 recombinant proteolytic trypsin produced are useful as an antigen to
 generate anti-human trypsin antibodies and in drug screening for
 compounds which act as trypsin inhibitors, antagonists, agonists, etc.
 AAS20775-AAS20790 encode for recombinant human beta-II trypsin active
 site mutants
 XX Sequence 771 BP; 147 A; 257 C; 243 G; 124 T; 0 U; 0 Other;
 Query Match 99.8%; Score 769.4; DB 6; Length 771;
 Best Local Similarity 99.9%; Pred. No. 2.8e-147;
 Matches 770; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGGCCCCCTCGAGAAAGAAATCGTGGGGGTGAGAGGCCCCCAGAGCAAGTGCCCTGG 60
 Db 1 GGGCCCCCTCGAGAAAGAAATCGTGGGGGTGAGAGGCCCCCAGAGCAAGTGCCCTGG 60
 QY 61 CAGGTGAGCCTGAGAGTCCACGGCCCATCTACTGGATGCACTTCTGGGGGGTCCCTCATC 120
 Db 61 CAGGTGAGCCTGAGAGTCCACGGCCCATCTACTGGATGCACTTCTGGGGGGTCCCTCATC 120
 QY 121 CACCCCTCAGTGGGTGCTACCGCCCGCGCGTGTGGGACCGGACGTCAGAGATCTGGCC 180
 Db 121 CACCCCTCAGTGGGTGCTACCGCCCGCGCGTGTGGGACCGGACGTCAGAGATCTGGCC 180
 QY 181 GCGCTCAGGTGCACTGCGGGGAGGAGCAGCCTTACTACAGGACGAGTCTGCGCGTC 240
 Db 181 GCGCTCAGGTGCACTGCGGGGAGGAGCAGCCTTACTACAGGACGAGTCTGCGCGTC 240
 QY 241 AGCAGGATCATCGTGCACCCAGTCTTACACCGCCAGATCGGAGCGGACATCGCCCTG 300


```
Db 241 AGCAGGATCATGTCGTCACCCACAGTTCCTACACGCGCCACGATCGAGCGGACATCGCCCTG 300
Qy 301 CTGAGCTGGAGGAGCGGTGAAGTCTCCAGCACAGTCTCCACAGGTCACTGCTGCGCCCT 360
Db 301 CTGAGCTGGAGGAGCGGTGAAGTCTCCAGCACAGTCTCCACAGGTCACTGCTGCGCCCT 360
Qy 361 GCCTCAGAGACTTCCCGCGGGATGCGTGGGTCACTGCTGGGGGATGTGGAC 420
Db 361 GCCTCAGAGACTTCCCGCGGGATGCGTGGGTCACTGCTGGGGGATGTGGAC 420
Qy 421 AATGATGAGCGCTCCACCGCCATTCTCTGAAGCAGGTGAAGGTCTCCCATATGGA 480
Db 421 AATGATGAGCGCTCCACCGCCATTCTCTGAAGCAGGTGAAGGTCTCCCATATGGA 480
Qy 481 AACCACATTTGTGAGGCAAAATACACTTGGCGCTACAGGGAGAGAGAGTGGCATC 540
Db 481 AACCACATTTGTGAGGCAAAATACACTTGGCGCTACAGGGAGAGAGAGTGGCATC 540
Qy 541 GTCCGTGACGACATGCTGTGTGCGGGAAACACCGAGGAGTCAATGCGAGGAGTCC 600
Db 541 GTCCGTGACGACATGCTGTGTGCGGGAAACACCGAGGAGTCAATGCGAGGAGTCC 600
Qy 601 GGAGGCGCCCTGGTGTGCAAGTGAATGGACCTGGTGTGAGGGGGGTGGTGTGAGTGG 660
Db 601 GGAGGCGCCCTGGTGTGCAAGTGAATGGACCTGGTGTGAGGGGGGTGGTGTGAGTGG 660
Qy 661 GGCGAGGGCTGTGCGGAGCCCAAGCGGCTGGCATCTACACCGCTGTACCTACTACTTG 720
Db 661 GGCGAGGGCTGTGCGGAGCCCAAGCGGCTGGCATCTACACCGCTGTACCTACTACTTG 720
Qy 721 GACTGGATCCACCACTATGTCCCAAAAGCGGTGAAGCGGCGCGCTGT 771
Db 721 GACTGGATCCACCACTATGTCCCAAAAGCGGTGAAGCGGCGCGCTGT 771
```

RESULT 3

```
AAZ40175
ID AAZ40175 standard; DNA; 771 BP.
XX
AC AAZ40175;
XX
DT 18-FEB-2000 (first entry)
XX
DE Human beta-tryptase coding sequence.
XX
KW Beta-tryptase; human; DNA expression construct; protein production;
KW combinatorial library screening; X ray crystallography; antigen;
KW antibody generation; ss.
XX
OS Homo sapiens.
XX
PN W09960139-A1.
XX
PD 25-NOV-1999.
XX
PF 29-OCT-1998; 98WO-US022994.
XX
PR 15-MAY-1998; 98US-00079970.
XX
PA (PROM-) PROMEGA CORP.
XX
PI Maffitt MA, Niles AL, Haak-Frendscho M;
XX
DR WPI; 2000-053300/04.
XX
DR P-PSDB; AAY55011.
XX
PT New DNA expression construct for production of enzymatically active
PT recombinant human beta-tryptase.
XX
PS Disclosure; Page 43-44; 50pp; English.
XX
CC This sequence encodes the human beta-tryptase. The invention relates to a
```

```
CC DNA expression construct comprising (5' to 3') a promoter linked to a
CC signal sequence which is linked to a sequence encoding human beta-
CC tryptase. The DNA construct is useful for transfecting host cells to
CC express, post translationally process and secrete enzymatically active
CC human tryptase. The method is useful for the production of large amounts
CC of tryptase with defined specifications. The transformant is useful for
CC pharmacological studies, combinatorial library screens and X ray
CC crystallographic studies. The tryptase produced allows for the
CC development of tryptase agonists and/or antagonists, is useful as an
CC antigen to generate antihuman tryptase antibodies in various animals, can
CC be used in screening for compounds which act as tryptase inhibitors,
CC antagonists, agonists etc. and to assay for the presence of tryptase in
CC biological or other solutions. Tryptase inhibitors, antagonists, agonists
CC etc. may be useful as therapeutics. The tryptase does not require any
CC post-expression or post-purification modifications or manipulations to
CC initiate tryptase activity and it has enzymatic activity which compares
CC favourably with cadaveric tryptase. The availability of enzymatically
CC active tryptase facilitates the large scale screening of combinatorial
CC libraries for specific tryptase inhibitors as potential therapeutics and
CC advances the understanding of the biological significance of tryptase in
CC mast cell mediated diseases. The tryptase can be used to detect low
CC levels of tryptase
XX
```

SQ Sequence 771 BP; 149 A; 256 C; 242 G; 124 T; 0 U; 0 Other;

	Query Match	Best Local Similarity	99.2%;	Score 764.6;	DB 3;	Length 771;
	Matches 767;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;	
Qy 1	GGGCCCCCTCGAGAAAAGAAATCGTCGGGGGTGAGGAGGCCCCCAGAGCAAGTGGCCCTGG	60				
Db 1	GGGCCCCCTCGAGAAAAGAAATCGTCGGGGGTGAGGAGGCCCCCAGAGCAAGTGGCCCTGG	60				
Qy 61	CAGGTGAGCTTGAGATCCAGGCGCCATCTGCGGTGATGCACTTCTGGGGGGTCCCTCATC	120				
Db 61	CAGGTGAGCTTGAGATCCAGGCGCCATCTGCGGTGATGCACTTCTGGGGGGTCCCTCATC	120				
Qy 121	CACCCCAAGTGGGTGCTGACCGCGCGGTGGGACCGGACGTCAAGATCTGGCC	180				
Db 121	CACCCCAAGTGGGTGCTGACCGCGCGGTGGGACCGGACGTCAAGATCTGGCC	180				
Qy 181	GCCTCAGGGTGAACCTGCGGAGCAGCACCTCTACTACAGGACCACTGCTGCGGTC	240				
Db 181	GCCTCAGGGTGAACCTGCGGAGCAGCACCTCTACTACAGGACCACTGCTGCGGTC	240				
Qy 241	AGCAGGATCATCTGCACCCACAGTTCACACCCCGCAGATCGGAGGAGCATGCGCCCTG	300				
Db 241	AGCAGGATCATCTGCACCCACAGTTCACACCCCGCAGATCGGAGGAGCATGCGCCCTG	300				
Qy 301	CTGGAGCTGGAGGAGCGGTGAAGGTCTCCAGCCACCGTCCACCGTCACTGCCCCCT	360				
Db 301	CTGGAGCTGGAGGAGCGGTGAAGGTCTCCAGCCACCGTCCACCGTCACTGCCCCCT	360				
Qy 361	GCCTCAGAGACTTCCCGCGGGATGCGTGGGTCACTGCTGGGGGATGTGGAC	420				
Db 361	GCCTCAGAGACTTCCCGCGGGATGCGTGGGTCACTGCTGGGGGATGTGGAC	420				
Qy 421	AATGATGAGCGCTCCACCGCCATTCTCTGAAGCAGGTGAAGGTCTCCCATATGGA	480				
Db 421	AATGATGAGCGCTCCACCGCCATTCTCTGAAGCAGGTGAAGGTCTCCCATATGGA	480				
Qy 481	AACCACATTTGTGAGGCAAAATACACTTGGCGCTACAGGGAGAGAGTGGCATC	540				
Db 481	AACCACATTTGTGAGGCAAAATACACTTGGCGCTACAGGGAGAGAGTGGCATC	540				
Qy 541	GTCCGTGACGACATGCTGTGTGCGGGAAACACCGAGGAGTCAATGCGAGGAGTCC	600				
Db 541	GTCCGTGACGACATGCTGTGTGCGGGAAACACCGAGGAGTCAATGCGAGGAGTCC	600				
Qy 601	GGAGGCGCCCTGGTGTGCAAGTGAATGGACCTGGTGTGAGGGGGTGGTGTGAGTGG	660				
Db 601	GGAGGCGCCCTGGTGTGCAAGTGAATGGACCTGGTGTGAGGGGGTGGTGTGAGTGG	660				

/partial
/product= "Beta-I tryptase"
/note= "this sequence lacks a start codon"

WO200198470-A2.

27-DEC-2001.

20-JUN-2001; 2001WO-US019681.

21-JUN-2000; 2000US-00598982.

(PROM-) PROMEGA CORP.

Maffit M, Niles AL, Haak-Frendscho M;

WPI; 2002-114578/15.

P-PSDB; AAU12006.

DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase having an active site mutation.

Disclosure; Page 72-74; 126pp; English.

The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The method is useful for producing enzymatically-active beta-II tryptase. The active site mutants of proteolytic tryptase provide a tool to investigate the structural and functional properties of the protease and its enzymatic activity, and for modelling studies. The enzymatically-active, recombinant proteolytic tryptase produced are useful as an antigen to generate anti-human tryptase antibodies and in drug screening for compounds which act as tryptase inhibitors, antagonists, agonists, etc. The present sequence encodes for human beta-I tryptase

Sequence 771 BP; 149 A; 257 C; 241 G; 124 T; 0 U; 0 Other;

Query Match 99.0%; Score 763; DB 6; Length 771;
Best Local Similarity 99.4%; Pred. No. 5,6e-146;
Matches 766; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGGCCCTCGAGAAAGAAATCGTGGGGGTGAGAGGCCCCCAGAGCAAGTGGCCCTGG 60
Db 1 GGGCCCTCGAGAAAGAAATCGTGGGGGTGAGAGGCCCCCAGAGCAAGTGGCCCTGG 60
QY 61 CAGGTGAGCCTGAGAGTCCACGGCCCTACTGAGTGCATCTCTGGGGGGTCCCTCATC 120
Db 61 CAGGTGAGCCTGAGAGTCCACGGCCCTACTGAGTGCATCTCTGGGGGGTCCCTCATC 120
QY 121 CACCCCAAGTGGGTGCTGACCGCGCGCGTGGGACCGGACGCTCAAGGATCTGGCC 180
Db 121 CACCCCAAGTGGGTGCTGACCGCGCGCGTGGGACCGGACGCTCAAGGATCTGGCC 180
QY 181 GCCCTCAGGTGGAATCGCGGGAGAGACACTTACTACAGGACCAAGCTCTGCGCGTC 240
Db 181 GCCCTCAGGTGGAATCGCGGGAGAGACACTTACTACAGGACCAAGCTCTGCGCGTC 240
QY 241 AGCAGGATCATCGTGGACCCACAGTCTTACACCGCCAGATCGGAGCGGACATGCCCTG 300
Db 241 AGCAGGATCATCGTGGACCCACAGTCTTACACCGCCAGATCGGAGCGGACATGCCCTG 300
QY 301 CTGAGCTGGAGGAGCGGGTGAAGTCTCCAGCCAGCTTCCACAGGTCACCCCTGCCCT 360
Db 301 CTGAGCTGGAGGAGCGGGTGAAGTCTCCAGCCAGCTTCCACAGGTCACCCCTGCCCT 360
QY 361 GCCTCAGAGACTTCCCGCCCGGAGTGCCTGCTGGGTCACTGGCTGGGGGATGTGGAC 420

Db 361 GCCTCAGAGACTTCCCGCCCGGAGTGCCTGCTGGGTCACTGGCTGGGGGATGTGGAC 420
QY 421 AATGATGAGCGCTCCACCGCCATTTCCTCTGAAGCAGGTGAAGTCCCATTAATGGAA 480
Db 421 AATGATGAGCGCTCCACCGCCATTTCCTCTGAAGCAGGTGAAGTCCCATTAATGGAA 480
QY 481 AACCAATTGTGACGCAAAATACACCTTGGCGCTTACCGGAGACGACGTCGCCATC 540
Db 481 AACCAATTGTGACGCAAAATACACCTTGGCGCTTACCGGAGACGACGTCGCCATC 540
QY 541 GTCCGTGACGACATGCTGTCGGGACACCGGAGGACTCATGCCAGGCGGACTCC 600
Db 541 GTCCGTGACGACATGCTGTCGGGAGACACCGGAGGACTCATGCCAGGCGGACTCC 600
QY 601 GGAGGGCCCTGCTGTCGAAGGTGAATGGACCTGGCTGAGCGGGGCTGTGACGTGG 660
Db 601 GGAGGGCCCTGCTGTCGAAGGTGAATGGACCTGGCTGAGCGGGGCTGTGACGTGG 660
QY 661 GCGAGGGCTGTGCGCCAGCCCAACCGGCTGGCATCTACCCGCTGCTACCTACTTGT 720
Db 661 GCGAGGGCTGTGCGCCAGCCCAACCGGCTGGCATCTACCCGCTGCTACCTACTTGT 720
QY 721 GACTGGATCCACCACTATGTGTCCTCCAAAGCGGTGAAGCGGCGCGGCTGT 771
Db 721 GACTGGATCCACCACTATGTGTCCTCCAAAGCGGTGAAGCGGCGCGGCTGT 771
RESULT 6
AAS20776
ID AAS20776 standard; DNA; 771 BP.
AC AAS20776;
XX 09-APR-2002 (first entry)
DE DNA encoding human beta-II tryptase active site mutant D91A #1.
XX Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
KW enzyme; mutant; ds.
XX Homo sapiens.
OS Synthetic.
XX WO200198470-A2.
XX 27-DEC-2001.
XX 20-JUN-2001; 2001WO-US019681.
XX 21-JUN-2000; 2000US-00598982.
XX (PROM-) PROMEGA CORP.
PI Maffit M, Niles AL, Haak-Frendscho M;
XX WPI; 2002-114578/15.
XX P-PSDB; AAU12010.
XX DNA construct for producing enzymatically-inactive proteolytic tryptase, comprises DNA sequence encoding proteolytic tryptase having an active site mutation.
PS Claim 7; Page 86-87; 126pp; English.
XX The present invention relates to recombinant human proteolytic tryptases, active site mutants of these tryptases and the methods for producing these. The method involves the production of a DNA expression construct comprising a promoter operably linked to a secretion signal sequence which is operably linked to a DNA sequence encoding a proteolytic tryptase with an active site mutation (the construct drives expression of a mature proteolytic tryptase that lacks enzymatic activity due to the active site mutation, in hosts transformed to contain the construct). The

CC method is useful for producing enzymatically-active beta-II tryptase. The
 CC active site mutants of proteolytic tryptase provide a tool to investigate
 CC the structural and functional properties of the protease and its
 CC enzymatic activity, and for modelling studies. The enzymatically-active,
 CC recombinant proteolytic tryptase produced are useful as an antigen to
 CC generate anti-human tryptase antibodies and in drug screening for
 CC compounds which act as tryptase inhibitors, antagonists, agonists, etc.
 CC AAS20775-AAS20790 encode for recombinant human beta-II tryptase active
 CC site mutants
 XX
 SQ Sequence 771 BP; 149 A; 256 C; 242 G; 124 T; 0 U; 0 Other;

Query Match 98.8%; Score 761.4; DB 6; Length 771;
 Best Local Similarity 99.2%; Pred. No. 1.2e-145;
 Matches 765; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGGCCCCCTCGAGAAAGAAATCGTGGGGGTGAGGAGGCCCCCGAGCAAGTGCCCTGG 60
 Db |||||
 QY 61 CAGGTGAGCTGAGATCCAGGCCCATCTGGATGCACTTCTCGGGGGTCCCTCATC 120
 Db |||||
 QY 61 CAGGTGAGCTGAGATCCAGGCCCATCTGGATGCACTTCTCGGGGGTCCCTCATC 120
 QY 121 CACCCCTCGAGAAAGAAATCGTGGGGGTGAGGAGGCCCCCGAGCAAGTGCCCTGG 180
 Db |||||
 QY 121 CACCCCTCGAGAAAGAAATCGTGGGGGTGAGGAGGCCCCCGAGCAAGTGCCCTGG 180
 QY 181 GCGCTCAGAGAGCTTCCCGCCGAGTCCAGCCGCGTGGTGGGACCGGACGTCATG 240
 Db |||||
 QY 181 GCGCTCAGAGAGCTTCCCGCCGAGTCCAGCCGCGTGGTGGGACCGGACGTCATG 240
 QY 241 AGCAGGATCATCTGTCAGCCACCTTCTACACCCGCGGATCGGAGCGGACATCGCC 300
 Db |||||
 QY 241 AGCAGGATCATCTGTCAGCCACCTTCTACACCCGCGGATCGGAGCGGACATCGCC 300
 QY 301 CTGAGCTGAGGAGCGGTTGAAGTCTCCAGCCAGCTCCAGCGTCCAGCTGCCCCCT 360
 Db |||||
 QY 301 CTGAGCTGAGGAGCGGTTGAAGTCTCCAGCCAGCTCCAGCGTCCAGCTGCCCCCT 360
 QY 361 GCCTCAGAGAGCTTCCCGCCGAGTCCAGCCGCGTGGTGGGACCGGACGTCATG 420
 Db |||||
 QY 361 GCCTCAGAGAGCTTCCCGCCGAGTCCAGCCGCGTGGTGGGACCGGACGTCATG 420
 QY 421 AATGATGAGCGCTCCCGCCGAGTCCAGCCGCGTGGTGGGACCGGACGTCATG 480
 Db |||||
 QY 421 AATGATGAGCGCTCCCGCCGAGTCCAGCCGCGTGGTGGGACCGGACGTCATG 480
 QY 481 AACACATTTGTGAGCGCAAAATACCACTTGGCGCTTACCGGGAGAGCGATCGGC 540
 Db |||||
 QY 481 AACACATTTGTGAGCGCAAAATACCACTTGGCGCTTACCGGGAGAGCGATCGGC 540
 QY 541 GTCCGTGAGCATGCTGTGTCGGGAAACACCGGAGGAGTCTATGCGAGGCGACTCC 600
 Db |||||
 QY 541 GTCCGTGAGCATGCTGTGTCGGGAAACACCGGAGGAGTCTATGCGAGGCGACTCC 600
 QY 601 GGAGGCCCCCTGCTGTCAGAGTGAATGCGCTGTCAGGCGGGGTGCTGAGCTGG 660
 Db |||||
 QY 601 GGAGGCCCCCTGCTGTCAGAGTGAATGCGCTGTCAGGCGGGGTGCTGAGCTGG 660
 QY 661 GCGAGGGCTGTGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
 Db |||||
 QY 661 GCGAGGGCTGTGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
 QY 721 GACTGATCCACCATATGTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 771
 Db |||||
 QY 721 GACTGATCCACCATATGTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 771

RESULT 7
 AAS20784
 ID AAS20784 standard; DNA; 771 BP.
 XX

AAS20784;
 09-APR-2002 (first entry)
 DNA encoding human beta-II tryptase active site mutant D91A #3.
 Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
 enzyme; mutant; ds.
 Homo sapiens.
 Synthetic.
 WO200198470-A2.
 27-DEC-2001.
 20-JUN-2001; 2001WO-US019681.
 21-JUN-2000; 2000US-00598982.
 (PROM-) PROMEGA CORP.
 Maffit M, Niles AL, Haak-Frendscho M;
 WPI; 2002-114578/15.
 P-PSDB; AAU12018.
 DNA construct for producing enzymatically-inactive proteolytic tryptase,
 comprises DNA sequence encoding proteolytic tryptase having an active
 site mutation.
 Claim 7; Page 107-109; 126pp; English.
 The present invention relates to recombinant human proteolytic tryptases,
 active site mutants of these tryptases and the methods for producing
 these. The method involves the production of a DNA expression construct
 comprising a promoter operably linked to a secretion signal sequence
 which is operably linked to a DNA sequence encoding a proteolytic
 tryptase with an active site mutation (the construct drives expression of
 a mature proteolytic tryptase that lacks enzymatic activity due to the
 active site mutation, in hosts transformed to contain the construct). The
 method is useful for producing enzymatically-active beta-II tryptase. The
 active site mutants of proteolytic tryptase provide a tool to investigate
 the structural and functional properties of the protease and its
 enzymatic activity, and for modelling studies. The enzymatically-active,
 recombinant proteolytic tryptase produced are useful as an antigen to
 generate anti-human tryptase antibodies and in drug screening for
 compounds which act as tryptase inhibitors, antagonists, agonists, etc.
 AAS20775-AAS20790 encode for recombinant human beta-II tryptase active
 site mutants
 SQ Sequence 771 BP; 149 A; 257 C; 241 G; 124 T; 0 U; 0 Other;

Query Match 98.5%; Score 759.8; DB 6; Length 771;
 Best Local Similarity 99.1%; Pred. No. 2.5e-145;
 Matches 764; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGGCCCCCTCGAGAAAGAAATCGTGGGGGTGAGGAGGCCCCCGAGCAAGTGCCCTGG 60
 Db |||||
 QY 61 CAGGTGAGCTGAGATCCAGGCCCATCTGGATGCACTTCTCGGGGGTCCCTCATC 120
 Db |||||
 QY 61 CAGGTGAGCTGAGATCCAGGCCCATCTGGATGCACTTCTCGGGGGTCCCTCATC 120
 QY 121 CACCCCTCGAGAAAGAAATCGTGGGGGTGAGGAGGCCCCCGAGCAAGTGCCCTGG 180
 Db |||||
 QY 121 CACCCCTCGAGAAAGAAATCGTGGGGGTGAGGAGGCCCCCGAGCAAGTGCCCTGG 180
 QY 181 GCGCTCAGAGAGCTTCCCGCCGAGTCCAGCCGCGTGGTGGGACCGGACGTCATG 240
 Db |||||
 QY 181 GCGCTCAGAGAGCTTCCCGCCGAGTCCAGCCGCGTGGTGGGACCGGACGTCATG 240

QY 241 AGCAGGATCATCGTGACCCACAGTTCTACACGCCAGATCGAGCGGACATCGCCCTG 300
 Db |||||
 QY 241 AGCAGGATCATCGTGACCCACAGTTCTACACGCCAGATCGAGCGGACATCGCCCTG 300
 Db |||||
 QY 301 CTGGAGCTGGAGAGCGGTTGAAGTCTCCAGCCAGTCCACACGGTCAACCTGCCCCCT 360
 Db |||||
 QY 301 CTGGAGCTGGAGAGCGGTTGAAGTCTCCAGCCAGTCCACACGGTCAACCTGCCCCCT 360
 Db |||||
 QY 361 GCCTCAGAGACCTTCCCGCGGGATCGGTGCTGGTCACTGGCTGGGGGATGTGGAC 420
 Db |||||
 QY 361 GCCTCAGAGACCTTCCCGCGGGATCGGTGCTGGTCACTGGCTGGGGGATGTGGAC 420
 Db |||||
 QY 421 AATGATGAGCGCTCCCGCCGCAATTTCTCTGAAGCAGGTGAAGTCCCATATGAA 480
 Db |||||
 QY 421 AATGATGAGCGCTCCCGCCGCAATTTCTCTGAAGCAGGTGAAGTCCCATATGAA 480
 Db |||||
 QY 481 AACCAATTGTGAGCGAAATACCACTTGGCGCTACACGGGAGACGCTCGGCATC 540
 Db |||||
 QY 481 AACCAATTGTGAGCGAAATACCACTTGGCGCTACACGGGAGACGCTCGGCATC 540
 Db |||||
 QY 541 GTCCGTGACGACATCGTGTGTCGGGAAACACCGAGGAGCTCATGCCAGGCGACTCC 600
 Db |||||
 QY 541 GTCCGTGACGACATCGTGTGTCGGGAAACACCGAGGAGCTCATGCCAGGCGACTCC 600
 Db |||||
 QY 601 GGAGGGCCCTGGTGTGCAAGGTGAATGGCACTGGCTGCAGCGCGGGTGTGCTCACTGG 660
 Db |||||
 QY 601 GGAGGGCCCTGGTGTGCAAGGTGAATGGCACTGGCTGCAGCGCGGGTGTGCTCACTGG 660
 Db |||||
 QY 661 GCGAGGCGCTGTGCCAGCCCAACCGGCTGGCATCTACACCGGTGCTCACTACTATTG 720
 Db |||||
 QY 661 GCGAGGCGCTGTGCCAGCCCAACCGGCTGGCATCTACACCGGTGCTCACTACTATTG 720
 Db |||||
 QY 721 GACTGGATCCACCACTATGTCCCAAAAGCGTGAAGCGCGCGCTCGT 771
 Db |||||
 QY 721 GACTGGATCCACCACTATGTCCCAAAAGCGTGAAGCGCGCGCTCGT 771
 Db |||||

RESULT 8

ID AAS20778
 XX AAS20778 standard; DNA; 771 BP.
 AC AAS20778;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE DNA encoding human beta-II tryptase active site mutant S194A #2.
 XX
 KW Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
 KW enzyme; mutant; ds.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 EN WO200198470-A2.
 XX
 XX 27-DEC-2001.
 XX
 XX 20-JUN-2001; 2001WO-US019681.
 XX
 XX 21-JUN-2000; 2000US-00598982.
 XX
 XX (PROM-) PROMEGA CORP.
 XX
 XX Maffit M, Niles AL, Haak-Frendscho M;
 XX
 DR WPI; 2002-114578/15.
 DR P-PSDB; AAU12012.
 XX
 XX DNA construct for producing enzymatically-inactive proteolytic tryptase,
 PT comprises DNA sequence encoding proteolytic tryptase having an active
 PT site mutation.
 XX
 PS Claim 7; Page 91-92; 126pp; English.

XX The present invention relates to recombinant human proteolytic tryptases,
 CC active site mutants of these tryptases and the methods for producing
 CC these. The method involves the production of a DNA expression construct
 CC comprising a promoter operably linked to a secretion signal sequence
 CC which is operably linked to a DNA sequence encoding a proteolytic
 CC tryptase with an active site mutation (the construct drives expression of
 CC a mature proteolytic tryptase that lacks enzymatic activity due to the
 CC active site mutation, in hosts transformed to contain the construct). The
 CC method is useful for producing enzymatically-active beta-II tryptase. The
 CC active site mutants of proteolytic tryptase provide a tool to investigate
 CC the structural and functional properties of the protease and its
 CC enzymatic activity, and for modelling studies. The enzymatically-active,
 CC recombinant proteolytic tryptase produced are useful as an antigen to
 CC generate anti-human tryptase antibodies and in drug screening for
 CC compounds which act as tryptase inhibitors, antagonists, agonists, etc.
 CC AAS20775-AAS20790 encode for recombinant human beta-II tryptase active
 CC site mutants

SQ Sequence 771 BP; 152 A; 255 C; 241 G; 123 T; 0 U; 0 Other;

Query Match 97.9%; Score 755; DB 6; Length 771;
 Best Local Similarity 98.7%; Pred. No. 2.4e-144;

Matches 761; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 GGGCCCTCGAGAAAGAAATCGTGGGGTTCAGGAGGCCCCAGCAGCAAGTGGCCCTGG 60
 Db 1 GGGCCCTCGAGAAAGAAATCGTGGGGTTCAGGAGGCCCCAGCAGCAAGTGGCCCTGG 60
 QY 61 CAGGTGAGCCTGAGAGTCCACGGCCCACTATGGATGCACTTCTGGGGGCTCCCTCATC 120
 Db 61 CAGGTGAGCCTGAGAGTCCACGGCCCACTATGGATGCACTTCTGGGGGCTCCCTCATC 120
 QY 121 CACCCCAAGTGGTGTCTGACCCCGCGCGTGTGGGACCGGACGTCGAAGATCTGGCC 180
 Db 121 CACCCCAAGTGGTGTCTGACCCCGCGCGTGTGGGACCGGACGTCGAAGATCTGGCC 180
 QY 181 GCCCTCAGGGTGCACCTCGGGGAGCAGCACCTTACTACAGGACCACTGCTGGCGGTC 240
 Db 181 GCCCTCAGGGTGCACCTCGGGGAGCAGCACCTTACTACAGGACCACTGCTGGCGGTC 240
 QY 241 AGCAGGATCATCGTGACCCACAGTTCTACACGCCAGATCGAGCGGACATCGCCCTG 300
 Db 241 AGCAGGATCATCGTGACCCACAGTTCTACACGCCAGATCGAGCGGACATCGCCCTG 300
 QY 301 CTGGAGCTGGAGAGCGGTTGAAGTCTCCAGCCAGTCCACACGGTCAACCTGCCCCCT 360
 Db 301 CTGGAGCTGGAGAGCGGTTGAAGTCTCCAGCCAGTCCACACGGTCAACCTGCCCCCT 360
 QY 361 GCCTCAGAGACCTTCCCGCGGGATCGGTGCTGGTCACTGGCTGGGGGATGTGGAC 420
 Db 361 GCCTCAGAGACCTTCCCGCGGGATCGGTGCTGGTCACTGGCTGGGGGATGTGGAC 420
 QY 421 AATGATGAGCGCTCCCGCCGCAATTTCTCTGAAGCAGGTGAAGTCCCATATGAA 480
 Db 421 AATGATGAGCGCTCCCGCCGCAATTTCTCTGAAGCAGGTGAAGTCCCATATGAA 480
 QY 481 AACCAATTGTGAGCGAAATACCACTTGGCGCTACACGGGAGACGCTCGGCATC 540
 Db 481 AACCAATTGTGAGCGAAATACCACTTGGCGCTACACGGGAGACGCTCGGCATC 540
 QY 541 GTCCGTGACGACATCGTGTGTCGGGAAACACCGAGGAGCTCATGCCAGGCGACTCC 600
 Db 541 GTCCGTGACGACATCGTGTGTCGGGAAACACCGAGGAGCTCATGCCAGGAGACGCC 600
 QY 601 GGAGGGCCCTGGTGTGCAAGGTGAATGGCACTGGCTGCAGCGCGGGTGTGCTCACTGG 660
 Db 601 GGAGGGCCCTGGTGTGCAAGGTGAATGGCACTGGCTGCAGCGCGGGTGTGCTCACTGG 660
 QY 661 GCGAGGCGCTGTGCCAGCCCAACCGGCTGGCATCTACACCGGTGCTCACTACTATTG 720
 Db 661 GCGAGGCGCTGTGCCAGCCCAACCGGCTGGCATCTACACCGGTGCTCACTACTATTG 720

QY 721 GACTGGATCCACCACTATGTCCTCCCAAAAGCCGTGAAGCGCGCCGCTCGT 771
 Db 721 GACTGGATCCACCACTATGTCCTCCCAAAAGCCGTGAAGCGCGCCGCTCGT 771

RESULT 9
 AAS20777 ID AAS20777 standard; DNA; 771 BP.
 XX AAS20777;
 XX 09-APR-2002 (first entry)
 XX DNA encoding human beta-II tryptase active site mutant S194A #1.
 XX Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
 XX enzyme; mutant; ds.
 XX Homo sapiens.
 OS Synthetic.
 XX W0200198470-A2.
 XX 27-DEC-2001.
 XX 20-JUN-2001; 2001WO-US019681.
 XX 21-JUN-2000; 2000US-00598982.
 XX (PROM-) PROMEGA CORP.
 XX Maffit M, Niles AL, Haak-Frendscho M;
 XX WPI; 2002-114578/15.
 DR P-PSDB; AAU12011.

XX DNA construct for producing enzymatically-inactive proteolytic tryptase,
 PT comprises DNA sequence encoding proteolytic tryptase having an active
 PT site mutation.
 XX Claim 7; Page 88-90; 126pp; English.
 XX The present invention relates to recombinant human proteolytic tryptases,
 CC active site mutants of these tryptases and the methods for producing
 CC these. The method involves the production of a DNA expression construct
 CC comprising a promoter operably linked to a secretion signal sequence
 CC which is operably linked to a DNA sequence encoding a proteolytic
 CC tryptase with an active site mutation (the construct drives expression of
 CC a mature proteolytic tryptase that lacks enzymatic activity due to the
 CC active site mutation, in hosts transformed to contain the construct). The
 CC method is useful for producing enzymatically-active beta-II tryptase. The
 CC active site mutants of proteolytic tryptase provide a tool to investigate
 CC the structural and functional properties of the protease and its
 CC enzymatic activity, and for modelling studies. The enzymatically-active,
 CC recombinant proteolytic tryptase produced are useful as an antigen to
 CC generate anti-human tryptase antibodies and in drug screening for
 CC compounds which act as tryptase inhibitors, antagonists, agonists, etc.
 CC AAS20775-AAS20790 encode for recombinant human beta-II tryptase active
 CC site mutants
 XX Sequence 771 BP; 150 A; 255 C; 241 G; 125 T; 0 U; 0 Other;

XX Query Match 97.9%; Score 755; DB 6; Length 771;
 XX Best Local Similarity 98.7%; Pred. No. 2.4e-144;
 XX Matches 761; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1 GGGCCCCCTCGAGAAAGAAATCGTCGGGGTCAGAGAGCCCCCAGAGCAAGTGGCCCTGG 60
 Db 1 GGGCCCCCTCGAGAAAGAAATCGTCGGGGTCAGAGAGCCCCCAGAGCAAGTGGCCCTGG 60
 QY 61 CAGGTGACCTGAGAGTCCAGGGCCCATCTACTGGATGCACTTCTGGGGGGTCCCTCATC 120
 Db 61 CAGGTGACCTGAGAGTCCAGGGCCCATCTACTGGATGCACTTCTGGGGGGTCCCTCATC 120

QY 121 CACCCAGTGGTGTGACCGCGCGCGTGGGACCGGACCGGACGCTCAAGGATCTGGCC 180
 Db 121 CACCCAGTGGTGTGACCGCGCGCGTGGGACCGGACCGGACGCTCAAGGATCTGGCC 180
 QY 181 GCCTCAGGGTGAACATGCGGGAGCAGCACTCTACTACAGGACCAAGTGTGTCGGCGTC 240
 Db 181 GCCTCAGGGTGAACATGCGGGAGCAGCACTCTACTACAGGACCAAGTGTGTCGGCGTC 240
 QY 241 AGCAGGATCATCTGTGACCCACAGTTTCTACACGCCCCAGATCGGAGCGGACATCGCCCTG 300
 Db 241 AGCAGGATCATCTGTGACCCACAGTTTCTACACGCCCCAGATCGGAGCGGACATCGCCCTG 300
 QY 301 CTGAGCTGAGGAGCGCGGTGAAGTCTCCAGGCACCTTCCACACGGTCAACCTCCCCCT 360
 Db 301 CTGAGCTGAGGAGCGCGGTGAAGTCTCCAGGCACCTTCCACACGGTCAACCTCCCCCT 360
 QY 361 GCCTCAGAGACCTTCCCGCGGGATGCGGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
 Db 361 GCCTCAGAGACCTTCCCGCGGGATGCGGTGCTGGGTCACTGGCTGGGGCGATGTGGAC 420
 QY 421 AATGATGAGCGCTCCCGACCGCCATTTCTCTGAAGCAGGTGAAGGTCCCATATGAA 480
 Db 421 AATGATGAGCGCTCCCGACCGCCATTTCTCTGAAGCAGGTGAAGGTCCCATATGAA 480
 QY 481 AACCACATTTGTGACGCAAAATACACCTTTGGCGCTTACACGGGAGACGCTCCGCATC 540
 Db 481 AACCACATTTGTGACGCAAAATACACCTTTGGCGCTTACACGGGAGACGCTCCGCATC 540
 QY 541 GTCCGTGACGACATGTGTGTCGGGGAACACCGGAGGAGTCACTATGCGAGGGGACTCC 600
 Db 541 GTCCGTGACGACATGTGTGTCGGGGAACACCGGAGGAGTCACTATGCGAGGGGACTCC 600
 QY 601 GGAGGGCCCTGTGTCGAAGTGAATGGACCTGGCTGACGGCGGCGTGTGTCAGCTGG 660
 Db 601 GGAGGGCCCTGTGTCGAAGTGAATGGACCTGGCTGACGGCGGCGTGTGTCAGCTGG 660
 QY 661 GGCAGGGCTGTGCCAGGCCAACCGGCTGGCATCTTACACCGCTGTCACTACTATTG 720
 Db 661 GGCAGGGCTGTGCCAGGCCAACCGGCTGGCATCTTACACCGCTGTCACTACTATTG 720
 QY 721 GACTGGATCCACCACTATGTCCTCCCAAAAGCCGTGAAGCGCGCCGCTCGT 771
 Db 721 GACTGGATCCACCACTATGTCCTCCCAAAAGCCGTGAAGCGCGCCGCTCGT 771

RESULT 10
 AAS20786 ID AAS20786 standard; DNA; 771 BP.
 XX AAS20786;
 XX 09-APR-2002 (first entry)
 XX DNA encoding human beta-II tryptase active site mutant S194A #6.
 XX Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
 XX enzyme; mutant; ds.
 XX Homo sapiens.
 OS Synthetic.
 XX W0200198470-A2.
 XX 27-DEC-2001.
 XX 20-JUN-2001; 2001WO-US019681.
 XX 21-JUN-2000; 2000US-00598982.
 XX (PROM-) PROMEGA CORP.
 XX Maffit M, Niles AL, Haak-Frendscho M;

Matches 760; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GGGCCCTCGAGAAAGATCGTCGGGGTCAGAGAGCCCGCCAGGACAAAGTGGCCCTGG 60
 Db 1 GGGCCCTCGAGAAAGATCGTCGGGGTCAGAGAGCCCGCCAGGACAAAGTGGCCCTGG 60
 QY 61 CAGTGAGCTGAGAGTCCACGGGCCATCTTGTGGGGGGTCCCTCATC 120
 Db 61 CAGTGAGCTGAGAGTCCACGGGCCATCTTGTGGGGGGTCCCTCATC 120
 QY 121 CACCCCAAGTGGTGTGACCGCCGGCGTGTGGGACCGGACGTCAGAGATCTGGCC 180
 Db 121 CACCCCAAGTGGTGTGACCGCCGGCGTGTGGGACCGGACGTCAGAGATCTGGCC 180
 QY 181 GCCTCAGGTGCAACTGCGGGAGCAGCACTCTTACTACAGGACCACTGCTGCCGTC 240
 Db 181 GCCTCAGGTGCAACTGCGGGAGCAGCACTCTTACTACAGGACCACTGCTGCCGTC 240
 QY 241 AGCAGGATCATCTGTGACCCACAGTCTTACACCGCCCGAGATCGGAGCGACATCGCCCTG 300
 Db 241 AGCAGGATCATCTGTGACCCACAGTCTTACACCGCCCGAGATCGGAGCGACATCGCCCTG 300
 QY 301 CTGAGCTGAGAGGCGGTGAGGTCTCCAGCCACGTCACACGGTCACTGCCCTT 360
 Db 301 CTGAGCTGAGAGGCGGTGAGGTCTCCAGCCACGTCACACGGTCACTGCCCTT 360
 QY 361 GCCTCAGAGACCTTCCCGCGGGATGCGGTGCTGGGTCTACTGGCTGGGGGATGTGGAC 420
 Db 361 GCCTCAGAGACCTTCCCGCGGGATGCGGTGCTGGGTCTACTGGCTGGGGGATGTGGAC 420
 QY 421 AATGATGAGCGCTCCACCGCCATTTCTCTGAAGCAGGTGAAGTCCCATATGAA 480
 Db 421 AATGATGAGCGCTCCACCGCCATTTCTCTGAAGCAGGTGAAGTCCCATATGAA 480
 QY 481 AACACATTTGTGACGCAAAATACACCTTGGCGCTTACAGGAGACGATCGGCATC 540
 Db 481 AACACATTTGTGACGCAAAATACACCTTGGCGCTTACAGGAGACGATCGGCATC 540
 QY 541 GTCGTGACGACATCTGTGTGCGGGAAACACCGGAGGACTCATCGAGGCGACTCC 600
 Db 541 GTCGTGACGACATCTGTGTGCGGGAAACACCGGAGGACTCATCTCAAGGCGAGGCC 600
 QY 601 GGAGGGCCCTGTGTGCAAGGTGAATGGCACTTGGCTGACGGCGGGCGTGGTCACTTG 660
 Db 601 GGAGGGCCCTGTGTGCAAGGTGAATGGCACTTGGCTGACGGCGGGCGTGGTCACTTG 660
 QY 661 GGCAGGGCTGTGCGGAGCCCAACGGGCTGGATCTACACCGCTGTACCTACTACTTG 720
 Db 661 GGCAGGGCTGTGCGGAGCCCAACGGGCTGGATCTACACCGCTGTACCTACTACTTG 720
 QY 721 GACTGGATCCACCACTATGTCCCAAAAGCCGTGAAGCGGCGCGCTCGT 771
 Db 721 GACTGGATCCACCACTATGTCCCAAAAGCCGTGAAGCGGCGCGCTCGT 771

RESULT 12
 AAS20779
 ID AAS20779 standard; DNA; 735 BP.
 XX AC AAS20779;
 XX DT 09-APR-2002 (first entry)
 XX DE DNA encoding human beta-II tryptase active site mutant H44A #2.
 XX KW Human; proteolytic tryptase; protease; recombinant beta-II tryptase;
 XX KW enzyme; mutant; ds.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX FN WO200198470-A2.

PD 27-DEC-2001.
 XX PF 20-JUN-2001; 2001WO-US019681.
 XX PR 21-JUN-2000; 2000US-0059982.
 XX PA (PROM-) PROMEGA CORP.
 XX PI Maffit M, Niles AL, Haak-Frendscho M;
 XX WI; 2002-114578/15.
 DR P-PSDB; AAU12013.
 XX PT DNA construct for producing enzymatically-inactive proteolytic tryptase,
 PT comprises DNA sequence encoding proteolytic tryptase having an active
 PT site mutation.
 XX PS Example 1c; Page 94-95; 126pp; English.
 XX CC The present invention relates to recombinant human proteolytic tryptases,
 CC active site mutants of these tryptases and the methods for producing
 CC these. The method involves the production of a DNA expression construct
 CC comprising a promoter operably linked to a secretion signal sequence
 CC which is operably linked to a DNA sequence encoding a proteolytic
 CC tryptase with an active site mutation (the construct drives expression of
 CC a mature proteolytic tryptase that lacks enzymatic activity due to the
 CC active site mutation, in hosts transformed to contain the construct). The
 CC method is useful for producing enzymatically-active beta-II tryptase. The
 CC active site mutants of proteolytic tryptase provide a tool to investigate
 CC the structural and functional properties of the protease and its
 CC enzymatic activity, and for modelling studies. The enzymatically-active,
 CC recombinant proteolytic tryptase produced are useful as an antigen to
 CC generate anti-human tryptase antibodies and in drug screening for
 CC compounds which act as tryptase inhibitors, antagonists, agonists, etc.
 CC AAS20775-AAS20790 encode for recombinant human beta-II tryptase active
 CC site mutants
 XX SQ Sequence 735 BP; 139 A; 245 C; 231 G; 120 T; 0 U; 0 Other;
 Query Match 95.3%; Score 735; DB 6; Length 735;
 Best Local Similarity 100.0%; Pred. No. 2.7e-140;
 Matches 735; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ATCGTCGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGAGGTGAGCTCAGAGTC 78
 Db 1 ATCGTCGGGGTCAGGAGGCCCCCAGGAGCAAGTGGCCCTGGAGGTGAGCTCAGAGTC 60
 QY 79 CACGGCCCATCTGATGCACTTCTGCGGGGCTCCCTCATCCACCCCGCTGAGTGTG 138
 Db 61 CACGGCCCATCTGATGCACTTCTGCGGGGCTCCCTCATCCACCCCGCTGAGTGTG 120
 QY 139 ACCGCGCGGGTGTGGGACCGGACGTCAGGATCTGGCGGCTCAGGGTGCACCTG 198
 Db 121 ACCGCGCGGGTGTGGGACCGGACGTCAGGATCTGGCGGCTCAGGGTGCACCTG 180
 QY 199 CGGAGAGCAGCACTCTACTACAGGACGAGCTGTGGCGGTGAGAGATCATCGTGAC 258
 Db 181 CGGAGAGCAGCACTCTACTACAGGACGAGCTGTGGCGGTGAGAGATCATCGTGAC 240
 QY 259 CCACAGTTCTACACCGCCCGAGATCGGAGCGACATCGCCCTGTGGAGCTGAGAGCG 318
 Db 241 CCACAGTTCTACACCGCCCGAGATCGGAGCGACATCGCCCTGTGGAGCTGAGAGCG 300
 QY 319 GTGAAGGTCTCCAGCCAGCTCCACAGGTCACTCCCTGCGCCCTGCTCAGAGACCTTCCC 378
 Db 301 GTGAAGGTCTCCAGCCAGCTCCACAGGTCACTCCCTGCGCCCTGCTCAGAGACCTTCCC 360
 QY 379 CCGGGGATGCGGTGCTGGTCACTGGCTGGGGGCGATGTGGCAATGATGAGCCCTCCCA 438
 Db 361 CCGGGGATGCGGTGCTGGTCACTGGCTGGGGGCGATGTGGCAATGATGAGCCCTCCCA 420
 QY 439 CCGCCATTCTCTGAAGCAGGTGAAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTG 498

XX	Mast cell tryptase II/beta; human; MCP-7; mast cell protease 7;
KW	blood clot; anticoagulant; myocardial infarction; reocclusion;
XX	thromboembolism; cerebral embolism; thrombosis; therapy; ss.
OS	Homo sapiens.
PH	Key Location/Qualifiers
FT	CDS 2..826
FT	/tag= a
XX	WO9824886-A1.
PN	11-JUN-1998.
XX	25-NOV-1997; 97WO-US021620.
PF	XX
PP	XX
PR	04-DEC-1996; 96US-0032354P.
PA	(BGHM) BRIGHAM & WOMENS HOSPITAL.
PI	Stevens RL;
XX	WPI; 1998-333308/29.
DR	P-PSDB; AAW64240.
XX	New compositions containing tryptase-7, e.g. mouse mast cell protease-7 -
PT	are used to treat clot formation in e.g. myocardial infarction,
PT	reocclusion following angioplasty or pulmonary thrombo-embolism.
XX	Disclosure; Page 66; 92pp; English.
PS	XX
CC	This nucleotide sequence includes a coding region for human mast cell
CC	tryptase II/beta (see AAW64240). The invention provides: compositions
CC	comprising an isolated tryptase-7 that may include chimeric proteins that
CC	contain (a) a human trypsin for all but the active site region and (b)
CC	the substrate-binding pocket of mouse tryptase-7 or its homologues (see
CC	AAW64233-39); a method for treating a blood clot by administering a
CC	nucleic acid molecule that codes for a tryptase-7, or an expression
CC	product, to decrease fibrinogen activity; a nucleic acid encoding a
CC	serine protease (SP); and a method of producing a mature SP by expressing
CC	the inactive zymogen in a host cell, and cleaving the enterokinase
CC	susceptibility domain. The tryptase-7 polypeptides can be used to treat
CC	disorders mediated by undesirable thrombus clot formation such as
CC	myocardial infarction and reocclusion following angioplasty of blood
CC	vessels associated with pulmonary thromboembolism, deep vein thrombosis,
CC	cerebral embolism, renal vein and peripheral arterial thrombosis. They
CC	are also useful for all surgical procedures that require decreased blood
CC	clots
XX	Sequence 1128 BP; 190 A; 409 C; 329 G; 200 T; 0 U; 0 Other;
SQ	Query Match 94.8%; Score 731; DB 2; Length 1128;
	Best Local Similarity 98.7%; Pred. No. 1.8e-139;
	Matches 737; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY	17 GAATCGTCGGGGTCTCAGGAGGCCCGACGAGCAATGGCCCTGGCAGGTGAGCTTGAGAG 76
Db	87 GCATCGTTGGGGTCTCAGGAGGCCCGACGAGCAATGGCCCTGGCAGGTGAGCTTGAGAG 146
QY	77 TCACGGCCCATCTACTGATGCATCTTGGGGGGTCTCCCTCATCCACCCCAGTGGGTGC 136
Db	147 TCACGGCCCATCTACTGATGCATCTTGGGGGGTCTCCCTCATCCACCCCAGTGGGTGC 206
QY	137 TGACCGCGCGGGTCTGCTGGGACCGGACGTCGAAGATCTGGCCGCTCAGGGTGC AAC 196
Db	207 TGACCGCGCGGACTCTGCTGGGACCGGACGTCGAAGATCTGGCCGCTCAGGGTGC AAC 266
QY	197 TGGCGGAGCAGCACCTCTACTACGAGACCCTGCTGCGGTGACGAGGATCATCTGTC 256
Db	267 TGGCGGAGCAGCACCTCTACTACGAGACCCTGCTGCGGTGACGAGGATCATCTGTC 326
QY	257 ACCACAGTTCTACACCGCCCGACGATCGGACGAGCATCGCCCTGCTGGAGCTGGAGGAGC 316

DR P-PSDB; AAW63175.
XX
XX Tryptase-6 complex inhibitory peptides - used to treat mast cell-mediated
PT inflammatory disorders e.g. asthma.
XX
XX Disclosure; Page 47-48; 69pp; English.
PS
XX This cDNA encodes the human mast cell tryptase II/beta which is a
CC homologue of the mouse mast cell protease (mMCP-6) zymogen. The invention
CC provides sequences shown in AAW63160 to AAW63169 that are inhibitors of
CC mMCP-6. These peptides which are tryptase-6 complex inhibitors, can be
CC used for treating a mast cell-mediated inflammatory disorder. The
CC inhibitors can be used to treat inflammatory disorders including asthma,
CC allergic rhinitis, urticaria and antioedema, eczematous dermatitis
CC (atopic dermatitis), anaphylaxis, hyperproliferative skin disease, peptic
CC ulcers, inflammatory bowel disorder, hyperresponsiveness and inflammatory
CC skin conditions
XX
XX Sequence 1128 BP; 190 A; 409 C; 329 G; 200 T; 0 U; 0 Other;
SQ
Query Match 94.8%; Score 731; DB 2; Length 1128;
Best Local Similarity 98.7%; Pred. No. 1.8e-139;
Matches 737; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 17 GAATGTCGGGGTTCAGGAGGCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
Db 87 GCATCGTTGGGGTTCAGGAGGCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 146
Qy 77 TCCAGGGCCCATCTAGTATGACTTCTGGGGGGTCCCTCATCCACCCAGTGGGTGC 136
Db 147 TCCAGGGCCCATCTAGTATGACTTCTGGGGGGTCCCTCATCCACCCAGTGGGTGC 206
Qy 137 TGACCGCGCGCGTGGGACCGGACGTCAGGATCTGCGCCCTCAGCAGGATCATCGTGC 196
Db 207 TGACCGGAGCGACTGCTGGGACCGGACGTCAGGATCTGCGCCCTCAGGAGTCAAC 266
Qy 197 TGGGGAGCAGCACTTACTTACCAGGACCGAGTCTGCGCGTCAAGGATCATCGTGC 256
Db 267 TGGGGAGCAGCACTTACTTACCAGGACCGAGTCTGCGCGTCAAGGATCATCGTGC 326
Qy 257 ACCACAGTTCTACACCGCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
Db 327 ACCACAGTTCTACACCGCCAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 386
Qy 317 CGGTGAAGGTCTCCAGCCAGCTCCACCGCTCACCGTCCCGCCCTCAGAGCCTTCC 376
Db 387 CGGTGAAGGTCTCCAGCCAGCTCCACCGTCCCGCCCTCAGAGCCTTCC 446
Qy 377 CCGCGGGATCGGTGCTGGGTCACTGGCTGGGGGATGTGACAAATGATGAGCGCCTCC 436
Db 447 CCGCGGGATCGGTGCTGGGTCACTGGCTGGGGGATGTGACAAATGATGAGCGCCTCC 506
Qy 437 CACCGCCATTTCTCTGAAGCAGGTGAAGTCCCCATTAATGGAAACCAATTTGTGACG 496
Db 507 CACCGCCATTTCTCTGAAGCAGGTGAAGTCCCCATTAATGGAAACCAATTTGTGACG 566
Qy 497 CAAATACCACTTGGGCCCTACACGGGAGACGCTCGCGATCGTCCGTGACGACATGC 556
Db 567 CAAATACCACTTGGGCCCTACACGGGAGACGCTCGCGATCGTCCGTGACGACATGC 626
Qy 557 TGTGTGCGGGAACACCCGGAGGACTCATGCGAGGGGACTCCGGAGGGGCCCTGGTGT 616
Db 627 TGTGTGCGGGAACACCCGGAGGACTCATGCGAGGGGACTCCGGAGGGGCCCTGGTGT 686
Qy 617 GCAAGGTGAATGGGACCTGGCTGCAGGGGGGGTGGTCACTGGGGCGAGGGCTGTGCC 676
Db 687 GCAAGGTGAATGGGACCTGGCTGCAGGGGGGGTGGTCACTGGGGCGAGGGCTGTGCC 746
Qy 677 AGCCCAACCGCGCTGGCATCTACACCGCTGTCACTACTTGGACTGGATCCACCACT 736
Db 747 AGCCCAACCGCGCTGGCATCTACACCGCTGTCACTACTTGGACTGGATCCACCACT 806
Qy 737 ATGTCCCCAAAAAGCCGTGAAGCGGCC 763

Db 807 ATGTCCCCAAAAAGCCGTGAGTCAGGC 833
Search completed: July 22, 2004, 11:01:39
Job time : 525 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 22, 2004, 10:45:20 ; Search time 3404 Seconds
(without alignments)
6763.731 Million cell updates/sec

Title: US-09-598-982-20

Perfect score: 771

Sequence: 1 gggccctcgagaaagaat.....cgtgaaggcgccgctgct 771

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	676.2	87.7	1030	12 BM919268	BM919268 AGENCOURT
2	581.8	75.5	589	13 BU071733	BU071733 im33a09.y
3	580.2	75.3	904	13 BQ720404	BQ720404 AGENCOURT
4	574.2	74.5	619	14 CD671851	CD671851 fg07g11.y

5	531.4	68.9	642	14	CD672689	fg15a06.y
6	525	68.1	635	14	CD671891	CD671891 fg08b10.y
7	516.6	67.0	722	13	BX091892	BX091892 K-EST0144
8	495.6	64.3	502	13	BQ082929	BQ082929 K-EST0144
9	488.4	63.3	581	13	BU787772	BU787772 i034c08.y
10	468.4	60.8	736	12	BG542089	BG542089 602571309
11	455.6	59.1	806	14	CF553058	CF553058 AGENCOURT
12	444.4	57.6	917	13	BQ721078	BQ721078 AGENCOURT
13	430.6	55.8	930	14	CB203717	CB203717 AGENCOURT
14	422.2	54.8	1000	12	BI413250	BI413250 602986390
15	420.4	54.5	639	9	AA131142	AA131142 z131b01.r
16	420	54.5	686	13	BU073263	BU073263 im33a09.x
17	401.4	52.1	811	12	BG697540	BG697540 602660760
18	400	51.9	678	12	BG483591	BG483591 602503309
19	375	48.6	512	10	BF724180	BF724180 bx01h02.y
20	371.4	48.2	929	14	CF583026	CF583026 AGENCOURT
21	358.6	46.5	690	14	CA439686	CA439686 UI-H-DT1-
22	357.6	46.4	699	14	CA438721	CA438721 UI-H-DT1-
23	351	45.5	693	12	BM991728	BM991728 UI-H-DT1-
24	350.2	45.4	376	10	BF850308	BF850308 CM3-EN007
25	349.6	45.3	692	12	BM989945	BM989945 UI-H-DT1-
26	348	45.1	688	12	BQ003361	BQ003361 UI-H-E11-
27	338	43.8	682	14	CA425354	CA425354 UI-H-DF0-
28	334.6	43.4	671	14	CB840425	CB840425 M15E-0715
29	334.2	43.3	371	10	BF359130	BF359130 QV3-ET006
30	324.2	42.0	859	14	CF583025	CF583025 AGENCOURT
31	319.4	41.4	581	14	CA867461	CA867461 i128f02.y
32	314.6	40.8	379	10	BF849396	BF849396 CM3-EN007
33	309.4	40.1	474	10	AW823937	AW823937 uf61e03.y
34	305.8	39.7	525	12	BI775716	BI775716 468400 MA
35	304.2	39.5	545	12	BI681216	BI681216 460544 MA
36	295	38.3	558	12	BI780801	BI780801 id09c06.y
37	289.4	37.5	291	10	BF876081	BF876081 IL3-ET011
38	286.6	37.2	617	14	CA943476	CA943476 i128f02.x
39	281.6	36.5	537	12	BM708916	BM708916 UI-E-CT11
40	279.6	36.3	620	13	BU731577	BU731577 UI-E-CT11
41	276.8	35.9	613	10	AW152543	AW152543 xf76b04.x
42	273.6	35.5	411	10	BE862270	BE862270 UI-M-BH0-
43	266.6	34.6	660	14	CB589106	CB589106 AGENCOURT
44	264.8	34.3	538	10	BE751979	BE751979 204246 MA
45	261.4	33.9	620	9	AA049080	AA049080 mj50f09.r

ALIGNMENTS

RESULT 1
BM919268
LOCUS
DEFINITION BM919268 6715837 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5748499
5' mRNA sequence.
ACCESSION BM919268
VERSION BM919268.1 GI:19369647
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1030)
NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12776 row: f column: 20
High quality sequence stop: 719.

I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10⁺ by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

```

Query Match      64.3%; Score 495.6; DB 13; Length 502;
Best Local Similarity 99.2%; Pred. No. 4.7e-82;
Matches 498; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 87 ATACTGGATGACATCTCTGGGGGGTCCCTCATCCACCCCGAGTGGGTGCTGACCGCGC 146
Db 1 ATACTGGATGACATCTCTGGGGGGTCCCTCATCCACCCCGAGTGGGTGCTGACCGCGC 60

QY 147 GCGGTGGTGGACCGAGTCAAGATCTGCGCCCTCAGGGTGCACCTGCGGGAGCA 206
Db 61 GCACCTGGTGGACCGAGTCAAGATCTGCGCCCTCAGGGTGCACCTGCGGGAGCA 120

QY 207 GCACCTCTACTACAGGACCGAGTCTGCGGTGACAGGATCATCTGCGACCCACAGTT 266
Db 121 GCACCTCTACTACAGGACCGAGTCTGCGGTGACAGGATCATCTGCGACCCACAGTT 180

QY 267 CTACACCGCCAGATCGGAGCGACATCGCCCTGTGGAGCTGGAGGACCGGTGAAGT 326
Db 181 CTACACCGCCAGATCGGAGCGACATCGCCCTGTGGAGCTGGAGGACCGGTGAAGT 240

QY 327 CTCAGCACAGTCCACAGTCACTGCGCCCTGCTCAGAGACCTTCCCGCGGGAT 386
Db 241 CTCAGCACAGTCCACAGTCACTGCGCCCTGCTCAGAGACCTTCCCGCGGGAT 300

QY 387 GCGGTGCTGGGTCACTGGCTGGGGGATGTGACAAATGATGAGCGCTCCACCGCCATT 446
Db 301 GCGGTGCTGGGTCACTGGCTGGGGGATGTGACAAATGATGAGCGCTCCACCGCCATT 360

QY 447 TCCTCTGAAGCAGGTGAAGTCCCAATATGAAACACACATTTGTGAGCGCAAAATACCA 506
Db 361 TCCTCTGAAGCAGGTGAAGTCCCAATATGAAACACACATTTGTGAGCGCAAAATACCA 420

QY 507 CTTGGCGCTACACGGAGACGATCGCGATCGTGGTACGACATGCTGTGTGCGG 566
Db 421 CTTGGCGCTACACGGAGACGATCGCGATCGTGGTACGACATGCTGTGTGCGG 480

QY 567 GAACACCGGAGGACTCATGC 588
Db 481 GAACACCGGAGGACTCATGC 502

```

RESULT 9

```

BU787772
LOCUS BU787772
DEFINITION BU787772 Human insulinoma Homo sapiens cDNA clone IMAGE:612847
5' similar to SW:TRYB_HUMAN P20231 BETA-TRYPTASE PRECURSOR ;, mRNA
sequence.

```

ACCESSION

```

VERSION BU787772.1 GI:23835713

```

KEYWORDS

```

EST.

```

SOURCE

```

Homo sapiens (human)

```

ORGANISM

```

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE

```

1 (bases 1 to 581)

```

AUTHORS

```

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blisstein,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,

```

TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other ESTs: i034c08.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 427.

FEATURES
source

```

1..581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6128247"
/tissue_type="insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Human insulinoma"
/note="Organ: pancreas; Vector: pBluescript SK-; Site: 1:  
XhoI; Site 2: EcoRI; Constructed with lambda ZAPII system  
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to  
pBluescript SK- by Dr. H. Inoue following the Washington  
University protocol  
(http://genome.wustl.edu/est/lambda_protocol.shtml).  
Please contact Hiroshi Inoue, MD/PhD for further  
information on this library (Metabolism Division, Permutt  
Laboratory, Washington University School of Medicine, Box  
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this  
is a Washington University Pancreas EST project library."

```

ORIGIN

```

Query Match      63.3%; Score 488.4; DB 13; Length 581;
Best Local Similarity 98.8%; Pred. No. 1.1e-80;
Matches 492; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 17 GAATGTCGGGGTTCAGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCTGAGAG 76
Db 84 GCATGTCGGGGTTCAGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCTGAGAG 143

QY 77 TCCACGGCCCATCTGAGTGCACCTTCTCGGGGGTCTCCCTCATCCACCCCGAGTGGTGC 136
Db 144 TCCACGGCCCATCTGAGTGCACCTTCTCGGGGGTCTCCCTCATCCACCCCGAGTGGTGC 203

QY 137 TGACCGCCCGCGTTCGCTGGGACCGGACGTCAGGATCTGCGCCCTTCAGGGTGCAC 196
Db 204 TGACCGCAGCGCACTCGCTGGGACCGGACGTCAGGATCTGCGCCCTTCAGGGTGCAC 263

QY 197 TCGGGAGCAGCACTCTACTACGAGCAGCTGCTCGCGTTCAGAGGATCATCTGTC 256
Db 264 TCGGGAGCAGCACTCTACTACGAGCAGCTGCTCGCGTTCAGAGGATCATCTGTC 323

QY 257 ACCACAGTTCCTACACCGCCAGATCGGAGCGGACATCGCCCTGCTGAGCTGGAGGAGC 316
Db 324 ACCACAGTTCCTACACCGCCAGATCGGAGCGGACATCGCCCTGCTGAGCTGGAGGAGC 383

QY 317 CGGTGAAGGTCTCCAGCCAGCTCCACACGGTCAACCTGCCCTCCCTCCCTCAGAGCTTCC 376
Db 384 CGGTGAAGGTCTCCAGCCAGCTCCACACGGTCAACCTGCCCTCCCTCAGAGCTTCC 443

QY 377 CCGCGGAGTACCGTGTGCTGGGTCTACTGGTGGGCGATGTGACAATGATGAGCGCTCC 436
Db 444 CCGCGGAGTACCGTGTGCTGGGTCTACTGGTGGGCGATGTGACAATGATGAGCGCTCC 503

QY 437 CACCGCCATTTCCTCTGAAGCAGGTGAAGTCCCCATAATGAAACACCATTTGTGAGC 496

```

```

Db      504  CACGCCATTTCCTCTAGCAGGTGAAGTCCCCATAATGAAACACATTGTGACG 563
      |||||||
Qy      497  CAAATACCACTTGGCG 514
      |||||||
Db      564  CAAATACCACTTGGCG 581
      |||||||

RESULT 10
BG542089
LOCUS      736 bp mRNA linear EST 03-APR-2001
DEFINITION 602571309f1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4695458 5',
mRNA sequence.
ACCESSION  BG542089
VERSION     BG542089.1 GI:13534322
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 736)
AUTHORS    NIH-MGC http://mgs.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LL0M1521 row: b column: 03
            High quality sequence stop: 725.

FEATURES   source
            Location/Qualifiers
            1..736
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:4695458"
            /lab_host="DH10B (T1 phage-resistant)"
            /clone_lib="NIH_MGC_77"
            /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
            SfiI (ggcgcttcggcc); Site 2: SfiI (ggcattatggcc); 5' and
            3' adaptors were used in cloning as follows: 5' adaptor
            sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
            5'-ATTCTAGGCGGCGGCGGCACATG-dt(30)BN-3' (where B = A,
            C, or G and N = A, C, G, or T). Average insert size 1.9
            kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
            by PCR. This library was enriched for full-length clones
            and was constructed by Clontech Laboratories (Palo Alto,
            CA). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 60.8%; Score 468.4; DB 12; Length 736;
Best Local Similarity 90.9%; Pred. No. 6.1e-77;
Matches 567; Conservative 0; Mismatches 46; Indels 11; Gaps 6;

Qy      17  GAATCTCGGGGTCAGAGGCCCGCCAGGACAACTGCGCTTGGCAGTGAAGCTTGAGAG 76
      |||||||
Db      113  GCATCTGTGGGGTTCAGAGGCCCGCCAGGACAACTGCGCTTGGCAGTGAAGCTTGAGAG 172
      |||||||
Qy      77  TCCACGGCCCATCTAGTATGACTTCTGCGGGGGCTCCCTCATCCACCCCGAGTGGGTGC 136
      |||||||
Db      173  TCCACGGCCCATCTAGTATGACTTCTGCGGGGGCTCCCTCATCCACCCCGAGTGGGTGC 232
      |||||||
Qy      137  TGACGGCGCGCGCTGCTGGGACCGGACGTCAGAGATCTGGCGCCCTCTAGGTGCAAC 196
      |||||||
Db      233  TGACGGCAGCGCAGCTGCTGGGACCGGACGTCAGAGATCTGGCGCCCTCTAGGTGCAAC 292
      |||||||
Qy      197  TGCGGGAGCAGCACTCTACTACCAAGGACCAAGCTGTCGGCGTCCAGCAGGATCATCGTGC 256
      |||||||

```

```

Db      293  TGGGGGAGCAGCACTCTACTACGAGCACCAGCTGTGTCGGGTAGCAGGATCATCTGTC 352
      |||||||
Qy      257  ACCCACAGTTCTACACCGCCAGATCGGAGCGGACATCGCCCTGCTCGAGCTGGAGAGC 316
      |||||||
Db      353  ACCCACAGTTCTACACCGCCAGATCGGAGCGGACATCGCCCTGCTCGAGCTGGAGAGC 412
      |||||||
Qy      317  CGGTGAAGGTCTCCAGCCACGTCCACACGGTCAACCTTGCCTGCTGCTCAGAGACCTTCC 376
      |||||||
Db      413  CGGTGAAGGTCTCCAGCCACGTCCACACGGTCAACCTTGCCTGCTGCTCAGAGACCTTCC 472
      |||||||
Qy      377  CCCC-GGGGATGCGCTGCTGGTCACTGCTGGGGCGATGTGGCAATGATGAGCGCTC 435
      |||||||
Db      473  CCGCGGGGATGCGCTGCTGGTCACTGCTGGGGCGATGTGGCAATGATGAGCGCTC 532
      |||||||
Qy      436  CCACCGCATTTCTCTGGAAGCAGG-TGAAGGTCCCATATGTAATGAAAAACACATTGTGA 494
      |||||||
Db      533  CCACCGCATTTCTCTGGAAGCAGGTGAAGTCCCATATGTAATGAAAAACACATTGTGA 592
      |||||||
Qy      495  CGCAAAATACACCTTGGCGCT-ACACGGGAGAG-ACGTCCGCATCTGTCCTGAGCAGAC 552
      |||||||
Db      593  CGCAAAATACACCTTGGCGCTTAACACGGGAGACGAAGGTCCGCTTCGTCGGTGAAC 652
      |||||||
Qy      553  ATGCT-----GTGTCGGCGGACACCGGAGGACTCATGCCAGGGCG--ACTCGGAGG 605
      |||||||
Db      653  GACATTCTGTGTGCGGGGACACCGGAGGACTCATGCCAGGGCGACTCCGGGAGG 712
      |||||||
Qy      606  GCCCTGGTGTGCAAGGTGAATGG 629
      |||||||
Db      713  GCCCTGGTGTGCAAGGTGACTGG 736
      |||||||

RESULT 11
CF553058
LOCUS      806 bp mRNA linear EST 22-SEP-2003
DEFINITION AGENCOURT 15594982 NIH_MGC_183 Homo sapiens cDNA clone
IMAGE:30529468 5', mRNA sequence.
ACCESSION  CF553058
VERSION     CF553058.1 GI:34889892
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 806)
AUTHORS    NIH-MGC http://mgs.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein
            cDNA Library Preparation: Invitrogen Corp
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM617 row: b column: 05
            High quality sequence start: 18
            High quality sequence stop: 611.
            Location/Qualifiers
            1..806
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:30529468"
            /lab_host="DH10B-Tona (T1 and T5 phage resistant)"
            /clone_lib="NIH_MGC_183"
            /note="Organ: Pooled muscle (cardiac and skeletal);
            Vector: pCMV-SPORT6.1; Site 1: EcoRV (destroyed); Site 2:
            NotI; Library is oligo-dT primed and directionally cloned

```

```

(Scorv site is destroyed upon cloning). Average insert
size 1.7. Library was constructed by Invitrogen."
ORIGIN
  Query Match      59.1%; Score 455.6; DB 14; Length 806;
  Best Local Similarity 94.0%; Pred. No. 1.5e-74;
  Matches 485; Conservative 0; Mismatches 29; Indels 2; Gaps 1;
  QY 17 GAATCGTGGGGGTGAGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
  DB 246 GTATGTCGGGGGTGAGAGGCCCCCAGGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 305
  QY 77 TCCAGGGCCATACATGATGATGATCTTCTGGGGGGGTCCCTCATCCACCCCAAGTGGGTGC 136
  DB 306 TCCGGGACCGATGATGATGATCTTCTGGGGGGGTCCCTCATCCACCCCAAGTGGGTGC 365
  QY 137 TCACCGCCGCGCGTGGGACCGGACGTCAGGATCTGCGCCCTCAGGGTGCAAC 196
  DB 366 TGACCGGCGCGCACTGCGCTGGGACCGGACGTCAGGATCTGCGCCACCTCAGGGTGCAAC 425
  QY 197 TCGGGGAGCAGCACCTCTACTACAGGACCAAGTCTGCGCGGTGACGAGGATCATCTGC 256
  DB 426 TCGGGGAGCAGCACCTCTACTACAGGACCAAGTCTGCGCGGTGACGAGGATCATCTGC 485
  QY 257 ACCCAAGTTTACACCGCCCAAGATCGGAGCGGACATCGCCCTGCTGGAGCTGGAGGAGC 316
  DB 486 ACCCAAGTTTACATCATCATCAGACTGGAGCGGATATCGCCCTGCTGGAGCTGGAGGAGC 545
  QY 317 CGGTGAAGTCTCCAGCCACGTCACAGGTCACCTGCGCCCTGCTGGAGCTGGAGGAGC 376
  DB 546 CCGTGAACATCTCCAGCGCGCTCCACAGGTCATCTGCGCCCTGCTGGAGCTGGAGGAGC 605
  QY 377 CCGCGGGATGCGGTGCTGGGTCACTGCTGGGGGATGAGCAATGATGAGCGCCCTCC 436
  DB 606 CCGCGGGATGCGGTGCTGGGTCACTGCTGGGGGATGAGCAATGATGAGCGCCCTCC 665
  QY 437 CACCGCCATTTCTCTGAAGCAGGTGAAGTCCCATTAATGAAACACACATTTGTGACG 496
  DB 666 CACCGCCATTTCTCTGAAGCAGGTGAAGTCCCATTAATGAAACACACATTTGTGACG 725
  QY 497 CAATATACACCTTGG--CGCTACACGGGAGACGA 530
  DB 726 CAATATACACCTTGGCGCCCTACACGGGAGACGA 761
  RESULT 12
  LOCUS BQ721078 917 bp mRNA linear EST 16-JUL-2002
  DEFINITION AGNCOURT_8109065 Lupski_sympathetic_trunk Homo sapiens cDNA clone
  IMAGE:6189508 5', mRNA sequence.
  ACCESSION BQ721078
  VERSION BQ721078.1 GI:21859975
  KEYWORDS EST.
  SOURCE Homo sapiens (human)
  ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE 1 (Bases 1 to 917)
  AUTHORS NIH-MGC http://mgc.nci.nih.gov/;
  TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL Unpublished (1999)
  COMMENT Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  Tissue Procurement: Dr. James R. Lupski
  cDNA Library Preparation: Life Technologies, Inc.
  DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
  Clone Distribution by: Agencourt Bioscience Corporation
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLAM13586 row: n column: 05
  High quality sequence stop: 609.
  Location/Qualifiers

```

```

1. 917
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6189508"
/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/clone_lib="Lupski_sympathetic trunk"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site 1:
NotI; Site 2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGCGGTCCG-3' and
5'-GACTAGTTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies."
ORIGIN
  Query Match      57.6%; Score 444.4; DB 13; Length 917;
  Best Local Similarity 98.5%; Pred. No. 1.9e-72;
  Matches 459; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
  QY 239 TGCTGGAGCTGGAGAGCGGTGAAGTCTTCAGCCACGTCACACGGTCAACCTGCCCC 358
  DB 1 TGCTGGAGCTGGAGAGCGGTGAAGTCTTCAGCCACGTCACACGGTCAACCTGCCCC 60
  QY 359 CTGCTCTAGAGACCTTCCCCCGGGATGCGGTGCTGGGTCACTGGTGGGCGGATGTGG 418
  DB 61 CTGCTCTAGAGACCTTCCCCCGGGATGCGGTGCTGGGTCACTGGTGGGCGGATGTGG 120
  QY 419 ACAATGATGAGCGCTCCACCGCCATTTCCTCTGAAGCAGGTGAAGTCCCCATAATGG 478
  DB 121 ACAATGATGAGCGCTCCACCGCCATTTCCTCTGAAGCAGGTGAAGTCCCCATAATGG 180
  QY 479 AAACCAACATTTGACGCAAAATACACCTTGGCGCTTACCGGGAGCAGCAGCTCCGCA 538
  DB 181 AAACCAACATTTGACGCAAAATACACCTTGGCGCTTACCGGGAGCAGCAGCTCCGCA 240
  QY 539 TCGTCCGTGACGA-CATGCTGTGTCGGGAAACCCCGAGGAGCTATGCCAGGCGAC 597
  DB 241 TCGTCCGTGACGATGCTGTGTCGGGAAACCCCGAGGAGCTATGCCAGGCGAC 300
  QY 598 TCCGAGAGGCGCTGTTGTGCAAGTGAATGGCAGCTGGCTGCAGCGCGGCTGTGTACG 657
  DB 301 TCCGAGAGGCGCTGTTGTGCAAGTGAATGGCAGCTGGCTGCAGCGCGGCTGTGTACG 360
  QY 658 TGGGCGGAGGCTGTGCCAGCCCAACCGGCTGGCATCTACCCGCTGTCACCTACTAC 717
  DB 361 TGGGCGGAGGCTGTGCCAGCCCAACCGGCTGGCATCTACCCGCTGTCACCTACTAC 420
  QY 718 TTGACTGTGATCCACCACTATGTCCCCAAAAGCGGTGAAGCGGC 763
  DB 421 TGGGACTGGATCCACCACTATGTCCCCAAAAGCGGTGAAGTCAGGC 466
  RESULT 13
  LOCUS CB203717 930 bp mRNA linear EST 05-FEB-2003
  DEFINITION AGNCOURT_1128628 NIH_MGC_135 Mus musculus cDNA clone
  IMAGE:30142408 5', mRNA sequence.
  ACCESSION CB203717
  VERSION CB203717.1 GI:28240351
  KEYWORDS EST.
  SOURCE Mus musculus (house mouse)
  ORGANISM Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  REFERENCE 1 (Bases 1 to 930)
  AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

```

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
cDNA Library Preparation: Invitrogen Corp
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM0051 row: j column: 17
High quality sequence stop: 681.

FEATURES
Location/Qualifiers
1..930
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clones="IMAGE:30142408"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 135"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRV; Site 2: NotI; Normalized full-length enriched library from pooled mouse embryonic limb, maxilla and mandible, day 12.5, 13.5, 14.5, and 15.5 (size selected for the 0.5-1 kb fragments) Cloned directionally, priming method: Oligo-dT. cDNA enrichment: 5x10⁶ bp, Average insert size 1.6k bp. Normalization (Cot value): 7.5 kb. Priming sequence: 5'-GACTAGTCTTCTAGTCGAGCGCGCCCTTT3' Tissue contributed by, David Rowe. Library constructed by ResGen, Invitrogen Corp."

ORIGIN
Query Match 55.8%; Score 430.6; DB 14; Length 930;
Best Local Similarity 76.7%; Pred. No. 7e-70;
Matches 552; Conservative 0; Mismatches 165; Indels 3; Gaps 2;

QY 17 GAATCTGTCGGGGTTCAGAGGCCCCAGAGCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
DB 40 GCATCTGGGAGGACATGAGGCTTCTGAGATGAGTGGCCCTGGCAGGTGAGCCTGAGAT 99
QY 77 TCCAGGCCCCATCTGATGATGACTTCTGCGGGGCTCCCTCATCACCCCCAGTGGGTGC 136
DB 100 TTAATAATTAATCTACTGGATACATTTCTGCGGAGGCTCTCTCATCCACCACAGTGGGTGC 159
QY 137 TGACCGCGCGCTGCTGGGAGCGGACGTCAAGGATCTGGCCGCTCAGGGTGAAC 196
DB 160 TCATCTGGGACACTGTGTGGACCGCACATCAAAAGCCCAAGCTCTTCGGGGTGCAGC 219
QY 197 TGGCGGAGCAGCACTCTACTACAGGACCAAGCTGCTCCGGTTCAGCAGGATCATCGTGC 256
DB 220 TTCTGAGCAGTATCTATCTATGGGACCAAGCTCTCTTTGAACCGGATCGTGGTGC 279
QY 257 ACCCAGAGTTTACACCGCCAGATCGAGGCGGACATCGCCCTGTGAGCTGAGGAGC 316
DB 280 ACCCCCACTATTACACGCGCCAGGTGGGCGAGAGTTTGGCTGTGAGCTTGAAGTCC 339
QY 317 CGGTGAGGTCTTCAGCAGCACTCCACAGCTCACCGCTGCGCCCTCCCTCAGAGCCTTCC 376
DB 340 CTGTGAAATGTCTCACCCATATTCACCCCATATCTCCCTGCCCCCTCGGAGACCTTCC 399
QY 377 CCCCAGGATGCGGTGCTGGGTCACTGTGCGGGGATGTGACAAATGATGAGCGCCTCC 436
DB 400 CCCCAGGATGCGGTGCTGGGTGACAGCTGGGGGACATTAATGACGAGCCTTCC 459
QY 437 CACCGCCATTTCTCTGAAGCAGGTGAGGTCCCATTAATGAAACACATTCTGTAGC 496
DB 460 CACCTCTTATCTCTGAAGCAAGTGAAGTTTCCCAITTTGGAACACAGCCTGTGTGACC 519
QY 497 CAAATATACCTTGGCGCTTACACGAGAGCAGCTCCGATCTCGTGAACGACATGC 556
DB 520 GGAAGTACCACTGGCTCTACACGGAGATGATTTTCCCATTTGTCCATGATGCGATGC 579

QY 557 TGTGTGCGGGAAACACCCGAGGAGTCTATCCAGGCGGACTCCGGAGGCGCCCTGGTGT 616
DB 580 TGTGTGCTGAAATACACGAGAGACTCTCTGCCAGGGCGATTTCAGGGGGCGCCACTGTGCT 639
QY 617 GCAAGTGAATGGCACTGCTGAGCGCGGCTGCTGAGTGGG-CGAGGGGCTGAGCC 675
DB 640 GCAAGTGAAGGGTACCTGCTGAGCGAGAGTGGTTCAGCTGGGCTGAGGGCTGGCCA 699
QY 676 CAGCCCAACCGCTGCTGATCATCACCCGCTGTCACC--TACTACTGCTGATGATCCACC 733
DB 700 CAGCCCAACCGCTGCTGATCATCACCCGCTGTCATCTTACTTATGATGATGATCCACC 759

RESULT 14
BI413250
LOCUS 602986390F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5142478 5',
DEFINITION mRNA sequence.
ACCESSION BI413250
VERSION BI413250.1 GI:15174173
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1000)
NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaps-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Inceye Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1351 row: c column: 23
High quality sequence start: 32
High quality sequence stop: 849.

FEATURES
Location/Qualifiers
1..1000
/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
/db_xref="taxon:10090"
/clones="IMAGE:5142478"
/tissue_type="pooled lung tumors"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI CGAP Lu33"
/note="Organ: lung; Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer [5' TGTTCACCAATCTGAAGTGGAGCGCGCTCTGTTTTTTTTTTT 3'] Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 54.8%; Score 422.2; DB 12; Length 1000;
Best Local Similarity 77.2%; Pred. No. 2.6e-68;
Matches 564; Conservative 0; Mismatches 163; Indels 4; Gaps 4;

QY 17 GAATCTGTCGGGGTTCAGGAGCCCCAGGACCAAGTGGCCCTGGCAGGTGAGCCTGAGAG 76
DB 73 GCATCTGGGAGGACATGAGGCTTCTGAGAGTGAAGTGGCCCTGGCAGGTGAGCCTGAGAT 132
QY 77 TCCAGGCCCCATCTGATGATGACTTCTGCGGGGGCTCCCTCATCCACCCCAAGTGGTGC 136

133	DB	TTAAATTAACTACTGGATACATTTCTGCGAGGCTCTCTATCCACCCACAGTGGGTGC	192
137	QY	TGACCGCGCGGGCGTGGTGGGACCGGACGCTCAAGGATCTGGCGCCCTCAAGGGTGCAC	196
193	DB	TCACTGGGCACACTGTGTGGACCGCACATCAAAGCCACAGCTCTTCCGGGTGCAGC	252
197	QY	TGGGGAGAGCACTCTATCTACAGACACAGCTGTGCTGCCGGTCAGCAGGATCATCTGTGC	256
253	DB	TTCTGTGACGATATCTATCTATATGGGACCAAGCTCTCTCTTTGAAACCGGATCTGTGGTGC	312
257	QY	ACCCACAGTTCTACACCGCCAGATCGGAGCGGACATCGCCCTCTGTGAGCTGAGGAGC	316
313	DB	ACCCCCACTATTACAGCGCGAGGGTGGGGCAGACGTTGCCCTCTGTGAGCTTGAGGTCC	372
317	QY	CGGTGAAGGTCTCCAGCCACGTCACACACGGTCAACCTTGCCGCCCTGCCCTCAGAGACCTTCC	376
373	DB	CTGTGATGTCTCACCCATATCACCCCATATCCCTGCCGCCCTGCCCTCGGAGACCTTCC	432
377	QY	CCCGGGGATGCGCTGTGTGGGTACTGGCTGGGGCGATGTGGACAAATGATGAGCGCCTCC	436
433	DB	CCCTCGGACATCGTGTGGGTGACAGGCTGGGGCGACATTGATAATGACGAGCCTCTCC	492
437	QY	CACGCCATTTCCTCTGACGAGTGAAGTTCGCCATTAATGGAAAAACACATTGTGA-C	495
493	DB	CACCTCCTTATCCTCTGAAGCAAGTGAAGTTCCTCATTTGTGGAAAAACAGCTGTGTGACC	552
496	QY	GCAAAATACCACCTTGGCGCCTACACGGGAGACGACGTCCTCGTGACGACATG	555
553	DB	GGAAGTAAACACACTGGCCCTCTACACGGGAGATGATTTCCCATGTTCATATGGCATG	612
556	QY	CTGTGTCCGGGAAACACCGGAGGAGTCTATGCCAGGGCGACTCCGGAGGGCCCTGTGTG	615
613	DB	CTGTGTCTGGAAATACACAGAGAGACTCTCTGCCAGGGCGATTCAGGGGGGCCACTGGTGC	672
616	QY	TGCAAGTGTATGCACTGCTGCAGCGCGGTGTGTCA-GCTGGGGCGAGGGCTGTGTC	674
673	DB	TGCAAAAGTGAAGGGTACTCTGCTGCAGCAGAGTGGTGTCACTGTGGGGTGAAGGGCTGCGC	732
675	QY	CCAGCCC-AACCGGCGCTGGCATCTACACCCGTGTCAAC-TACTACTTGGACTTGGATCCAC	732
733	DB	ACAGCCCAACAGCCTTGGCATCTACACCCGGGTGACCATCTACTTATAGATTCGATCCAC	792
733	QY	CACATATGCC	743
793	Db	GCTTATGTCC	803

RESULT 15	
AA131142	
LOCUS	639 bp mRNA linear EST 14-MAY-1997
DEFINITION	zl31b01.r1 Soares_pregnant_uterus NbHPU Homo sapiens cDNA clone IMAGE:503497 5' similar to gb:M30038 ALPHA-TRYPTASE PRECURSOR (HUMAN); mRNA sequence.
ACCESSION	AA131142
VERSION	AA131142.1 GI:1692796
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 639)
AUTHORS	Hallier L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, P., Thierry-Mieg, J., Trevas, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R., and Marra, M.
TITLE	Generation and analysis of 280,000 human expressed sequence tags
JOURNAL	Genome Res. 6 (9), 807-828 (1996)
MEDLINE	97044478
PUBMED	8889549

Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 This clone is available royalty-free through LLMU ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 894 Std Error: 0.00
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 349.
 Location/Qualifiers
 source
 1..639
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:3808485"
 /db_xref="taxon:9606"
 /clone="IMAGE:503497"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="Soares_pregnant_uterus_NbHPU"
 /notes="Organ: uterus; Vector: p7T3-pac; Site.1: Not I;
 Site.2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo(dT) primer [5',
 ACTGGAAGATCGCGCGCCCTTTTTTTTTTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified p7T3 vector. Library
 went through one round of normalization. Library
 constructed by M. Fatima Bonaldo."

ORIGIN

Query Match	54.5%;	Score 420.4;	DB 9;	Length 639;
Best Local Similarity	94.0%;	Pred. No. 4.8e-68;		
Matches	458;	Conservative 0;	Mismatches 27;	Indels 2; Gaps 2;

```

QY      276  CGAGATCGAGCGGACATGCCCCTGCTGGAGCTGGAGAGCCGGTGAAGTCTCCAGCCA 335
Db      276  |||||
QY      336  CGTCCACACGGTCACCTGCCCCCTGCTCAGAGACCTTCCCCCGGGGATCGGTGCTG 395
Db      336  |||||
QY      61   CGTCCACACGGTCATGCTGCCCTGCTCGGAGACCTTCCCCCGGGGATCGGTGCTG 120
Db      61   |||||
QY      396  GGTCACTGGCTGGGCGATGTGGACAATGATGAGCGCTCCACCGCCATTCTCTGTAA 455
Db      396  |||||
QY      455  GGTCACTGGCTGGGCGATGTGGACAATGATGAGCGCTCCACCGCCATTCTCTGTAA 180
Db      455  |||||
QY      456  GCAGGTGAGGTCGCCATATGAAACACACATTGTGAGCGAAATACACCTGGCGC 515
Db      456  |||||
QY      181  GCAGGTGAGGTCGCCATATGAAACACACATTGTGAGCGAAATACACCTGGCGC 240
Db      181  |||||
QY      516  CTACACGGAGACGACGTCCGATCGCTCGGTGACGACATGCTGTGCGGGGAACACCCG 575
Db      516  |||||
QY      241  CTACACGGAGACGACGTCCGATCATCGTGACGACATGCTGTGCGGGGAACACCCG 300
Db      241  |||||
QY      576  GAGGACTCATGCGAGCGGACTCCGAGGCCCCCTGGTGTGAAGTGAATGCGACCTG 635
Db      576  |||||
QY      301  GAGAGCTTCATGCGAGGGGACTCTCGAGGGCCCCCTGGTGTGCAAGTGAAATGGCACCTG 360
Db      301  |||||
QY      636  GCTGCGAGGGGGCGTGGTCAGTGGGGCGAGGGCTGTGCCAGCCCAACCGGCTCGCAT 695
Db      636  |||||
QY      361  GCTACAGGGCGGGCGTGGTCATCTGGGACGAGGGCTGTG--CAGTCCCAACCGGCTGGCAT 419
Db      361  |||||
QY      696  CTACACCGGTGTCACTTACTCTGG--ACTGGATCCACCACTATGTGTCCCCAAAAGCCGT 754
Db      696  |||||
QY      420  CTACACCGGTGTCACTTACTCTGGAACTGGATCCACCANTATGTGTCCCCAAAAGCCGT 479
Db      420  |||||
QY      755  GAAGCGG 761
Db      480  GAGTCAG 486
  
```

Search completed: July 22, 2004, 13:24:27
Job time : 3410 secs
